

GanCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2006, 10:38:34 ; Search time 93 Seconds
(without alignments)
2.906 Million cell updates/sec

Title: US-10-764-316-6-COPY
Perfect score: 2743
Sequence: 1 9cgggcccgtatccatttgt.....aaaaaaaaaaaaaaaaaaaaa 2743

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1733 seqs, 49269 residues

Total number of hits satisfying chosen parameters: 3466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1733 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78.4	2.9	80	1	BY799992
2	73.8	2.7	78	1	AA587192
3	55.4	2.0	61	1	AA079243
4	50	1.8	50	1	AU103749
5	48.4	1.8	50	1	AU103750
6	46.8	1.7	50	1	AU103751
7	46.8	1.7	50	1	AU103772
8	41.8	1.5	52	1	T92783
9	39.8	1.5	46	1	CF298283
10	38.6	1.4	46	1	BG610636
11	38.4	1.4	43	1	CV733592
12	37.6	1.4	47	1	CF317896
13	37.2	1.4	44	1	CF305383
14	37.2	1.4	46	1	CV732719
15	37	1.3	37	1	CF329026
16	37	1.3	42	1	AL046183
17	37	1.3	44	1	CF332388
18	36.8	1.3	43	1	CV730946
19	36.8	1.3	44	1	CF302212
20	36.8	1.3	46	1	CF332152
21	36.8	1.3	46	1	CV732463
22	36.6	1.3	43	1	CV725460
23	36.6	1.3	44	1	CF331239
24	36.6	1.3	45	1	CF332233
25	36.6	1.3	45	1	CV729880
26	36.4	1.3	38	1	CV724890
27	36.4	1.3	43	1	CV733486
28	36.4	1.3	44	1	CF316377
29	36.2	1.3	42	1	CF292085
30	36.2	1.3	42	1	CV734468
31	36.2	1.3	42	1	CV734501
32	36.2	1.3	44	1	DY231327
33	36	1.3	37	1	AJ659250

ACCESSION:CF328866	37	1	CF328866	37	1	CF328866
ACCESSION:CV731657	37	1	CV731657	37	1	CV731657
ACCESSION:CV730040	38	1	CV730040	38	1	CV730040
ACCESSION:CF300591	39	1	CF300591	39	1	CF300591
ACCESSION:CV726948	39	1	CV726948	39	1	CV726948
ACCESSION:CV727347	39	1	CV727347	39	1	CV727347
ACCESSION:CF309581	40	1	CF309581	40	1	CF309581
ACCESSION:CV733657	41	1	CV733657	41	1	CV733657
ACCESSION:CV726108	43	1	CV726108	43	1	CV726108
ACCESSION:CV728159	43	1	CV728159	43	1	CV728159
ACCESSION:CV734232	43	1	CV734232	43	1	CV734232
ACCESSION:CV726790	44	1	CV726790	44	1	CV726790
ACCESSION:CF331757	45	1	CF331757	45	1	CF331757
ACCESSION:CV734230	45	1	CV734230	45	1	CV734230
ACCESSION:CV729079	37	1	CV729079	37	1	CV729079
ACCESSION:CV730711	37	1	CV730711	37	1	CV730711
ACCESSION:CV734007	37	1	CV734007	37	1	CV734007
ACCESSION:CF315184	38	1	CF315184	38	1	CF315184
ACCESSION:CV727074	38	1	CV727074	38	1	CV727074
ACCESSION:CV727193	38	1	CV727193	38	1	CV727193
ACCESSION:CF291979	39	1	CF291979	39	1	CF291979
ACCESSION:CV732133	39	1	CV732133	39	1	CV732133
ACCESSION:CF301837	41	1	CF301837	41	1	CF301837
ACCESSION:CV725219	41	1	CV725219	41	1	CV725219
ACCESSION:CF302691	43	1	CF302691	43	1	CF302691
ACCESSION:CV725096	43	1	CV725096	43	1	CV725096
ACCESSION:DV573571	43	1	DV573571	43	1	DV573571
ACCESSION:DV573572	43	1	DV573572	43	1	DV573572
ACCESSION:CF298596	44	1	CF298596	44	1	CF298596
ACCESSION:CN545689	44	1	CN545689	44	1	CN545689
ACCESSION:CF334384	44	1	CF334384	44	1	CF334384
ACCESSION:CF315871	35	1	CF315871	35	1	CF315871
ACCESSION:CF334198	35	1	CF334198	35	1	CF334198
ACCESSION:CF335633	35	1	CF335633	35	1	CF335633
ACCESSION:CV725312	35	1	CV725312	35	1	CV725312
ACCESSION:CV725444	35	1	CV725444	35	1	CV725444
ACCESSION:CV725518	35	1	CV725518	35	1	CV725518
ACCESSION:CV725797	35	1	CV725797	35	1	CV725797
ACCESSION:CV726506	35	1	CV726506	35	1	CV726506
ACCESSION:CV727085	35	1	CV727085	35	1	CV727085
ACCESSION:CV727326	35	1	CV727326	35	1	CV727326
ACCESSION:CV728725	35	1	CV728725	35	1	CV728725
ACCESSION:CV728984	35	1	CV728984	35	1	CV728984
ACCESSION:CV729199	35	1	CV729199	35	1	CV729199
ACCESSION:CV730453	35	1	CV730453	35	1	CV730453
ACCESSION:CV730547	35	1	CV730547	35	1	CV730547
ACCESSION:CV731689	35	1	CV731689	35	1	CV731689
ACCESSION:CV733059	35	1	CV733059	35	1	CV733059
ACCESSION:CV733251	35	1	CV733251	35	1	CV733251
ACCESSION:CV733296	35	1	CV733296	35	1	CV733296
ACCESSION:CV733344	35	1	CV733344	35	1	CV733344
ACCESSION:CV733739	35	1	CV733739	35	1	CV733739
ACCESSION:CV734164	35	1	CV734164	35	1	CV734164
ACCESSION:AZ623128	35	1	AZ623128	35	1	AZ623128
ACCESSION:AZ803371	35	1	AZ803371	35	1	AZ803371
ACCESSION:AJ791385	36	1	AJ791385	36	1	AJ791385
ACCESSION:AL587891	36	1	AL587891	36	1	AL587891
ACCESSION:AM046410	36	1	AM046410	36	1	AM046410
ACCESSION:CF279874	36	1	CF279874	36	1	CF279874
ACCESSION:CF317028	36	1	CF317028	36	1	CF317028
ACCESSION:CF31913	36	1	CF31913	36	1	CF31913
ACCESSION:CF331983	36	1	CF331983	36	1	CF331983
ACCESSION:CF333863	36	1	CF333863	36	1	CF333863
ACCESSION:BE876160	36	1	BE876160	36	1	BE876160
ACCESSION:CV724782	36	1	CV724782	36	1	CV724782
ACCESSION:CV725281	36	1	CV725281	36	1	CV725281
ACCESSION:CV725289	36	1	CV725289	36	1	CV725289
ACCESSION:CV725592	36	1	CV725592	36	1	CV725592
ACCESSION:CV726151	36	1	CV726151	36	1	CV726151
ACCESSION:CV726321	36	1	CV726321	36	1	CV726321
ACCESSION:CV727111	36	1	CV727111	36	1	CV727111
ACCESSION:CV728675	36	1	CV728675	36	1	CV728675

C 107 35 1.3 36 1 CV728870 ACCESSION: CV728870
C 108 35 1.3 36 1 CV729206 ACCESSION: CV729206
C 109 35 1.3 36 1 CV730235 ACCESSION: CV730235
C 110 35 1.3 36 1 CV730921 ACCESSION: CV730921
C 111 35 1.3 36 1 CV730953 ACCESSION: CV730953
C 112 35 1.3 36 1 CV732578 ACCESSION: CV732578
C 113 35 1.3 36 1 CV732659 ACCESSION: CV732659
C 114 35 1.3 36 1 CV733597 ACCESSION: CV733597
C 115 35 1.3 36 1 CV734403 ACCESSION: CV734403
C 116 35 1.3 36 1 A2470916 ACCESSION: A2470916
C 117 35 1.3 36 1 A2628484 ACCESSION: A2628484
C 118 35 1.3 36 1 A2793484 ACCESSION: A2793484
C 119 35 1.3 36 1 A2949866 ACCESSION: A2949866
C 120 35 1.3 36 1 A2957867 ACCESSION: A2957867
C 121 35 1.3 36 1 C2914006 ACCESSION: C2914006
C 122 35 1.3 36 1 D0834235 ACCESSION: D0834235
C 123 35 1.3 36 1 DX046307 ACCESSION: DX046307
C 124 35 1.3 37 1 BG033620 ACCESSION: BG033620
C 125 35 1.3 37 1 CF291818 ACCESSION: CF291818
C 126 35 1.3 37 1 CF300002 ACCESSION: CF300002
C 127 35 1.3 37 1 CF300328 ACCESSION: CF300328
C 128 35 1.3 37 1 CF301560 ACCESSION: CF301560
C 129 35 1.3 37 1 CF301864 ACCESSION: CF301864
C 130 35 1.3 37 1 CF307971 ACCESSION: CF307971
C 131 35 1.3 37 1 CF316114 ACCESSION: CF316114
C 132 35 1.3 37 1 CF321294 ACCESSION: CF321294
C 133 35 1.3 37 1 CF326975 ACCESSION: CF326975
C 134 35 1.3 37 1 CF333624 ACCESSION: CF333624
C 135 35 1.3 37 1 CF336769 ACCESSION: CF336769
C 136 35 1.3 37 1 CF324637 ACCESSION: CF324637
C 137 35 1.3 37 1 CV725878 ACCESSION: CV725878
C 138 35 1.3 37 1 CV726514 ACCESSION: CV726514
C 139 35 1.3 37 1 CV726571 ACCESSION: CV726571
C 140 35 1.3 37 1 CV727266 ACCESSION: CV727266
C 141 35 1.3 37 1 CV727448 ACCESSION: CV727448
C 142 35 1.3 37 1 CV727567 ACCESSION: CV727567
C 143 35 1.3 37 1 CV727819 ACCESSION: CV727819
C 144 35 1.3 37 1 CV728196 ACCESSION: CV728196
C 145 35 1.3 37 1 CV728197 ACCESSION: CV728197
C 146 35 1.3 37 1 CV730003 ACCESSION: CV730003
C 147 35 1.3 37 1 CV730176 ACCESSION: CV730176
C 148 35 1.3 37 1 CV731472 ACCESSION: CV731472
C 149 35 1.3 37 1 A2321759 ACCESSION: A2321759
C 150 35 1.3 37 1 A2463801 ACCESSION: A2463801
C 151 35 1.3 37 1 A2831214 ACCESSION: A2831214
C 152 35 1.3 37 1 C2914427 ACCESSION: C2914427
C 153 35 1.3 37 1 DX071328 ACCESSION: DX071328
C 154 35 1.3 37 1 DX072665 ACCESSION: DX072665
C 155 35 1.3 37 1 DR102924T ACCESSION: DR102924T
C 156 35 1.3 37 1 DR102927 ACCESSION: DR102927
C 157 35 1.3 38 1 CF291176 ACCESSION: CF291176
C 158 35 1.3 38 1 CF301164 ACCESSION: CF301164
C 159 35 1.3 38 1 CF301819 ACCESSION: CF301819
C 160 35 1.3 38 1 CF321261 ACCESSION: CF321261
C 161 35 1.3 38 1 CF328351 ACCESSION: CF328351
C 162 35 1.3 38 1 CF329605 ACCESSION: CF329605
C 163 35 1.3 38 1 CF329690 ACCESSION: CF329690
C 164 35 1.3 38 1 CF329730 ACCESSION: CF329730
C 165 35 1.3 38 1 BF525501 ACCESSION: BF525501
C 166 35 1.3 38 1 BF526154 ACCESSION: BF526154
C 167 35 1.3 38 1 CV724657 ACCESSION: CV724657
C 168 35 1.3 38 1 CV725198 ACCESSION: CV725198
C 169 35 1.3 38 1 CV725495 ACCESSION: CV725495
C 170 35 1.3 38 1 CV726250 ACCESSION: CV726250
C 171 35 1.3 38 1 CV726534 ACCESSION: CV726534
C 172 35 1.3 38 1 CV726895 ACCESSION: CV726895
C 173 35 1.3 38 1 CV726983 ACCESSION: CV726983
C 174 35 1.3 38 1 CV727096 ACCESSION: CV727096
C 175 35 1.3 38 1 CV727478 ACCESSION: CV727478
C 176 35 1.3 38 1 CV727598 ACCESSION: CV727598
C 177 35 1.3 38 1 CV727921 ACCESSION: CV727921
C 178 35 1.3 38 1 CV728176 ACCESSION: CV728176
C 179 35 1.3 38 1 CV728223 ACCESSION: CV728223

C 180 35 1.3 38 1 CV728809 ACCESSION: CV728809
C 181 35 1.3 38 1 CV728835 ACCESSION: CV728835
C 182 35 1.3 38 1 CV729857 ACCESSION: CV729857
C 183 35 1.3 38 1 CV731476 ACCESSION: CV731476
C 184 35 1.3 38 1 DR064343 ACCESSION: DR064343
C 185 35 1.3 38 1 DW337683 ACCESSION: DW337683
C 186 35 1.3 38 1 A2785034 ACCESSION: A2785034
C 187 35 1.3 38 1 BG287495 ACCESSION: BG287495
C 188 35 1.3 39 1 B1694035 ACCESSION: B1694035
C 189 35 1.3 39 1 CF298508 ACCESSION: CF298508
C 190 35 1.3 39 1 CF302356 ACCESSION: CF302356
C 191 35 1.3 39 1 CF315736 ACCESSION: CF315736
C 192 35 1.3 39 1 CF321323 ACCESSION: CF321323
C 193 35 1.3 39 1 CF330732 ACCESSION: CF330732
C 194 35 1.3 39 1 BF032623 ACCESSION: BF032623
C 195 35 1.3 39 1 BE891613 ACCESSION: BE891613
C 196 35 1.3 39 1 CV724457 ACCESSION: CV724457
C 197 35 1.3 39 1 CV724623 ACCESSION: CV724623
C 198 35 1.3 39 1 CV725192 ACCESSION: CV725192
C 199 35 1.3 39 1 CV725228 ACCESSION: CV725228
C 200 35 1.3 39 1 CV725383 ACCESSION: CV725383
C 201 35 1.3 39 1 CV725570 ACCESSION: CV725570
C 202 35 1.3 39 1 CV726046 ACCESSION: CV726046
C 203 35 1.3 39 1 CV726057 ACCESSION: CV726057
C 204 35 1.3 39 1 CV726327 ACCESSION: CV726327
C 205 35 1.3 39 1 CV726361 ACCESSION: CV726361
C 206 35 1.3 39 1 CV726728 ACCESSION: CV726728
C 207 35 1.3 39 1 CV726866 ACCESSION: CV726866
C 208 35 1.3 39 1 CV726936 ACCESSION: CV726936
C 209 35 1.3 39 1 CV726971 ACCESSION: CV726971
C 210 35 1.3 39 1 CV727002 ACCESSION: CV727002
C 211 35 1.3 39 1 CV727016 ACCESSION: CV727016
C 212 35 1.3 39 1 CV727114 ACCESSION: CV727114
C 213 35 1.3 39 1 CV727215 ACCESSION: CV727215
C 214 35 1.3 39 1 CV727351 ACCESSION: CV727351
C 215 35 1.3 39 1 CV727680 ACCESSION: CV727680
C 216 35 1.3 39 1 CV728240 ACCESSION: CV728240
C 217 35 1.3 39 1 CV728278 ACCESSION: CV728278
C 218 35 1.3 39 1 CV729217 ACCESSION: CV729217
C 219 35 1.3 39 1 CV730113 ACCESSION: CV730113
C 220 35 1.3 39 1 CV732729 ACCESSION: CV732729
C 221 35 1.3 39 1 CV733026 ACCESSION: CV733026
C 222 35 1.3 39 1 CV733160 ACCESSION: CV733160
C 223 35 1.3 39 1 CV733431 ACCESSION: CV733431
C 224 35 1.3 39 1 CV733935 ACCESSION: CV733935
C 225 35 1.3 39 1 CV733973 ACCESSION: CV733973
C 226 35 1.3 39 1 AZ639088 ACCESSION: AZ639088
C 227 35 1.3 40 1 AL037510 ACCESSION: AL037510
C 228 35 1.3 40 1 AL449576 ACCESSION: AL449576
C 229 35 1.3 40 1 BG166502 ACCESSION: BG166502
C 230 35 1.3 40 1 CF311814 ACCESSION: CF311814
C 231 35 1.3 40 1 CF327027 ACCESSION: CF327027
C 232 35 1.3 40 1 CF328199 ACCESSION: CF328199
C 233 35 1.3 40 1 CF328306 ACCESSION: CF328306
C 234 35 1.3 40 1 CF334545 ACCESSION: CF334545
C 235 35 1.3 40 1 CV724551 ACCESSION: CV724551
C 236 35 1.3 40 1 CV725014 ACCESSION: CV725014
C 237 35 1.3 40 1 CV725673 ACCESSION: CV725673
C 238 35 1.3 40 1 CV726807 ACCESSION: CV726807
C 239 35 1.3 40 1 CV727416 ACCESSION: CV727416
C 240 35 1.3 40 1 CV727587 ACCESSION: CV727587
C 241 35 1.3 40 1 CV727805 ACCESSION: CV727805
C 242 35 1.3 40 1 CV727843 ACCESSION: CV727843
C 243 35 1.3 40 1 CV727858 ACCESSION: CV727858
C 244 35 1.3 40 1 CV728325 ACCESSION: CV728325
C 245 35 1.3 40 1 CV728655 ACCESSION: CV728655
C 246 35 1.3 40 1 CV730371 ACCESSION: CV730371
C 247 35 1.3 40 1 CV731031 ACCESSION: CV731031
C 248 35 1.3 40 1 CV731319 ACCESSION: CV731319
C 249 35 1.3 40 1 CV731528 ACCESSION: CV731528
C 250 35 1.3 40 1 CV732353 ACCESSION: CV732353
C 251 35 1.3 40 1 CV732629 ACCESSION: CV732629
C 252 35 1.3 40 1 CV732676 ACCESSION: CV732676

C 253	35	1.3	40	1	CV733006	ACCSSION: CV733006	326	35	1.3	43	1	CV062138	ACCSSION: CV062138
C 254	35	1.3	40	1	CV733017	ACCSSION: CV733017	C 327	35	1.3	43	1	CV724539	ACCSSION: CV724539
C 255	35	1.3	40	1	CV733422	ACCSSION: CV733422	C 328	35	1.3	43	1	CV724959	ACCSSION: CV724959
C 256	35	1.3	40	1	CV733638	ACCSSION: CV733638	C 329	35	1.3	43	1	CV724969	ACCSSION: CV724969
C 257	35	1.3	40	1	AZ831983	ACCSSION: AZ831983	C 330	35	1.3	43	1	CV725127	ACCSSION: CV725127
C 258	35	1.3	40	1	DU835034	ACCSSION: DU835034	C 331	35	1.3	43	1	CV725506	ACCSSION: CV725506
C 259	35	1.3	41	1	AJ792759	ACCSSION: AJ792759	C 332	35	1.3	43	1	CV725680	ACCSSION: CV725680
C 260	35	1.3	41	1	CF291539	ACCSSION: CF291539	C 333	35	1.3	43	1	CV725720	ACCSSION: CV725720
C 261	35	1.3	41	1	CF318677	ACCSSION: CF318677	C 334	35	1.3	43	1	CV725822	ACCSSION: CV725822
C 262	35	1.3	41	1	CF320203	ACCSSION: CF320203	C 335	35	1.3	43	1	CV726349	ACCSSION: CV726349
C 263	35	1.3	41	1	CF330464	ACCSSION: CF330464	C 336	35	1.3	43	1	CV726694	ACCSSION: CV726694
C 264	35	1.3	41	1	CF334638	ACCSSION: CF334638	C 337	35	1.3	43	1	CV726751	ACCSSION: CV726751
C 265	35	1.3	41	1	CV725868	ACCSSION: CV725868	C 338	35	1.3	43	1	CV727328	ACCSSION: CV727328
C 266	35	1.3	41	1	CV725993	ACCSSION: CV725993	C 339	35	1.3	43	1	CV727684	ACCSSION: CV727684
C 267	35	1.3	41	1	CV726255	ACCSSION: CV726255	C 340	35	1.3	43	1	CV728681	ACCSSION: CV728681
C 268	35	1.3	41	1	CV726393	ACCSSION: CV726393	C 341	35	1.3	43	1	CV728686	ACCSSION: CV728686
C 269	35	1.3	41	1	CV726923	ACCSSION: CV726923	C 342	35	1.3	43	1	CV728737	ACCSSION: CV728737
C 270	35	1.3	41	1	CV727015	ACCSSION: CV727015	C 343	35	1.3	43	1	CV728887	ACCSSION: CV728887
C 271	35	1.3	41	1	CV727210	ACCSSION: CV727210	C 344	35	1.3	43	1	CV729000	ACCSSION: CV729000
C 272	35	1.3	41	1	CV727412	ACCSSION: CV727412	C 345	35	1.3	43	1	CV729158	ACCSSION: CV729158
C 273	35	1.3	41	1	CV727841	ACCSSION: CV727841	C 346	35	1.3	43	1	CV729970	ACCSSION: CV729970
C 274	35	1.3	41	1	CV728055	ACCSSION: CV728055	C 347	35	1.3	43	1	CV730586	ACCSSION: CV730586
C 275	35	1.3	41	1	CV728228	ACCSSION: CV728228	C 348	35	1.3	43	1	CV730813	ACCSSION: CV730813
C 276	35	1.3	41	1	CV728716	ACCSSION: CV728716	C 349	35	1.3	43	1	CV731060	ACCSSION: CV731060
C 277	35	1.3	41	1	CV728978	ACCSSION: CV728978	C 350	35	1.3	43	1	CV731475	ACCSSION: CV731475
C 278	35	1.3	41	1	CV729041	ACCSSION: CV729041	C 351	35	1.3	43	1	CV732091	ACCSSION: CV732091
C 279	35	1.3	41	1	CV731427	ACCSSION: CV731427	C 352	35	1.3	43	1	CV732291	ACCSSION: CV732291
C 280	35	1.3	41	1	CV731668	ACCSSION: CV731668	C 353	35	1.3	43	1	CV732533	ACCSSION: CV732533
C 281	35	1.3	41	1	CV732073	ACCSSION: CV732073	C 354	35	1.3	43	1	CV732864	ACCSSION: CV732864
C 282	35	1.3	41	1	CV733839	ACCSSION: CV733839	C 355	35	1.3	43	1	CV733072	ACCSSION: CV733072
C 283	35	1.3	41	1	CV734304	ACCSSION: CV734304	C 356	35	1.3	43	1	CV733143	ACCSSION: CV733143
C 284	35	1.3	41	1	AZ775066	ACCSSION: AZ775066	C 357	35	1.3	43	1	CV733227	ACCSSION: CV733227
C 285	35	1.3	41	1	AZ827008	ACCSSION: AZ827008	C 358	35	1.3	43	1	CV733316	ACCSSION: CV733316
C 286	35	1.3	41	1	DU834001	ACCSSION: DU834001	C 359	35	1.3	43	1	CV734334	ACCSSION: CV734334
C 287	35	1.3	41	1	DU834619	ACCSSION: DU834619	C 360	35	1.3	43	1	CV734334	ACCSSION: CV734334
C 288	35	1.3	41	1	DU835000	ACCSSION: DU835000	C 361	35	1.3	43	1	CV734334	ACCSSION: CV734334
C 289	35	1.3	41	1	DX049410	ACCSSION: DX049410	C 362	34.8	1.3	40	1	AZ355703	ACCSSION: AZ355703
C 290	35	1.3	42	1	AJ691919	ACCSSION: AJ691919	C 363	34.8	1.3	43	1	CV066153	ACCSSION: CV066153
C 291	35	1.3	42	1	BG292448	ACCSSION: BG292448	C 364	34.4	1.3	36	1	CV725617	ACCSSION: CV725617
C 292	35	1.3	42	1	CF318540	ACCSSION: CF318540	C 365	34.4	1.3	41	1	CV725617	ACCSSION: CV725617
C 293	35	1.3	42	1	CF318962	ACCSSION: CF318962	C 366	34.4	1.3	41	1	CV725617	ACCSSION: CV725617
C 294	35	1.3	42	1	CF319867	ACCSSION: CF319867	C 367	34	1.2	34	1	CV725617	ACCSSION: CV725617
C 295	35	1.3	42	1	CF320056	ACCSSION: CF320056	C 368	34	1.2	34	1	CV726231	ACCSSION: CV726231
C 296	35	1.3	42	1	CF322408	ACCSSION: CF322408	C 369	34	1.2	34	1	CV726784	ACCSSION: CV726784
C 297	35	1.3	42	1	BF334329	ACCSSION: BF334329	C 370	34	1.2	34	1	CV727320	ACCSSION: CV727320
C 298	35	1.3	42	1	AW334133	ACCSSION: AW334133	C 371	34	1.2	34	1	CV729064	ACCSSION: CV729064
C 299	35	1.3	42	1	CV062024	ACCSSION: CV062024	C 372	34	1.2	34	1	CV730592	ACCSSION: CV730592
C 300	35	1.3	42	1	CV725428	ACCSSION: CV725428	C 373	34	1.2	34	1	CV730644	ACCSSION: CV730644
C 301	35	1.3	42	1	CV726363	ACCSSION: CV726363	C 374	34	1.2	34	1	CV731182	ACCSSION: CV731182
C 302	35	1.3	42	1	CV726372	ACCSSION: CV726372	C 375	34	1.2	34	1	CV734338	ACCSSION: CV734338
C 303	35	1.3	42	1	CV728634	ACCSSION: CV728634	C 376	34	1.2	34	1	AZ465350	ACCSSION: AZ465350
C 304	35	1.3	42	1	CV728806	ACCSSION: CV728806	C 377	34	1.2	34	1	AZ501040	ACCSSION: AZ501040
C 305	35	1.3	42	1	CV729215	ACCSSION: CV729215	C 378	34	1.2	34	1	AZ809643	ACCSSION: AZ809643
C 306	35	1.3	42	1	CV729267	ACCSSION: CV729267	C 379	34	1.2	34	1	DU835285	ACCSSION: DU835285
C 307	35	1.3	42	1	CV731493	ACCSSION: CV731493	C 380	34	1.2	34	1	DX037933	ACCSSION: DX037933
C 308	35	1.3	42	1	CV731845	ACCSSION: CV731845	C 381	34	1.2	35	1	CV730365	ACCSSION: CV730365
C 309	35	1.3	42	1	CV732835	ACCSSION: CV732835	C 382	34	1.2	37	1	CF291807	ACCSSION: CF291807
C 310	35	1.3	42	1	CV732860	ACCSSION: CV732860	C 383	34	1.2	42	1	CF330901	ACCSSION: CF330901
C 311	35	1.3	42	1	CV733275	ACCSSION: CV733275	C 384	34	1.2	42	1	CV726166	ACCSSION: CV726166
C 312	35	1.3	42	1	CV733323	ACCSSION: CV733323	C 385	33.8	1.2	41	1	DX045841	ACCSSION: DX045841
C 313	35	1.3	42	1	CV733544	ACCSSION: CV733544	C 386	33.8	1.2	42	1	CV728107	ACCSSION: CV728107
C 314	35	1.3	42	1	CV733603	ACCSSION: CV733603	C 387	33.6	1.2	40	1	CF331029	ACCSSION: CF331029
C 315	35	1.3	42	1	CV733690	ACCSSION: CV733690	C 388	33.6	1.2	42	1	AL038483	ACCSSION: AL038483
C 316	35	1.3	42	1	CV733938	ACCSSION: CV733938	C 389	33.4	1.2	35	1	BE894837	ACCSSION: BE894837
C 317	35	1.3	42	1	CV734112	ACCSSION: CV734112	C 390	33.4	1.2	35	1	CV785671	ACCSSION: CV785671
C 318	35	1.3	42	1	CV734112	ACCSSION: CV734112	C 391	33.4	1.2	35	1	DN955388	ACCSSION: DN955388
C 319	35	1.3	42	1	CV733544	ACCSSION: CV733544	C 392	33.4	1.2	36	1	BE894682	ACCSSION: BE894682
C 320	35	1.3	43	1	AJ923543	ACCSSION: AJ923543	C 393	33.4	1.2	36	1	CV724804	ACCSSION: CV724804
C 321	35	1.3	43	1	AL587884	ACCSSION: AL587884	C 394	33.4	1.2	36	1	CZ912531	ACCSSION: CZ912531
C 322	35	1.3	43	1	BG028362	ACCSSION: BG028362	C 395	33.4	1.2	36	1	DU830895	ACCSSION: DU830895
C 323	35	1.3	43	1	BI908698	ACCSSION: BI908698	C 396	33.4	1.2	37	1	AL048768	ACCSSION: AL048768
C 324	35	1.3	43	1	CF302744	ACCSSION: CF302744	C 397	33.4	1.2	37	1	CV732356	ACCSSION: CV732356
C 325	35	1.3	43	1	CF334344	ACCSSION: CF334344	C 398	33.4	1.2	37	1	AZ824309	ACCSSION: AZ824309

C 399	33.4	1.2	37	1	DX062077	ACCESSION: DX062077	C 472	32	1.2	32	1	CF313717	ACCESSION: CF313717
C 400	33.4	1.2	38	1	CF302184	ACCESSION: CF302184	C 473	32	1.2	32	1	CF321046	ACCESSION: CF321046
C 401	33.4	1.2	38	1	CF316791	ACCESSION: CF316791	C 474	32	1.2	32	1	CF328471	ACCESSION: CF328471
C 402	33.4	1.2	38	1	AW333985	ACCESSION: AW333985	C 475	32	1.2	32	1	CF331270	ACCESSION: CF331270
C 403	33.4	1.2	38	1	DR074451	ACCESSION: DR074451	C 476	32	1.2	32	1	AW327277	ACCESSION: AW327277
C 404	33.4	1.2	38	1	AZ589726	ACCESSION: AZ589726	C 477	32	1.2	32	1	CV724815	ACCESSION: CV724815
C 405	33.4	1.2	38	1	DX060574	ACCESSION: DX060574	C 478	32	1.2	32	1	CV725190	ACCESSION: CV725190
C 406	33.4	1.2	38	1	CF319510	ACCESSION: CF319510	C 479	32	1.2	32	1	CV725571	ACCESSION: CV725571
C 407	33.4	1.2	39	1	CF0786273	ACCESSION: CF0786273	C 480	32	1.2	32	1	CV726012	ACCESSION: CV726012
C 408	33.4	1.2	39	1	CNS0040NT	ACCESSION: AL054298	C 481	32	1.2	32	1	CV726385	ACCESSION: CV726385
C 409	33.4	1.2	40	1	AL638703	ACCESSION: AL638703	C 482	32	1.2	32	1	CV727659	ACCESSION: CV727659
C 410	33.4	1.2	40	1	CF336399	ACCESSION: CF336399	C 483	32	1.2	32	1	CV728625	ACCESSION: CV728625
C 411	33.4	1.2	40	1	DV082973	ACCESSION: DV082973	C 484	32	1.2	32	1	CV729255	ACCESSION: CV729255
C 412	33.4	1.2	40	1	DX076358	ACCESSION: DX076358	C 485	32	1.2	32	1	CV732146	ACCESSION: CV732146
C 413	33.4	1.2	41	1	CF300448	ACCESSION: CF300448	C 486	32	1.2	32	1	CV732586	ACCESSION: CV732586
C 414	33.4	1.2	41	1	CF302032	ACCESSION: CF302032	C 487	32	1.2	32	1	AZ459536	ACCESSION: AZ459536
C 415	33.4	1.2	41	1	CF305364	ACCESSION: CF305364	C 488	32	1.2	32	1	AZ470832	ACCESSION: AZ470832
C 416	33.4	1.2	41	1	AV742106	ACCESSION: AV742106	C 489	32	1.2	32	1	AZ611890	ACCESSION: AZ611890
C 417	33.4	1.2	41	1	CV731029	ACCESSION: CV731029	C 490	32	1.2	32	1	AZ778018	ACCESSION: AZ778018
C 418	33.4	1.2	41	1	DX049794	ACCESSION: DX049794	C 491	32	1.2	32	1	DU835386	ACCESSION: DU835386
C 419	33.2	1.2	38	1	AL038652	ACCESSION: AL038652	C 492	32	1.2	32	1	DR85121T	ACCESSION: AL986044
C 420	33.2	1.2	39	1	CF328529	ACCESSION: CF328529	C 493	32	1.2	33	1	AL587609	ACCESSION: AL587609
C 421	33	1.2	33	1	CF291613	ACCESSION: CF291613	C 494	32	1.2	33	1	B0431798	ACCESSION: B0431798
C 422	33	1.2	33	1	CF311229	ACCESSION: CF311229	C 495	32	1.2	34	1	AZ345610	ACCESSION: AZ345610
C 423	33	1.2	33	1	CF326967	ACCESSION: CF326967	C 496	32	1.2	35	1	BF338797	ACCESSION: BF338797
C 424	33	1.2	33	1	CF328313	ACCESSION: CF328313	C 497	32	1.2	35	1	DR073823	ACCESSION: DR073823
C 425	33	1.2	33	1	CF336752	ACCESSION: CF336752	C 498	32	1.2	39	1	AM046479	ACCESSION: AM046479
C 426	33	1.2	33	1	CF337105	ACCESSION: CF337105	C 499	32	1.2	40	1	CV723737	ACCESSION: CV723737
C 427	33	1.2	33	1	CV725203	ACCESSION: CV725203	C 500	31.8	1.2	35	1	BQ590703	ACCESSION: BQ590703
C 428	33	1.2	33	1	CV725846	ACCESSION: CV725846	C 501	31.8	1.2	35	1	CV724720	ACCESSION: CV724720
C 429	33	1.2	33	1	CV725871	ACCESSION: CV725871	C 502	31.8	1.2	36	1	AZ945733	ACCESSION: AZ945733
C 430	33	1.2	33	1	CV729599	ACCESSION: CV729599	C 503	31.8	1.2	36	1	CZ919025	ACCESSION: CZ919025
C 431	33	1.2	33	1	CV726801	ACCESSION: CV726801	C 504	31.8	1.2	37	1	CF298167	ACCESSION: CF298167
C 432	33	1.2	33	1	CV726984	ACCESSION: CV726984	C 505	31.8	1.2	38	1	DN988546	ACCESSION: DN988546
C 433	33	1.2	33	1	CV732151	ACCESSION: CV732151	C 506	31.8	1.2	39	1	TA116F09P	ACCESSION: AL462333
C 434	33	1.2	33	1	CV732198	ACCESSION: CV732198	C 507	31.4	1.1	33	1	CZ908819	ACCESSION: CZ908819
C 435	33	1.2	33	1	CV732853	ACCESSION: CV732853	C 508	31.4	1.1	36	1	CF298131	ACCESSION: CF298131
C 436	33	1.2	33	1	CV733051	ACCESSION: CV733051	C 509	31.4	1.1	37	1	CF278363	ACCESSION: CF278363
C 437	33	1.2	33	1	CV734457	ACCESSION: CV734457	C 510	31.4	1.1	39	1	CA853500	ACCESSION: CA853500
C 438	33	1.2	33	1	CK013914	ACCESSION: CK013914	C 511	31.2	1.1	38	1	CF321807	ACCESSION: CF321807
C 439	33	1.2	33	1	AZ486795	ACCESSION: AZ486795	C 512	31.2	1.1	39	1	CF308197	ACCESSION: CF308197
C 440	33	1.2	33	1	AZ627839	ACCESSION: AZ627839	C 513	31	1.1	31	1	AJ659810	ACCESSION: AJ659810
C 441	33	1.2	33	1	CZ917348	ACCESSION: CZ917348	C 514	31	1.1	31	1	AJ693992	ACCESSION: AJ693992
C 442	33	1.2	33	1	DU830405	ACCESSION: DU830405	C 515	31	1.1	31	1	AM044121	ACCESSION: AM044121
C 443	33	1.2	33	1	DX033863	ACCESSION: DX033863	C 516	31	1.1	31	1	BX569502	ACCESSION: BX569502
C 444	33	1.2	34	1	AL587876	ACCESSION: AL587876	C 517	31	1.1	31	1	CF278807	ACCESSION: CF278807
C 445	33	1.2	34	1	BU431799	ACCESSION: BU431799	C 518	31	1.1	31	1	CF300345	ACCESSION: CF300345
C 446	33	1.2	34	1	CV734277	ACCESSION: CV734277	C 519	31	1.1	31	1	AZ333315	ACCESSION: AZ333315
C 447	33	1.2	34	1	BI761940	ACCESSION: BI761940	C 520	31	1.1	31	1	AZ510092	ACCESSION: AZ510092
C 448	33	1.2	36	1	AJ792257	ACCESSION: AJ792257	C 521	31	1.1	31	1	AZ623538	ACCESSION: AZ623538
C 449	33	1.2	38	1	CV064759	ACCESSION: CV064759	C 522	31	1.1	31	1	AZ627692	ACCESSION: AZ627692
C 450	33	1.2	39	1	CF327755	ACCESSION: CF327755	C 523	31	1.1	31	1	AZ778697	ACCESSION: AZ778697
C 451	32.8	1.2	37	1	CF292043	ACCESSION: CF292043	C 524	31	1.1	31	1	AZ821215	ACCESSION: AZ821215
C 452	32.4	1.2	34	1	CF302250	ACCESSION: CF302250	C 525	31	1.1	31	1	AZ826618	ACCESSION: AZ826618
C 453	32.4	1.2	34	1	CF315464	ACCESSION: CF315464	C 526	31	1.1	31	1	AZ826618	ACCESSION: AZ826618
C 454	32.4	1.2	34	1	CZ906552	ACCESSION: CZ906552	C 527	31	1.1	31	1	CZ917108	ACCESSION: CZ917108
C 455	32.4	1.2	34	1	DX054666	ACCESSION: DX054666	C 528	31	1.1	31	1	DU835031	ACCESSION: DU835031
C 456	32.4	1.2	34	1	DX058168	ACCESSION: DX058168	C 529	31	1.1	31	1	DX063750	ACCESSION: DX063750
C 457	32.4	1.2	34	1	DR41AAT	ACCESSION: AL980969	C 530	31	1.1	34	1	AV674152	ACCESSION: AV674152
C 458	32.4	1.2	36	1	AM047864	ACCESSION: AM047864	C 531	31	1.1	34	1	AM334249	ACCESSION: AM334249
C 459	32.4	1.2	38	1	CN545543	ACCESSION: CN545543	C 532	31	1.1	36	1	CV066718	ACCESSION: CV066718
C 460	32.2	1.2	37	1	CN545945	ACCESSION: CN545945	C 533	30.8	1.1	34	1	BQ587432	ACCESSION: BQ587432
C 461	32.2	1.2	38	1	AL037916	ACCESSION: AL037916	C 534	30.8	1.1	34	1	DU832879	ACCESSION: DU832879
C 462	32.2	1.2	39	1	CN546173	ACCESSION: CN546173	C 535	30.8	1.1	34	1	DX048708	ACCESSION: DX048708
C 463	32.2	1.2	40	1	BQ591342	ACCESSION: BQ591342	C 536	30.6	1.1	37	1	CV848473	ACCESSION: CV848473
C 464	32	1.2	32	1	AJ923479	ACCESSION: AJ923479	C 537	30.4	1.1	37	1	CV848473	ACCESSION: CV848473
C 465	32	1.2	32	1	AM044529	ACCESSION: AM044529	C 538	30.4	1.1	32	1	CF302459	ACCESSION: CF302459
C 466	32	1.2	32	1	AM044934	ACCESSION: AM044934	C 539	30.4	1.1	32	1	CN546365	ACCESSION: CN546365
C 467	32	1.2	32	1	AM045405	ACCESSION: AM045405	C 540	30.4	1.1	32	1	DV083947	ACCESSION: DV083947
C 468	32	1.2	32	1	CF291773	ACCESSION: CF291773	C 541	30.4	1.1	32	1	AZ314322	ACCESSION: AZ314322
C 469	32	1.2	32	1	CF299386	ACCESSION: CF299386	C 542	30.4	1.1	32	1	AZ579652	ACCESSION: AZ579652
C 470	32	1.2	32	1	CF309233	ACCESSION: CF309233	C 543	30.4	1.1	32	1	DU834670	ACCESSION: DU834670
C 471	32	1.2	32	1	CF309345	ACCESSION: CF309345	C 544	30.4	1.1	32	1	DX033610	ACCESSION: DX033610

C 545	30.4	1.1	32	1	DR1P7S	ACCESSION:AL733323	C 618	29.4	1.1	36	1	CN546685	ACCESSION:CN546685
C 546	30.4	1.1	33	1	CF334899	ACCESSION:CF334899	C 619	29.4	1.1	34	1	CV091545	ACCESSION:CV091545
C 547	30.4	1.1	34	1	AZ307192	ACCESSION:AZ307192	C 620	29.2	1.1	36	1	AL038356	ACCESSION:AL038356
C 548	30.4	1.1	35	1	CN545906	ACCESSION:CN545906	C 621	29.2	1.1	35	1	T50295	ACCESSION:T50295
C 549	30.4	1.1	36	1	CN546158	ACCESSION:CN546158	C 622	29.2	1.1	35	1	AZ351309	ACCESSION:AZ351309
C 550	30.4	1.1	36	1	CN546709	ACCESSION:CN546709	C 623	29.2	1.1	35	1	CZ914519	ACCESSION:CZ914519
C 551	30.4	1.1	36	1	DU834429	ACCESSION:DU834429	C 624	29	1.1	29	1	AM044739	ACCESSION:AM044739
C 552	30.4	1.1	37	1	CN545897	ACCESSION:CN545897	C 625	29	1.1	29	1	AM048584	ACCESSION:AM048584
C 553	30.4	1.1	37	1	DN988462	ACCESSION:DN988462	C 626	29	1.1	29	1	CF279536	ACCESSION:CF279536
C 554	30.4	1.1	38	1	CN546437	ACCESSION:CN546437	C 627	29	1.1	29	1	CF299920	ACCESSION:CF299920
C 555	30.4	1.1	38	1	CN546551	ACCESSION:CN546551	C 628	29	1.1	29	1	CF312601	ACCESSION:CF312601
C 556	30.4	1.1	38	1	CN546633	ACCESSION:CN546633	C 629	29	1.1	29	1	CN545237	ACCESSION:CN545237
C 557	30.2	1.1	36	1	CZ916174	ACCESSION:CZ916174	C 630	29	1.1	29	1	CN546188	ACCESSION:CN546188
C 558	30	1.1	30	1	AL038650	ACCESSION:AL038650	C 631	29	1.1	29	1	CN546382	ACCESSION:CN546382
C 559	30	1.1	30	1	AM044444	ACCESSION:AM044444	C 632	29	1.1	29	1	CN546438	ACCESSION:CN546438
C 560	30	1.1	30	1	BG666435	ACCESSION:BG666435	C 633	29	1.1	29	1	CN546557	ACCESSION:CN546557
C 561	30	1.1	30	1	CF280699	ACCESSION:CF280699	C 634	29	1.1	29	1	CV999708	ACCESSION:CV999708
C 562	30	1.1	30	1	CF292086	ACCESSION:CF292086	C 635	29	1.1	29	1	DR073120	ACCESSION:DR073120
C 563	30	1.1	30	1	CF299555	ACCESSION:CF299555	C 636	29	1.1	29	1	AZ389966	ACCESSION:AZ389966
C 564	30	1.1	30	1	CF312417	ACCESSION:CF312417	C 637	29	1.1	29	1	AZ414283	ACCESSION:AZ414283
C 565	30	1.1	30	1	CF322226	ACCESSION:CF322226	C 638	29	1.1	29	1	AZ451930	ACCESSION:AZ451930
C 566	30	1.1	30	1	CF327835	ACCESSION:CF327835	C 639	29	1.1	29	1	AZ468402	ACCESSION:AZ468402
C 567	30	1.1	30	1	CF336555	ACCESSION:CF336555	C 640	29	1.1	29	1	AZ486793	ACCESSION:AZ486793
C 568	30	1.1	30	1	CN545913	ACCESSION:CN545913	C 641	29	1.1	29	1	AZ661709	ACCESSION:AZ661709
C 569	30	1.1	30	1	CN546459	ACCESSION:CN546459	C 642	29	1.1	29	1	AZ784208	ACCESSION:AZ784208
C 570	30	1.1	30	1	CN546474	ACCESSION:CN546474	C 643	29	1.1	29	1	AZ806470	ACCESSION:AZ806470
C 571	30	1.1	30	1	CN546789	ACCESSION:CN546789	C 644	29	1.1	29	1	AZ812242	ACCESSION:AZ812242
C 572	30	1.1	30	1	CV728764	ACCESSION:CV728764	C 645	29	1.1	29	1	AZ868731	ACCESSION:AZ868731
C 573	30	1.1	30	1	CX014987	ACCESSION:CX014987	C 646	29	1.1	29	1	CZ919318	ACCESSION:CZ919318
C 574	30	1.1	30	1	DR073060	ACCESSION:DR073060	C 647	29	1.1	29	1	DU833998	ACCESSION:DU833998
C 575	30	1.1	30	1	AZ357603	ACCESSION:AZ357603	C 648	29	1.1	29	1	DU835145	ACCESSION:DU835145
C 576	30	1.1	30	1	AZ455741	ACCESSION:AZ455741	C 649	29	1.1	29	1	AG193759	ACCESSION:AG193759
C 577	30	1.1	30	1	AZ481739	ACCESSION:AZ481739	C 650	29	1.1	29	1	TA334G09Q	ACCESSION:TA334G09Q
C 578	30	1.1	30	1	AZ582114	ACCESSION:AZ582114	C 651	29	1.1	30	1	BG865511	ACCESSION:BG865511
C 579	30	1.1	30	1	CZ917652	ACCESSION:CZ917652	C 652	29	1.1	30	1	CN545845	ACCESSION:CN545845
C 580	30	1.1	30	1	CZ919796	ACCESSION:CZ919796	C 653	29	1.1	31	1	CZ514262	ACCESSION:CZ514262
C 581	30	1.1	30	1	CW020481	ACCESSION:CW020481	C 654	29	1.1	32	1	CN546517	ACCESSION:CN546517
C 582	30	1.1	30	1	DU835531	ACCESSION:DU835531	C 655	29	1.1	32	1	DN955775	ACCESSION:DN955775
C 583	30	1.1	31	1	AG191161	ACCESSION:AG191161	C 656	29	1.1	32	1	BU431802	ACCESSION:BU431802
C 584	30	1.1	31	1	BG292912	ACCESSION:BG292912	C 657	29	1.1	35	1	CV064432	ACCESSION:CV064432
C 585	30	1.1	31	1	CN545579	ACCESSION:CN545579	C 658	29	1.1	36	1	AM044046	ACCESSION:AM044046
C 586	30	1.1	31	1	CN545867	ACCESSION:CN545867	C 659	28.8	1.0	32	1	CF318239	ACCESSION:CF318239
C 587	30	1.1	31	1	CN545921	ACCESSION:CN545921	C 660	28.8	1.0	32	1	AZ627842	ACCESSION:AZ627842
C 588	30	1.1	31	1	CN546024	ACCESSION:CN546024	C 661	28.8	1.0	34	1	AJ800678	ACCESSION:AJ800678
C 589	30	1.1	31	1	CN546130	ACCESSION:CN546130	C 662	28.8	1.0	36	1	AM043639	ACCESSION:AM043639
C 590	30	1.1	31	1	AZ597046	ACCESSION:AZ597046	C 663	28.4	1.0	30	1	CN546288	ACCESSION:CN546288
C 591	30	1.1	31	1	CZ917966	ACCESSION:CZ917966	C 664	28.4	1.0	30	1	AZ443322	ACCESSION:AZ443322
C 592	30	1.1	32	1	AZ400441	ACCESSION:AZ400441	C 665	28.4	1.0	30	1	AZ458127	ACCESSION:AZ458127
C 593	30	1.1	33	1	AU013658	ACCESSION:AU013658	C 666	28.4	1.0	30	1	CZ917310	ACCESSION:CZ917310
C 594	30	1.1	33	1	DN955605	ACCESSION:DN955605	C 667	28.4	1.0	30	1	DU833997	ACCESSION:DU833997
C 595	30	1.1	35	1	CV066327	ACCESSION:CV066327	C 668	28.4	1.0	32	1	CN546007	ACCESSION:CN546007
C 596	29.8	1.1	33	1	CN545607	ACCESSION:CN545607	C 669	28.4	1.0	33	1	CN546531	ACCESSION:CN546531
C 597	29.8	1.1	33	1	DX050853	ACCESSION:DX050853	C 670	28.4	1.0	33	1	CV725332	ACCESSION:CV725332
C 598	29.8	1.1	37	1	CF301193	ACCESSION:CF301193	C 671	28.4	1.0	34	1	BG531309	ACCESSION:BG531309
C 599	29.6	1.1	36	1	CN546175	ACCESSION:CN546175	C 672	28.4	1.0	34	1	BG612023	ACCESSION:BG612023
C 600	29.6	1.1	37	1	AL587823	ACCESSION:AL587823	C 673	28.4	1.0	35	1	CN546161	ACCESSION:CN546161
C 601	29.4	1.1	31	1	BQ591372	ACCESSION:BQ591372	C 674	28.4	1.0	35	1	CN546416	ACCESSION:CN546416
C 602	29.4	1.1	31	1	CD577356	ACCESSION:CD577356	C 675	28.4	1.0	35	1	CN546519	ACCESSION:CN546519
C 603	29.4	1.1	31	1	CN545785	ACCESSION:CN545785	C 676	28.4	1.0	35	1	CN546666	ACCESSION:CN546666
C 604	29.4	1.1	31	1	CN546374	ACCESSION:CN546374	C 677	28.2	1.0	33	1	AJ791259	ACCESSION:AJ791259
C 605	29.4	1.1	31	1	AZ486763	ACCESSION:AZ486763	C 678	28.2	1.0	33	1	CF335736	ACCESSION:CF335736
C 606	29.4	1.1	31	1	AZ785111	ACCESSION:AZ785111	C 679	28.2	1.0	33	1	CZ919845	ACCESSION:CZ919845
C 607	29.4	1.1	31	1	DU835198	ACCESSION:DU835198	C 680	28.2	1.0	33	1	DR85L9T	ACCESSION:DR85L9T
C 608	29.4	1.1	31	1	DX033882	ACCESSION:DX033882	C 681	28.2	1.0	34	1	CN973659	ACCESSION:CN973659
C 609	29.4	1.1	32	1	AL038680	ACCESSION:AL038680	C 682	28.2	1.0	35	1	AJ746854	ACCESSION:AJ746854
C 610	29.4	1.1	34	1	CN545857	ACCESSION:CN545857	C 683	28	1.0	28	1	AJ666435	ACCESSION:AJ666435
C 611	29.4	1.1	34	1	CN546360	ACCESSION:CN546360	C 684	28	1.0	28	1	AM043789	ACCESSION:AM043789
C 612	29.4	1.1	34	1	CN546656	ACCESSION:CN546656	C 685	28	1.0	28	1	AM043903	ACCESSION:AM043903
C 613	29.4	1.1	35	1	CN545982	ACCESSION:CN545982	C 686	28	1.0	28	1	AM043968	ACCESSION:AM043968
C 614	29.4	1.1	35	1	CN546734	ACCESSION:CN546734	C 687	28	1.0	28	1	AM044512	ACCESSION:AM044512
C 615	29.4	1.1	36	1	AL036993	ACCESSION:AL036993	C 688	28	1.0	28	1	CF282351	ACCESSION:CF282351
C 616	29.4	1.1	36	1	CN545377	ACCESSION:CN545377	C 689	28	1.0	28	1	CF321885	ACCESSION:CF321885
C 617	29.4	1.1	36	1	CN546215	ACCESSION:CN546215	C 690	28	1.0	28	1	CF330748	ACCESSION:CF330748

691	28	1.0	28	1	CF330938	ACCESSION: CF330938	C 764	27	1.0	27	1	DR072930	ACCESSION: DR072930
C 692	28	1.0	28	1	CN546364	ACCESSION: CN546364	C 765	27	1.0	27	1	AZ344642	ACCESSION: AZ344642
C 693	28	1.0	28	1	CN546703	ACCESSION: CN546703	C 766	27	1.0	27	1	AZ401672	ACCESSION: AZ401672
C 694	28	1.0	28	1	DR073098	ACCESSION: DR073098	C 767	27	1.0	27	1	AZ486791	ACCESSION: AZ486791
C 695	28	1.0	28	1	AZ399637	ACCESSION: AZ399637	C 768	27	1.0	27	1	AZ511894	ACCESSION: AZ511894
C 696	28	1.0	28	1	AZ401766	ACCESSION: AZ401766	C 769	27	1.0	27	1	AZ580921	ACCESSION: AZ580921
C 697	28	1.0	28	1	AZ471744	ACCESSION: AZ471744	C 770	27	1.0	27	1	AZ616094	ACCESSION: AZ616094
C 698	28	1.0	28	1	AZ493138	ACCESSION: AZ493138	C 771	27	1.0	27	1	AZ623186	ACCESSION: AZ623186
C 699	28	1.0	28	1	AZ553365	ACCESSION: AZ553365	C 772	27	1.0	27	1	AZ627847	ACCESSION: AZ627847
C 700	28	1.0	28	1	AZ785035	ACCESSION: AZ785035	C 773	27	1.0	27	1	AZ809295	ACCESSION: AZ809295
C 701	28	1.0	28	1	AZ824519	ACCESSION: AZ824519	C 774	27	1.0	27	1	CZ917070	ACCESSION: CZ917070
C 702	28	1.0	28	1	AZ833425	ACCESSION: AZ833425	C 775	27	1.0	27	1	DX046035	ACCESSION: DX046035
C 703	28	1.0	28	1	AZ865569	ACCESSION: AZ865569	C 776	27	1.0	27	1	DX056021	ACCESSION: DX056021
C 704	28	1.0	28	1	CZ912316	ACCESSION: CZ912316	C 777	27	1.0	27	1	AG829428	ACCESSION: AG829428
C 705	28	1.0	28	1	CZ913960	ACCESSION: CZ913960	C 778	27	1.0	27	1	TA355806P	ACCESSION: TA355806P
C 706	28	1.0	28	1	DU828712	ACCESSION: DU828712	C 779	27	1.0	28	1	AL048439	ACCESSION: AL048439
C 707	28	1.0	28	1	DU835260	ACCESSION: DU835260	C 780	27	1.0	28	1	CF322082	ACCESSION: CF322082
C 708	28	1.0	28	1	DU835584	ACCESSION: DU835584	C 781	27	1.0	28	1	CF337400	ACCESSION: CF337400
C 709	28	1.0	28	1	DX072153	ACCESSION: DX072153	C 782	27	1.0	28	1	CN545498	ACCESSION: CN545498
C 710	28	1.0	28	1	TA291A01Q	ACCESSION: AL486613	C 783	27	1.0	28	1	CN546292	ACCESSION: CN546292
C 711	28	1.0	28	1	TA379D11P	ACCESSION: AL497637	C 784	27	1.0	28	1	CN546304	ACCESSION: CN546304
C 712	28	1.0	29	1	CN545883	ACCESSION: CN545883	C 785	27	1.0	28	1	DN988459	ACCESSION: DN988459
C 713	28	1.0	29	1	CZ912823	ACCESSION: CZ912823	C 786	27	1.0	28	1	ACCESSION: CZ918534	ACCESSION: CZ918534
C 714	28	1.0	29	1	CZ914240	ACCESSION: CZ914240	C 787	27	1.0	32	1	CA853459	ACCESSION: CA853459
C 715	28	1.0	30	1	CN545968	ACCESSION: CN545968	C 788	27	1.0	32	1	R16114	ACCESSION: R16114
C 716	28	1.0	30	1	CN546523	ACCESSION: CN546523	C 789	26.8	1.0	30	1	CZ913832	ACCESSION: CZ913832
C 717	28	1.0	30	1	CZ919540	ACCESSION: CZ919540	C 790	26.8	1.0	32	1	CF332296	ACCESSION: CF332296
C 718	28	1.0	31	1	AW245279	ACCESSION: AW245279	C 791	26.8	1.0	32	1	CV733741	ACCESSION: CV733741
C 719	28	1.0	31	1	CV057897	ACCESSION: CV057897	C 792	26.6	1.0	33	1	CF300359	ACCESSION: CF300359
C 720	28	1.0	32	1	AM046790	ACCESSION: AM046790	C 793	26.4	1.0	28	1	CF307749	ACCESSION: CF307749
C 721	28	1.0	32	1	C0577661	ACCESSION: C0577661	C 794	26.4	1.0	28	1	AW332443	ACCESSION: AW332443
C 722	28	1.0	32	1	AZ397471	ACCESSION: AZ397471	C 795	26.4	1.0	28	1	CN545659	ACCESSION: CN545659
C 723	28	1.0	33	1	AV743346	ACCESSION: AV743346	C 796	26.4	1.0	28	1	CK001046	ACCESSION: CK001046
C 724	27.8	1.0	31	1	AW249485	ACCESSION: AW249485	C 797	26.4	1.0	28	1	DR062845	ACCESSION: DR062845
C 725	27.8	1.0	33	1	AX014884	ACCESSION: AX014884	C 798	26.4	1.0	28	1	AZ514352	ACCESSION: AZ514352
C 726	27.8	1.0	33	1	CV727574	ACCESSION: CV727574	C 799	26.4	1.0	28	1	AZ824574	ACCESSION: AZ824574
C 727	27.6	1.0	34	1	AJ656734	ACCESSION: AJ656734	C 800	26.4	1.0	28	1	CZ916890	ACCESSION: CZ916890
C 728	27.6	1.0	34	1	BQ594010	ACCESSION: BQ594010	C 801	26.4	1.0	28	1	TA29A09P	ACCESSION: AL453073
C 729	27.4	1.0	29	1	BQ590537	ACCESSION: BQ590537	C 802	26.4	1.0	29	1	CF328476	ACCESSION: CF328476
C 730	27.4	1.0	29	1	CN545226	ACCESSION: CN545226	C 803	26.2	1.0	31	1	CF328476	ACCESSION: AU268044
C 731	27.4	1.0	29	1	CN545618	ACCESSION: CN545618	C 804	26.2	1.0	31	1	CF297930	ACCESSION: CF297930
C 732	27.4	1.0	29	1	CN546518	ACCESSION: CN546518	C 805	26.2	1.0	32	1	AZ451251	ACCESSION: AZ451251
C 733	27.4	1.0	29	1	AZ825156	ACCESSION: AZ825156	C 806	26	0.9	26	1	AM043187	ACCESSION: AM043187
C 734	27.4	1.0	29	1	CZ914157	ACCESSION: CZ914157	C 807	26	0.9	26	1	AM045820	ACCESSION: AM045820
C 735	27.4	1.0	29	1	DU834266	ACCESSION: DU834266	C 808	26	0.9	26	1	AM046959	ACCESSION: AM046959
C 736	27.4	1.0	30	1	AL038672	ACCESSION: AL038672	C 809	26	0.9	26	1	AM047208	ACCESSION: AM047208
C 737	27.4	1.0	30	1	AU267300	ACCESSION: AU267300	C 810	26	0.9	26	1	CF278359	ACCESSION: CF278359
C 738	27.4	1.0	30	1	CN546316	ACCESSION: CN546316	C 811	26	0.9	26	1	CF282426	ACCESSION: CF282426
C 739	27.4	1.0	30	1	DR31A15T	ACCESSION: AL987581	C 812	26	0.9	26	1	CF297087	ACCESSION: CF297087
C 740	27.4	1.0	31	1	CN545916	ACCESSION: CN545916	C 813	26	0.9	26	1	CF299701	ACCESSION: CF299701
C 741	27.4	1.0	33	1	AZ759642	ACCESSION: AZ759642	C 814	26	0.9	26	1	CF302874	ACCESSION: CF302874
C 742	27.4	1.0	34	1	DN988790	ACCESSION: DN988790	C 815	26	0.9	26	1	CF311369	ACCESSION: CF311369
C 743	27.2	1.0	32	1	CF298526	ACCESSION: CF298526	C 816	26	0.9	26	1	CF311439	ACCESSION: CF311439
C 744	27.2	1.0	32	1	CF334956	ACCESSION: CF334956	C 817	26	0.9	26	1	AW327613	ACCESSION: AW327613
C 745	27.2	1.0	32	1	AW250841	ACCESSION: AW250841	C 818	26	0.9	26	1	CN545213	ACCESSION: CN545213
C 746	27.2	1.0	32	1	CZ467504	ACCESSION: CZ467504	C 819	26	0.9	26	1	CN545225	ACCESSION: CN545225
C 747	27	1.0	27	1	AM048211	ACCESSION: AM048211	C 820	26	0.9	26	1	CN545546	ACCESSION: CN545546
C 748	27	1.0	27	1	CF291968	ACCESSION: CF291968	C 821	26	0.9	26	1	CN545888	ACCESSION: CN545888
C 749	27	1.0	27	1	CF297925	ACCESSION: CF297925	C 822	26	0.9	26	1	CN546608	ACCESSION: CN546608
C 750	27	1.0	27	1	CF330557	ACCESSION: CF330557	C 823	26	0.9	26	1	CN546649	ACCESSION: CN546649
C 751	27	1.0	27	1	CF335229	ACCESSION: CF335229	C 824	26	0.9	26	1	DN953783	ACCESSION: DN953783
C 752	27	1.0	27	1	AW327923	ACCESSION: AW327923	C 825	26	0.9	26	1	DN955188	ACCESSION: DN955188
C 753	27	1.0	27	1	CN545326	ACCESSION: CN545326	C 826	26	0.9	26	1	DR073125	ACCESSION: DR073125
C 754	27	1.0	27	1	CN545492	ACCESSION: CN545492	C 827	26	0.9	26	1	AZ359871	ACCESSION: AZ359871
C 755	27	1.0	27	1	CN545530	ACCESSION: CN545530	C 828	26	0.9	26	1	AZ376664	ACCESSION: AZ376664
C 756	27	1.0	27	1	CN545597	ACCESSION: CN545597	C 829	26	0.9	26	1	AZ389765	ACCESSION: AZ389765
C 757	27	1.0	27	1	CN545938	ACCESSION: CN545938	C 830	26	0.9	26	1	AZ414673	ACCESSION: AZ414673
C 758	27	1.0	27	1	CN545962	ACCESSION: CN545962	C 831	26	0.9	26	1	AZ414673	ACCESSION: AZ414673
C 759	27	1.0	27	1	CN546052	ACCESSION: CN546052	C 832	26	0.9	26	1	AZ593300	ACCESSION: AZ593300
C 760	27	1.0	27	1	CN546271	ACCESSION: CN546271	C 833	26	0.9	26	1	AZ612722	ACCESSION: AZ612722
C 761	27	1.0	27	1	CN546337	ACCESSION: CN546337	C 834	26	0.9	26	1	AZ624441	ACCESSION: AZ624441
C 762	27	1.0	27	1	CN546559	ACCESSION: CN546559	C 835	26	0.9	26	1	AZ627846	ACCESSION: AZ627846
C 763	27	1.0	27	1	CN546574	ACCESSION: CN546574	C 836	26	0.9	26	1	AZ652515	ACCESSION: AZ652515

C 837	26	0.9	26	1	AZ800453	ACCSSION:AZ800453	C 910	25	0.9	26	1	AL587774	ACCSSION:AL587774
C 838	26	0.9	26	1	AZ963974	ACCSSION:AZ963974	C 911	25	0.9	26	1	AM048107	ACCSSION:AM048107
C 839	26	0.9	26	1	CZ490199	ACCSSION:CZ490199	C 912	25	0.9	26	1	CF296851	ACCSSION:CF296851
C 840	26	0.9	26	1	CZ910095	ACCSSION:CZ910095	C 913	25	0.9	26	1	CN545723	ACCSSION:CN545723
C 841	26	0.9	26	1	DUB32827	ACCSSION:DUB32827	C 914	25	0.9	27	1	AJ789548	ACCSSION:AJ789548
C 842	26	0.9	26	1	DUB35360	ACCSSION:DUB35360	C 915	25	0.9	31	1	TA244G08P	ACCSSION:TA244G08P
C 843	26	0.9	26	1	DX034224	ACCSSION:DX034224	C 916	24.8	0.9	28	1	CZ469056	ACCSSION:CZ469056
C 844	26	0.9	26	1	TA324D07P	ACCSSION:TA324D07P	C 917	24.4	0.9	26	1	AM042970	ACCSSION:AM042970
C 845	26	0.9	27	1	CN545777	ACCSSION:CN545777	C 918	24.4	0.9	26	1	CR546444	ACCSSION:CR546444
C 846	26	0.9	27	1	CN545880	ACCSSION:CN545880	C 919	24.4	0.9	26	1	AZ355083	ACCSSION:AZ355083
C 847	26	0.9	27	1	TA257667	ACCSSION:TA257667	C 920	24.4	0.9	26	1	AZ623156	ACCSSION:AZ623156
C 848	26	0.9	27	1	TA257670P	ACCSSION:TA257670P	C 921	24.4	0.9	26	1	AZ635695	ACCSSION:AZ635695
C 849	26	0.9	29	1	AJ658334	ACCSSION:AJ658334	C 922	24.4	0.9	26	1	CZ917641	ACCSSION:CZ917641
C 850	26	0.9	30	1	AZ819924	ACCSSION:AZ819924	C 923	24.4	0.9	26	1	AG2019575	ACCSSION:AG2019575
C 851	26	0.9	30	1	CN545889	ACCSSION:CN545889	C 924	24.4	0.9	26	1	AG201580	ACCSSION:AG201580
C 852	26	0.9	30	1	AZ962183	ACCSSION:AZ962183	C 925	24.4	0.9	27	1	DT471186	ACCSSION:DT471186
C 853	26	0.9	31	1	AM044314	ACCSSION:AM044314	C 926	24.4	0.9	27	1	N52529	ACCSSION:N52529
C 854	26	0.9	32	1	CD577496	ACCSSION:CD577496	C 927	24.4	0.9	27	1	AZ862643	ACCSSION:AZ862643
C 855	25.8	0.9	29	1	BQ583967	ACCSSION:BQ583967	C 928	24.4	0.9	28	1	CF299294	ACCSSION:CF299294
C 856	25.8	0.9	29	1	CN545957	ACCSSION:CN545957	C 929	24.4	0.9	28	1	TS2836	ACCSSION:TS2836
C 857	25.6	0.9	32	1	R59306	ACCSSION:R59306	C 930	24.4	0.9	28	1	AZ481286	ACCSSION:AZ481286
C 858	25.6	0.9	32	1	AZ326012	ACCSSION:AZ326012	C 931	24.4	0.9	29	1	CF299155	ACCSSION:CF299155
C 859	25.6	0.9	32	1	CZ915120	ACCSSION:CZ915120	C 932	24.2	0.9	29	1	DR073498	ACCSSION:DR073498
C 860	25.6	0.9	32	1	CZ918635	ACCSSION:CZ918635	C 933	24.2	0.9	29	1	CL693162	ACCSSION:CL693162
C 861	25.4	0.9	27	1	AZ434285	ACCSSION:AZ434285	C 934	24.2	0.9	29	1	TA378G07P	ACCSSION:TA378G07P
C 862	25.4	0.9	27	1	AZ458228	ACCSSION:AZ458228	C 935	24	0.9	24	1	AM043978	ACCSSION:AM043978
C 863	25.4	0.9	27	1	AZ941721	ACCSSION:AZ941721	C 936	24	0.9	24	1	AJ921827	ACCSSION:AJ921827
C 864	25.4	0.9	27	1	AZ970621	ACCSSION:AZ970621	C 937	24	0.9	24	1	AM045511	ACCSSION:AM045511
C 865	25.4	0.9	27	1	DX070376	ACCSSION:DX070376	C 938	24	0.9	24	1	AM046329	ACCSSION:AM046329
C 866	25.4	0.9	28	1	R37697	ACCSSION:R37697	C 939	24	0.9	24	1	AM046329	ACCSSION:AM046329
C 867	25.4	0.9	28	1	TS6352	ACCSSION:TS6352	C 940	24	0.9	24	1	AM048042	ACCSSION:AM048042
C 868	25.4	0.9	28	1	AZ836072	ACCSSION:AZ836072	C 941	24	0.9	24	1	BG670391	ACCSSION:BG670391
C 869	25.2	0.9	30	1	CF299716	ACCSSION:CF299716	C 942	24	0.9	24	1	BX554611	ACCSSION:BX554611
C 870	25.2	0.9	30	1	CZ919253	ACCSSION:CZ919253	C 943	24	0.9	24	1	CF276855	ACCSSION:CF276855
C 871	25.2	0.9	31	1	DX082113	ACCSSION:DX082113	C 944	24	0.9	24	1	CF301561	ACCSSION:CF301561
C 872	25.2	0.9	31	1	CZ918715	ACCSSION:CZ918715	C 945	24	0.9	24	1	CF320862	ACCSSION:CF320862
C 873	25	0.9	25	1	CF291048	ACCSSION:CF291048	C 946	24	0.9	24	1	CN545449	ACCSSION:CN545449
C 874	25	0.9	25	1	CF291646	ACCSSION:CF291646	C 947	24	0.9	24	1	CN545307	ACCSSION:CN545307
C 875	25	0.9	25	1	CF299288	ACCSSION:CF299288	C 948	24	0.9	24	1	CN545784	ACCSSION:CN545784
C 876	25	0.9	25	1	CF300333	ACCSSION:CF300333	C 949	24	0.9	24	1	CN546689	ACCSSION:CN546689
C 877	25	0.9	25	1	CF316323	ACCSSION:CF316323	C 950	24	0.9	24	1	DR073080	ACCSSION:DR073080
C 878	25	0.9	25	1	CF317714	ACCSSION:CF317714	C 951	24	0.9	24	1	DR074082	ACCSSION:DR074082
C 879	25	0.9	25	1	CF319073	ACCSSION:CF319073	C 952	24	0.9	24	1	AZ328848	ACCSSION:AZ328848
C 880	25	0.9	25	1	CF330786	ACCSSION:CF330786	C 953	24	0.9	24	1	AZ328848	ACCSSION:AZ328848
C 881	25	0.9	25	1	CN545505	ACCSSION:CN545505	C 954	24	0.9	24	1	AZ363562	ACCSSION:AZ363562
C 882	25	0.9	25	1	CN546041	ACCSSION:CN546041	C 955	24	0.9	24	1	AZ386491	ACCSSION:AZ386491
C 883	25	0.9	25	1	CN546397	ACCSSION:CN546397	C 956	24	0.9	24	1	AZ390642	ACCSSION:AZ390642
C 884	25	0.9	25	1	CN546477	ACCSSION:CN546477	C 957	24	0.9	24	1	AZ459280	ACCSSION:AZ459280
C 885	25	0.9	25	1	CN546728	ACCSSION:CN546728	C 958	24	0.9	24	1	AZ644621	ACCSSION:AZ644621
C 886	25	0.9	25	1	CV999835	ACCSSION:CV999835	C 959	24	0.9	24	1	AZ834990	ACCSSION:AZ834990
C 887	25	0.9	25	1	DR073093	ACCSSION:DR073093	C 960	24	0.9	24	1	AZ984490	ACCSSION:AZ984490
C 888	25	0.9	25	1	DR073104	ACCSSION:DR073104	C 961	24	0.9	24	1	AZ993423	ACCSSION:AZ993423
C 889	25	0.9	25	1	DR073105	ACCSSION:DR073105	C 962	24	0.9	24	1	DUB29467	ACCSSION:DUB29467
C 890	25	0.9	25	1	DR073133	ACCSSION:DR073133	C 963	24	0.9	24	1	DUB30197	ACCSSION:DUB30197
C 891	25	0.9	25	1	L32039	ACCSSION:L32039	C 964	24	0.9	24	1	DX047568	ACCSSION:DX047568
C 892	25	0.9	25	1	AZ344725	ACCSSION:AZ344725	C 965	24	0.9	24	1	DX049347	ACCSSION:DX049347
C 893	25	0.9	25	1	AZ350777	ACCSSION:AZ350777	C 966	24	0.9	24	1	DX053980	ACCSSION:DX053980
C 894	25	0.9	25	1	AZ389458	ACCSSION:AZ389458	C 967	24	0.9	24	1	DX072040	ACCSSION:DX072040
C 895	25	0.9	25	1	AZ609234	ACCSSION:AZ609234	C 968	24	0.9	24	1	DX080492	ACCSSION:DX080492
C 896	25	0.9	25	1	AZ623157	ACCSSION:AZ623157	C 969	24	0.9	24	1	DX082296	ACCSSION:DX082296
C 897	25	0.9	25	1	AZ788646	ACCSSION:AZ788646	C 970	24	0.9	24	1	TA169D12P	ACCSSION:TA169D12P
C 898	25	0.9	25	1	AZ949287	ACCSSION:AZ949287	C 971	24	0.9	24	1	TA27B08Q	ACCSSION:TA27B08Q
C 899	25	0.9	25	1	AZ980407	ACCSSION:AZ980407	C 972	24	0.9	24	1	TA354C06P	ACCSSION:TA354C06P
C 900	25	0.9	25	1	CZ914066	ACCSSION:CZ914066	C 973	24	0.9	24	1	TA371F11P	ACCSSION:TA371F11P
C 901	25	0.9	25	1	CZ918479	ACCSSION:CZ918479	C 974	24	0.9	24	1	TA95B08P	ACCSSION:TA95B08P
C 902	25	0.9	25	1	DUB29648	ACCSSION:DUB29648	C 975	24	0.9	25	1	AL587648	ACCSSION:AL587648
C 903	25	0.9	25	1	DUB32111	ACCSSION:DUB32111	C 976	24	0.9	25	1	CF317007	ACCSSION:CF317007
C 904	25	0.9	25	1	DUB34405	ACCSSION:DUB34405	C 977	24	0.9	25	1	CF638767	ACCSSION:CF638767
C 905	25	0.9	25	1	DUB34424	ACCSSION:DUB34424	C 978	24	0.9	25	1	N33150	ACCSSION:N33150
C 906	25	0.9	25	1	DUB34577	ACCSSION:DUB34577	C 979	24	0.9	25	1	AZ381039	ACCSSION:AZ381039
C 907	25	0.9	25	1	DX075967	ACCSSION:DX075967	C 980	24	0.9	26	1	CF639306	ACCSSION:CF639306
C 908	25	0.9	25	1	TA324E10P	ACCSSION:TA324E10P	C 981	24	0.9	27	1	R31539	ACCSSION:R31539
C 909	25	0.9	26	1	AL038686	ACCSSION:AL038686	C 982	24	0.9	28	1	AZ358038	ACCSSION:AZ358038

c 983	23.8	0.9	27	1	CF299084	ACCESSION:CF299084	c1056	23	0.8	27	1	N34459	ACCESSION:N34459
c 984	23.8	0.9	27	1	CF318113	ACCESSION:CF318113	c1057	23	0.8	28	1	AJ922298	ACCESSION:AJ922298
c 985	23.8	0.9	27	1	R59382	ACCESSION:R59382	c1058	23	0.8	28	1	DX072773	ACCESSION:DX072773
c 986	23.8	0.9	28	1	C2914142	ACCESSION:C2914142	c1059	22.8	0.8	26	1	BM658913	ACCESSION:BM658913
c 987	23.8	0.9	28	1	DX071727	ACCESSION:DX071727	c1060	22.8	0.8	26	1	EX563414	ACCESSION:EX563414
c 988	23.4	0.9	25	1	A2404078	ACCESSION:A2404078	c1061	22.8	0.8	26	1	KW020478	ACCESSION:KW020478
c 989	23.4	0.9	25	1	DUR333936	ACCESSION:DUR333936	c1062	22.8	0.8	27	1	C2908520	ACCESSION:C2908520
c 990	23.4	0.9	25	1	DUR34323	ACCESSION:DUR34323	c1063	22.8	0.8	28	1	CV091538	ACCESSION:CV091538
c 991	23.4	0.9	26	1	CF299646	ACCESSION:CF299646	c1064	22.8	0.8	28	1	TA327D04P	ACCESSION:TA327D04P
c 992	23.4	0.9	26	1	A2316353	ACCESSION:A2316353	c1065	22.4	0.8	24	1	CF281313	ACCESSION:CF281313
c 993	23.4	0.9	28	1	AL587582	ACCESSION:AL587582	c1066	22.4	0.8	24	1	AW247159	ACCESSION:AW247159
c 994	23.4	0.9	28	1	AU257468	ACCESSION:AU257468	c1067	22.4	0.8	24	1	A2438069	ACCESSION:A2438069
c 995	23.4	0.9	29	1	DR064440	ACCESSION:DR064440	c1068	22.4	0.8	24	1	A2458112	ACCESSION:A2458112
c 996	23.4	0.9	29	1	DR072912	ACCESSION:DR072912	c1069	22.4	0.8	24	1	A2607198	ACCESSION:A2607198
c 997	23.4	0.9	29	1	T67079	ACCESSION:T67079	c1070	22.4	0.8	24	1	AZ621257	ACCESSION:AZ621257
c 998	23.2	0.8	28	1	AA852828	ACCESSION:AA852828	c1071	22.4	0.8	24	1	DUR35497	ACCESSION:DUR35497
c 999	23.2	0.8	29	1	CF314795	ACCESSION:CF314795	c1072	22.4	0.8	24	1	DX045709	ACCESSION:DX045709
c1000	23.2	0.8	29	1	DR074680	ACCESSION:DR074680	c1073	22.4	0.8	25	1	N27663	ACCESSION:N27663
c1001	23.2	0.8	29	1	A2827060	ACCESSION:A2827060	c1074	22.4	0.8	27	1	CF310745	ACCESSION:CF310745
c1002	23.2	0.8	29	1	C2171125	ACCESSION:C2171125	c1075	22.4	0.8	28	1	AL039138	ACCESSION:AL039138
c1003	23	0.8	23	1	AJ695799	ACCESSION:AJ695799	c1076	22.4	0.8	28	1	DX082097	ACCESSION:DX082097
c1004	23	0.8	23	1	AJ747297	ACCESSION:AJ747297	c1077	22.2	0.8	27	1	CF298133	ACCESSION:CF298133
c1005	23	0.8	23	1	AM047432	ACCESSION:AM047432	c1078	22.2	0.8	27	1	CF328811	ACCESSION:CF328811
c1006	23	0.8	23	1	AM047142	ACCESSION:AM047142	c1079	22.2	0.8	27	1	CF333518	ACCESSION:CF333518
c1007	23	0.8	23	1	CF279238	ACCESSION:CF279238	c1080	22.2	0.8	27	1	N89936	ACCESSION:N89936
c1008	23	0.8	23	1	CF297943	ACCESSION:CF297943	c1081	22.2	0.8	27	1	CL654516	ACCESSION:CL654516
c1009	23	0.8	23	1	CF310501	ACCESSION:CF310501	c1082	22	0.8	22	1	AJ747407	ACCESSION:AJ747407
c1010	23	0.8	23	1	CF319212	ACCESSION:CF319212	c1083	22	0.8	22	1	CF299342	ACCESSION:CF299342
c1011	23	0.8	23	1	CF322953	ACCESSION:CF322953	c1084	22	0.8	22	1	CF300133	ACCESSION:CF300133
c1012	23	0.8	23	1	CF329042	ACCESSION:CF329042	c1085	22	0.8	22	1	CF310366	ACCESSION:CF310366
c1013	23	0.8	23	1	CF334657	ACCESSION:CF334657	c1086	22	0.8	22	1	CF311269	ACCESSION:CF311269
c1014	23	0.8	23	1	CN545940	ACCESSION:CN545940	c1087	22	0.8	22	1	CF311713	ACCESSION:CF311713
c1015	23	0.8	23	1	CN546520	ACCESSION:CN546520	c1088	22	0.8	22	1	CF312498	ACCESSION:CF312498
c1016	23	0.8	23	1	C0577495	ACCESSION:C0577495	c1089	22	0.8	22	1	CF330679	ACCESSION:CF330679
c1017	23	0.8	23	1	CX004980	ACCESSION:CX004980	c1090	22	0.8	22	1	CF333430	ACCESSION:CF333430
c1018	23	0.8	23	1	DR063413	ACCESSION:DR063413	c1091	22	0.8	22	1	CF334781	ACCESSION:CF334781
c1019	23	0.8	23	1	DR072928	ACCESSION:DR072928	c1092	22	0.8	22	1	CF336250	ACCESSION:CF336250
c1020	23	0.8	23	1	DR073135	ACCESSION:DR073135	c1093	22	0.8	22	1	CF337580	ACCESSION:CF337580
c1021	23	0.8	23	1	DR074008	ACCESSION:DR074008	c1094	22	0.8	22	1	CF338524	ACCESSION:CF338524
c1022	23	0.8	23	1	A2309219	ACCESSION:A2309219	c1095	22	0.8	22	1	AW332181	ACCESSION:AW332181
c1023	23	0.8	23	1	A2309851	ACCESSION:A2309851	c1096	22	0.8	22	1	AW332399	ACCESSION:AW332399
c1024	23	0.8	23	1	A2312314	ACCESSION:A2312314	c1097	22	0.8	22	1	CN545550	ACCESSION:CN545550
c1025	23	0.8	23	1	A2313922	ACCESSION:A2313922	c1098	22	0.8	22	1	DN955212	ACCESSION:DN955212
c1026	23	0.8	23	1	A2351354	ACCESSION:A2351354	c1099	22	0.8	22	1	DN955228	ACCESSION:DN955228
c1027	23	0.8	23	1	A2357645	ACCESSION:A2357645	c1100	22	0.8	22	1	DR063422	ACCESSION:DR063422
c1028	23	0.8	23	1	A2419236	ACCESSION:A2419236	c1101	22	0.8	22	1	DR072980	ACCESSION:DR072980
c1029	23	0.8	23	1	A2461220	ACCESSION:A2461220	c1102	22	0.8	22	1	DR072989	ACCESSION:DR072989
c1030	23	0.8	23	1	A2465327	ACCESSION:A2465327	c1103	22	0.8	22	1	DR073101	ACCESSION:DR073101
c1031	23	0.8	23	1	A2481702	ACCESSION:A2481702	c1104	22	0.8	22	1	DR073127	ACCESSION:DR073127
c1032	23	0.8	23	1	A2588254	ACCESSION:A2588254	c1105	22	0.8	22	1	DR073458	ACCESSION:DR073458
c1033	23	0.8	23	1	A2593340	ACCESSION:A2593340	c1106	22	0.8	22	1	DR074014	ACCESSION:DR074014
c1034	23	0.8	23	1	A2610785	ACCESSION:A2610785	c1107	22	0.8	22	1	AZ310066	ACCESSION:AZ310066
c1035	23	0.8	23	1	A2647637	ACCESSION:A2647637	c1108	22	0.8	22	1	AZ351527	ACCESSION:AZ351527
c1036	23	0.8	23	1	A2654903	ACCESSION:A2654903	c1109	22	0.8	22	1	AZ357630	ACCESSION:AZ357630
c1037	23	0.8	23	1	A2778751	ACCESSION:A2778751	c1110	22	0.8	22	1	AZ388103	ACCESSION:AZ388103
c1038	23	0.8	23	1	A2787184	ACCESSION:A2787184	c1111	22	0.8	22	1	AZ401908	ACCESSION:AZ401908
c1039	23	0.8	23	1	AZ792751	ACCESSION:AZ792751	c1112	22	0.8	22	1	AZ424307	ACCESSION:AZ424307
c1040	23	0.8	23	1	AZ859570	ACCESSION:AZ859570	c1113	22	0.8	22	1	AZ428818	ACCESSION:AZ428818
c1041	23	0.8	23	1	AZ939608	ACCESSION:AZ939608	c1114	22	0.8	22	1	AZ459654	ACCESSION:AZ459654
c1042	23	0.8	23	1	BH000534	ACCESSION:BH000534	c1115	22	0.8	22	1	AZ463503	ACCESSION:AZ463503
c1043	23	0.8	23	1	DUR30086	ACCESSION:DUR30086	c1116	22	0.8	22	1	AZ463652	ACCESSION:AZ463652
c1044	23	0.8	23	1	DUR34017	ACCESSION:DUR34017	c1117	22	0.8	22	1	AZ582403	ACCESSION:AZ582403
c1045	23	0.8	23	1	DX071679	ACCESSION:DX071679	c1118	22	0.8	22	1	AZ607658	ACCESSION:AZ607658
c1046	23	0.8	23	1	TA151C02Q	ACCESSION:TA151C02Q	c1119	22	0.8	22	1	AZ654691	ACCESSION:AZ654691
c1047	23	0.8	23	1	TA274B03P	ACCESSION:TA274B03P	c1120	22	0.8	22	1	AZ760533	ACCESSION:AZ760533
c1048	23	0.8	23	1	TA353A10P	ACCESSION:TA353A10P	c1121	22	0.8	22	1	AZ779844	ACCESSION:AZ779844
c1049	23	0.8	24	1	AZ786257	ACCESSION:AZ786257	c1122	22	0.8	22	1	AZ785019	ACCESSION:AZ785019
c1050	23	0.8	25	1	CF301712	ACCESSION:CF301712	c1123	22	0.8	22	1	AZ787098	ACCESSION:AZ787098
c1051	23	0.8	25	1	AZ386891	ACCESSION:AZ386891	c1124	22	0.8	22	1	AZ787606	ACCESSION:AZ787606
c1052	23	0.8	25	1	AZ832800	ACCESSION:AZ832800	c1125	22	0.8	22	1	AZ792704	ACCESSION:AZ792704
c1053	23	0.8	26	1	BQ583199	ACCESSION:BQ583199	c1126	22	0.8	22	1	AZ810674	ACCESSION:AZ810674
c1054	23	0.8	26	1	R26779	ACCESSION:R26779	c1127	22	0.8	22	1	AZ820439	ACCESSION:AZ820439
c1055	23	0.8	27	1	N29432	ACCESSION:N29432	c1128	22	0.8	22	1	AZ841661	ACCESSION:AZ841661

c1129	22	0.8	22	1	AZ843514	ACCSSION:AZ843514	1202	21	0.8	21	1	CF338057	ACCSSION:CF338057
c1130	22	0.8	22	1	AZ946102	ACCSSION:AZ946102	c1203	21	0.8	21	1	CF338522	ACCSSION:CF338522
c1131	22	0.8	22	1	DUB34428	ACCSSION:DUB34428	c1204	21	0.8	21	1	CN546489	ACCSSION:CN546489
c1132	22	0.8	22	1	DUB35320	ACCSSION:DUB35320	c1205	21	0.8	21	1	CN546504	ACCSSION:CN546504
c1133	22	0.8	22	1	DX033920	ACCSSION:DX033920	c1206	21	0.8	21	1	CN546595	ACCSSION:CN546595
c1134	22	0.8	22	1	DX046124	ACCSSION:DX046124	c1207	21	0.8	21	1	CO779794	ACCSSION:CO779794
c1135	22	0.8	22	1	DX056961	ACCSSION:DX056961	c1208	21	0.8	21	1	DR063419	ACCSSION:DR063419
c1136	22	0.8	22	1	DX069868	ACCSSION:DX069868	c1209	21	0.8	21	1	DR072918	ACCSSION:DR072918
c1137	22	0.8	22	1	DX080494	ACCSSION:DX080494	c1210	21	0.8	21	1	AZ348593	ACCSSION:AZ348593
c1138	22	0.8	22	1	AG194579	ACCSSION:AG194579	c1211	21	0.8	21	1	AZ350611	ACCSSION:AZ350611
c1139	22	0.8	22	1	TA131B09P	ACCSSION:AL464164	c1212	21	0.8	21	1	AZ386711	ACCSSION:AZ386711
c1140	22	0.8	22	1	TA329F10P	ACCSSION:AL492691	c1213	21	0.8	21	1	AZ386794	ACCSSION:AZ386794
c1141	22	0.8	22	1	TA35C12Q	ACCSSION:AL454256	c1214	21	0.8	21	1	AZ389287	ACCSSION:AZ389287
c1142	22	0.8	22	1	TA380A07P	ACCSSION:AL497713	c1215	21	0.8	21	1	AZ389687	ACCSSION:AZ389687
c1143	22	0.8	23	1	CF329694	ACCSSION:CF329694	c1216	21	0.8	21	1	AZ406936	ACCSSION:AZ406936
c1144	22	0.8	23	1	CF332379	ACCSSION:CF332379	c1217	21	0.8	21	1	AZ412739	ACCSSION:AZ412739
c1145	22	0.8	23	1	DT495201	ACCSSION:DT495201	c1218	21	0.8	21	1	AZ412931	ACCSSION:AZ412931
c1146	22	0.8	23	1	AZ425710	ACCSSION:AZ425710	c1219	21	0.8	21	1	AZ415029	ACCSSION:AZ415029
c1147	22	0.8	23	1	AZ801003	ACCSSION:AZ801003	c1220	21	0.8	21	1	AZ465890	ACCSSION:AZ465890
c1148	22	0.8	24	1	CA853764	ACCSSION:CA853764	c1221	21	0.8	21	1	AZ611116	ACCSSION:AZ611116
c1149	22	0.8	24	1	CF312319	ACCSSION:CF312319	c1222	21	0.8	21	1	AZ611423	ACCSSION:AZ611423
c1150	22	0.8	24	1	AZ812579	ACCSSION:AZ812579	c1223	21	0.8	21	1	AZ615628	ACCSSION:AZ615628
c1151	22	0.8	25	1	N59260	ACCSSION:N59260	c1224	21	0.8	21	1	AZ627843	ACCSSION:AZ627843
c1152	22	0.8	25	1	CZ914626	ACCSSION:CZ914626	c1225	21	0.8	21	1	AZ627845	ACCSSION:AZ627845
c1153	22	0.8	25	1	CZ916641	ACCSSION:CZ916641	c1226	21	0.8	21	1	AZ657727	ACCSSION:AZ657727
c1154	22	0.8	25	1	TA154D03P	ACCSSION:AL472971	c1227	21	0.8	21	1	AZ766552	ACCSSION:AZ766552
c1155	22	0.8	27	1	AM046273	ACCSSION:AM046273	c1228	21	0.8	21	1	AZ769976	ACCSSION:AZ769976
c1156	22	0.8	27	1	CZ914111	ACCSSION:CZ914111	c1229	21	0.8	21	1	AZ793486	ACCSSION:AZ793486
c1157	21.8	0.8	25	1	CF319499	ACCSSION:CF319499	c1230	21	0.8	21	1	AZ799327	ACCSSION:AZ799327
c1158	21.8	0.8	25	1	AW249476	ACCSSION:AW249476	c1231	21	0.8	21	1	AZ810054	ACCSSION:AZ810054
c1159	21.8	0.8	25	1	DN954014	ACCSSION:DN954014	c1232	21	0.8	21	1	AZ815424	ACCSSION:AZ815424
c1160	21.8	0.8	25	1	AZ330737	ACCSSION:AZ330737	c1233	21	0.8	21	1	AZ819181	ACCSSION:AZ819181
c1161	21.8	0.8	25	1	AZ442170	ACCSSION:AZ442170	c1234	21	0.8	21	1	AZ832198	ACCSSION:AZ832198
c1162	21.8	0.8	25	1	DX053323	ACCSSION:DX053323	c1235	21	0.8	21	1	AZ843603	ACCSSION:AZ843603
c1163	21.8	0.8	26	1	CF337311	ACCSSION:CF337311	c1236	21	0.8	21	1	AZ960063	ACCSSION:AZ960063
c1164	21.4	0.8	23	1	CF334077	ACCSSION:CF334077	c1237	21	0.8	21	1	BH000837	ACCSSION:BH000837
c1165	21.4	0.8	23	1	DR072900	ACCSSION:DR072900	c1238	21	0.8	21	1	DUB28985	ACCSSION:DUB28985
c1166	21.4	0.8	23	1	DT501689	ACCSSION:DT501689	c1239	21	0.8	21	1	DUB30099	ACCSSION:DUB30099
c1167	21.4	0.8	23	1	AZ382013	ACCSSION:AZ382013	c1240	21	0.8	21	1	DUB32906	ACCSSION:DUB32906
c1168	21.4	0.8	23	1	AZ486853	ACCSSION:AZ486853	c1241	21	0.8	21	1	DUB34573	ACCSSION:DUB34573
c1169	21.4	0.8	23	1	AZ627841	ACCSSION:AZ627841	c1242	21	0.8	21	1	DUB35098	ACCSSION:DUB35098
c1170	21.4	0.8	23	1	AZ645254	ACCSSION:AZ645254	c1243	21	0.8	21	1	DX046130	ACCSSION:DX046130
c1171	21.4	0.8	23	1	CL693171	ACCSSION:CL693171	c1244	21	0.8	21	1	DX050095	ACCSSION:DX050095
c1172	21.4	0.8	23	1	DUB28758	ACCSSION:DUB28758	c1245	21	0.8	21	1	DX056929	ACCSSION:DX056929
c1173	21.4	0.8	23	1	TA55C06P	ACCSSION:AL455778	c1246	21	0.8	21	1	DX059939	ACCSSION:DX059939
c1174	21.4	0.8	24	1	CD743368	ACCSSION:CD743368	c1247	21	0.8	21	1	DX075742	ACCSSION:DX075742
c1175	21.4	0.8	24	1	CF292725	ACCSSION:CF292725	c1248	21	0.8	21	1	DX082155	ACCSSION:DX082155
c1176	21.4	0.8	24	1	AZ404871	ACCSSION:AZ404871	c1249	21	0.8	21	1	DX082624	ACCSSION:DX082624
c1177	21.4	0.8	24	1	AZ486788	ACCSSION:AZ486788	c1250	21	0.8	22	1	AL038477	ACCSSION:AL038477
c1178	21.4	0.8	25	1	AU265663	ACCSSION:AU265663	c1251	21	0.8	22	1	CF282024	ACCSSION:CF282024
c1179	21.4	0.8	25	1	AV737092	ACCSSION:AV737092	c1252	21	0.8	22	1	CO778290	ACCSSION:CO778290
c1180	21.4	0.8	25	1	CG726337	ACCSSION:CG726337	c1253	21	0.8	22	1	AZ304806	ACCSSION:AZ304806
c1181	21.4	0.8	26	1	AG194089	ACCSSION:AG194089	c1254	21	0.8	22	1	AZ374487	ACCSSION:AZ374487
c1182	21.2	0.8	26	1	AM043942	ACCSSION:AM043942	c1255	21	0.8	22	1	AZ505769	ACCSSION:AZ505769
c1183	21.2	0.8	26	1	CF280688	ACCSSION:CF280688	c1256	21	0.8	22	1	AZ823875	ACCSSION:AZ823875
c1184	21.2	0.8	26	1	AW333508	ACCSSION:AW333508	c1257	21	0.8	23	1	AL048776	ACCSSION:AL048776
c1185	21.2	0.8	26	1	AZ358846	ACCSSION:AZ358846	c1258	21	0.8	23	1	DT503381	ACCSSION:DT503381
c1186	21.2	0.8	26	1	CZ917639	ACCSSION:CZ917639	c1259	21	0.8	26	1	AL037096	ACCSSION:AL037096
c1187	21	0.8	21	1	AJ658282	ACCSSION:AJ658282	c1260	21	0.8	26	1	TA321G11P	ACCSSION:AL492371
c1188	21	0.8	21	1	AL666203	ACCSSION:AL666203	c1261	20.8	0.8	24	1	AZ626101	ACCSSION:AZ626101
c1189	21	0.8	21	1	AL048777	ACCSSION:AL048777	c1262	20.8	0.8	24	1	AZ627850	ACCSSION:AZ627850
c1190	21	0.8	21	1	AM047262	ACCSSION:AM047262	c1263	20.8	0.8	24	1	CL693181	ACCSSION:CL693181
c1191	21	0.8	21	1	CF282216	ACCSSION:CF282216	c1264	20.8	0.8	24	1	DUB29360	ACCSSION:DUB29360
c1192	21	0.8	21	1	CF292703	ACCSSION:CF292703	c1265	20.8	0.8	25	1	AZ476141	ACCSSION:AZ476141
c1193	21	0.8	21	1	CF295642	ACCSSION:CF295642	c1266	20.8	0.8	25	1	CZ910207	ACCSSION:CZ910207
c1194	21	0.8	21	1	CF295642	ACCSSION:CF295642	c1267	20.8	0.8	25	1	CZ917081	ACCSSION:CZ917081
c1195	21	0.8	21	1	CF298322	ACCSSION:CF298322	c1268	20.8	0.8	26	1	AZ437459	ACCSSION:AZ437459
c1196	21	0.8	21	1	CF300809	ACCSSION:CF300809	c1269	20.4	0.7	22	1	CF298427	ACCSSION:CF298427
c1197	21	0.8	21	1	CF312715	ACCSSION:CF312715	c1270	20.4	0.7	22	1	DT494457	ACCSSION:DT494457
c1198	21	0.8	21	1	CF316073	ACCSSION:CF316073	c1271	20.4	0.7	22	1	DT497428	ACCSSION:DT497428
c1199	21	0.8	21	1	CF326952	ACCSSION:CF326952	c1272	20.4	0.7	22	1	DT502811	ACCSSION:DT502811
c1200	21	0.8	21	1	CF327391	ACCSSION:CF327391	c1273	20.4	0.7	22	1	BH000233	ACCSSION:BH000233
c1201	21	0.8	21	1	CF332956	ACCSSION:CF332956	c1274	20.4	0.7	22	1	DUB35072	ACCSSION:DUB35072

1275	20.4	0.7	22	1	DX060105	ACCESSION:DX060105	1348	20	0.7	20	1	AZ650271	ACCESSION:AZ650271
1276	20.4	0.7	22	1	TX03G05P	ACCESSION:AL497383	1349	20	0.7	20	1	AZ760838	ACCESSION:AZ760838
1277	20.4	0.7	23	1	AL038397	ACCESSION:AL038397	1350	20	0.7	20	1	AZ764504	ACCESSION:AZ764504
1278	20.4	0.7	23	1	AL038592	ACCESSION:AL038592	c1351	20	0.7	20	1	AZ765211	ACCESSION:AZ765211
1279	20.4	0.7	23	1	AL038609	ACCESSION:AL038609	1352	20	0.7	20	1	AZ772091	ACCESSION:AZ772091
1280	20.4	0.7	23	1	AL038688	ACCESSION:AL038688	c1353	20	0.7	20	1	AZ779425	ACCESSION:AZ779425
c1281	20.4	0.7	23	1	BX559898	ACCESSION:BX559898	1354	20	0.7	20	1	AZ784041	ACCESSION:AZ784041
c1282	20.4	0.7	23	1	CF279593	ACCESSION:CF279593	c1355	20	0.7	20	1	AZ793467	ACCESSION:AZ793467
1283	20.4	0.7	23	1	DT496947	ACCESSION:DT496947	c1356	20	0.7	20	1	AZ798529	ACCESSION:AZ798529
1284	20.4	0.7	24	1	AL048765	ACCESSION:AL048765	1357	20	0.7	20	1	AZ805163	ACCESSION:AZ805163
1285	20.4	0.7	24	1	CF326993	ACCESSION:CF326993	1358	20	0.7	20	1	AZ806521	ACCESSION:AZ806521
1286	20.4	0.7	24	1	DT496307	ACCESSION:DT496307	1359	20	0.7	20	1	AZ806585	ACCESSION:AZ806585
c1287	20.4	0.7	25	1	CF310471	ACCESSION:CF310471	1360	20	0.7	20	1	AZ809306	ACCESSION:AZ809306
1288	20.4	0.7	25	1	DX046299	ACCESSION:DX046299	1361	20	0.7	20	1	AZ810986	ACCESSION:AZ810986
c1289	20.2	0.7	25	1	CF300714	ACCESSION:CF300714	1362	20	0.7	20	1	AZ813908	ACCESSION:AZ813908
1290	20.2	0.7	25	1	A2427752	ACCESSION:A2427752	1363	20	0.7	20	1	AZ817323	ACCESSION:AZ817323
1291	20.2	0.7	25	1	AZ867155	ACCESSION:AZ867155	1364	20	0.7	20	1	AZ817414	ACCESSION:AZ817414
1292	20.2	0.7	25	1	TA12F02Q	ACCESSION:AL451366	1365	20	0.7	20	1	AZ817467	ACCESSION:AZ817467
c1293	20	0.7	20	1	AJ666402	ACCESSION:AJ666402	c1366	20	0.7	20	1	AZ817608	ACCESSION:AZ817608
1294	20	0.7	20	1	AL038427	ACCESSION:AL038427	c1367	20	0.7	20	1	AZ818489	ACCESSION:AZ818489
1295	20	0.7	20	1	AL038429	ACCESSION:AL038429	c1368	20	0.7	20	1	AZ818816	ACCESSION:AZ818816
1296	20	0.7	20	1	AL038570	ACCESSION:AL038570	1369	20	0.7	20	1	AZ837491	ACCESSION:AZ837491
1297	20	0.7	20	1	AL038750	ACCESSION:AL038750	1370	20	0.7	20	1	AZ841342	ACCESSION:AZ841342
1298	20	0.7	20	1	CF280913	ACCESSION:CF280913	c1371	20	0.7	20	1	AZ841558	ACCESSION:AZ841558
1299	20	0.7	20	1	CF282035	ACCESSION:CF282035	1372	20	0.7	20	1	AZ858052	ACCESSION:AZ858052
1300	20	0.7	20	1	CF282414	ACCESSION:CF282414	1373	20	0.7	20	1	AZ858419	ACCESSION:AZ858419
c1301	20	0.7	20	1	CF299822	ACCESSION:CF299822	1374	20	0.7	20	1	AZ936914	ACCESSION:AZ936914
1302	20	0.7	20	1	CF301720	ACCESSION:CF301720	c1375	20	0.7	20	1	AZ949180	ACCESSION:AZ949180
1303	20	0.7	20	1	CF302027	ACCESSION:CF302027	c1376	20	0.7	20	1	AZ963973	ACCESSION:AZ963973
1304	20	0.7	20	1	CF310604	ACCESSION:CF310604	1377	20	0.7	20	1	CF979138	ACCESSION:CF979138
1305	20	0.7	20	1	CF313067	ACCESSION:CF313067	c1378	20	0.7	20	1	DU834188	ACCESSION:DU834188
c1306	20	0.7	20	1	CF313569	ACCESSION:CF313569	1379	20	0.7	20	1	DU835125	ACCESSION:DU835125
1307	20	0.7	20	1	CF319133	ACCESSION:CF319133	1380	20	0.7	20	1	DX045751	ACCESSION:DX045751
1308	20	0.7	20	1	CF321721	ACCESSION:CF321721	1381	20	0.7	20	1	DX055580	ACCESSION:DX055580
1309	20	0.7	20	1	CF328565	ACCESSION:CF328565	c1382	20	0.7	20	1	DX070282	ACCESSION:DX070282
c1310	20	0.7	20	1	CF333173	ACCESSION:CF333173	1383	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1311	20	0.7	20	1	CF334170	ACCESSION:CF334170	c1384	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1312	20	0.7	20	1	CF336525	ACCESSION:CF336525	1385	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1313	20	0.7	20	1	CF337494	ACCESSION:CF337494	c1386	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1314	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1387	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1315	20	0.7	20	1	CF334823	ACCESSION:CF334823	1388	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1316	20	0.7	20	1	CF334823	ACCESSION:CF334823	1389	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1317	20	0.7	20	1	CF334823	ACCESSION:CF334823	1390	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1318	20	0.7	20	1	CF334823	ACCESSION:CF334823	1391	20	0.7	21	1	DX070282	ACCESSION:DX070282
1319	20	0.7	20	1	CF334823	ACCESSION:CF334823	1392	20	0.7	21	1	DX070282	ACCESSION:DX070282
1320	20	0.7	20	1	CF334823	ACCESSION:CF334823	1393	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1321	20	0.7	20	1	CF334823	ACCESSION:CF334823	1394	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1322	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1395	20	0.7	21	1	DX070282	ACCESSION:DX070282
1323	20	0.7	20	1	CF334823	ACCESSION:CF334823	1396	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1324	20	0.7	20	1	CF334823	ACCESSION:CF334823	1397	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1325	20	0.7	20	1	CF334823	ACCESSION:CF334823	1398	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1326	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1399	20	0.7	21	1	DX070282	ACCESSION:DX070282
1327	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1400	20	0.7	21	1	DX070282	ACCESSION:DX070282
1328	20	0.7	20	1	CF334823	ACCESSION:CF334823	1401	20	0.7	21	1	DX070282	ACCESSION:DX070282
1329	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1402	20	0.7	21	1	DX070282	ACCESSION:DX070282
1330	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1403	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1331	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1404	20	0.7	21	1	DX070282	ACCESSION:DX070282
1332	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1405	20	0.7	21	1	DX070282	ACCESSION:DX070282
1333	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1406	20	0.7	21	1	DX070282	ACCESSION:DX070282
1334	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1407	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1335	20	0.7	20	1	CF334823	ACCESSION:CF334823	1408	20	0.7	21	1	DX070282	ACCESSION:DX070282
1336	20	0.7	20	1	CF334823	ACCESSION:CF334823	1409	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1337	20	0.7	20	1	CF334823	ACCESSION:CF334823	1410	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1338	20	0.7	20	1	CF334823	ACCESSION:CF334823	1411	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1339	20	0.7	20	1	CF334823	ACCESSION:CF334823	1412	20	0.7	21	1	DX070282	ACCESSION:DX070282
1340	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1413	20	0.7	21	1	DX070282	ACCESSION:DX070282
1341	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1414	20	0.7	21	1	DX070282	ACCESSION:DX070282
1342	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1415	20	0.7	21	1	DX070282	ACCESSION:DX070282
1343	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1416	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1344	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1417	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1345	20	0.7	20	1	CF334823	ACCESSION:CF334823	1418	20	0.7	21	1	DX070282	ACCESSION:DX070282
1346	20	0.7	20	1	CF334823	ACCESSION:CF334823	c1419	20	0.7	21	1	DX070282	ACCESSION:DX070282
c1347	20	0.7	20	1	CF334823	ACCESSION:CF334823	1420	20	0.7	21	1	DX070282	ACCESSION:DX070282

C1421	19.4	0.7	21	1	ACCSSION:AZ792613	1494	19	0.7	19	1	AZ450180	ACCSSION:AZ450180
1422	19.4	0.7	21	1	ACCSSION:AZ822825	C1495	19	0.7	19	1	AZ453930	ACCSSION:AZ453930
1423	19.4	0.7	21	1	ACCSSION:AZ833429	1496	19	0.7	19	1	AZ460906	ACCSSION:AZ460906
1424	19.4	0.7	21	1	ACCSSION:CL693165	C1497	19	0.7	19	1	AZ471494	ACCSSION:AZ471494
C1425	19.4	0.7	21	1	ACCSSION:DU828988	C1498	19	0.7	19	1	AZ476576	ACCSSION:AZ476576
1426	19.4	0.7	22	1	ACCSSION:AL038142	C1499	19	0.7	19	1	AZ486786	ACCSSION:AZ486786
C1427	19.4	0.7	22	1	ACCSSION:BX556059	C1500	19	0.7	19	1	AZ490852	ACCSSION:AZ490852
1428	19.4	0.7	22	1	ACCSSION:CL693160	1501	19	0.7	19	1	AZ508040	ACCSSION:AZ508040
C1429	19.4	0.7	23	1	ACCSSION:AJ666332	1502	19	0.7	19	1	AZ579119	ACCSSION:AZ579119
1430	19.4	0.7	23	1	ACCSSION:AL048745	1503	19	0.7	19	1	AZ583970	ACCSSION:AZ583970
C1431	19.4	0.7	23	1	ACCSSION:CF333801	1504	19	0.7	19	1	AZ585865	ACCSSION:AZ585865
1432	19.2	0.7	24	1	ACCSSION:AM043222	1505	19	0.7	19	1	AZ593210	ACCSSION:AZ593210
C1433	19.2	0.7	24	1	ACCSSION:AZ304870	C1506	19	0.7	19	1	AZ616154	ACCSSION:AZ616154
1434	19.2	0.7	24	1	ACCSSION:AZ309553	C1507	19	0.7	19	1	AZ627844	ACCSSION:AZ627844
1435	19.2	0.7	24	1	ACCSSION:AZ448207	1508	19	0.7	19	1	AZ631701	ACCSSION:AZ631701
C1436	19.2	0.7	24	1	ACCSSION:AZ814559	1509	19	0.7	19	1	AZ633821	ACCSSION:AZ633821
C1437	19.2	0.7	24	1	ACCSSION:CL676551	1510	19	0.7	19	1	AZ643659	ACCSSION:AZ643659
C1438	19	0.7	19	1	ACCSSION:AJ668179	C1511	19	0.7	19	1	AZ644698	ACCSSION:AZ644698
C1439	19	0.7	19	1	ACCSSION:AJ669138	1512	19	0.7	19	1	AZ648335	ACCSSION:AZ648335
1440	19	0.7	19	1	ACCSSION:BQ588729	C1513	19	0.7	19	1	AZ649888	ACCSSION:AZ649888
C1441	19	0.7	19	1	ACCSSION:CB174047	1514	19	0.7	19	1	AZ764497	ACCSSION:AZ764497
C1442	19	0.7	19	1	ACCSSION:CF279008	1515	19	0.7	19	1	AZ764522	ACCSSION:AZ764522
C1443	19	0.7	19	1	ACCSSION:CF291089	1516	19	0.7	19	1	AZ764534	ACCSSION:AZ764534
1444	19	0.7	19	1	ACCSSION:CF291090	1517	19	0.7	19	1	AZ770387	ACCSSION:AZ770387
C1445	19	0.7	19	1	ACCSSION:CF295598	1518	19	0.7	19	1	AZ778858	ACCSSION:AZ778858
C1446	19	0.7	19	1	ACCSSION:CF302327	1519	19	0.7	19	1	AZ779901	ACCSSION:AZ779901
C1447	19	0.7	19	1	ACCSSION:CF304589	1520	19	0.7	19	1	AZ781876	ACCSSION:AZ781876
C1448	19	0.7	19	1	ACCSSION:CF309801	C1521	19	0.7	19	1	AZ787634	ACCSSION:AZ787634
1449	19	0.7	19	1	ACCSSION:CF309943	1522	19	0.7	19	1	AZ788058	ACCSSION:AZ788058
C1450	19	0.7	19	1	ACCSSION:CF311496	C1523	19	0.7	19	1	AZ789590	ACCSSION:AZ789590
C1451	19	0.7	19	1	ACCSSION:CF311513	1524	19	0.7	19	1	AZ792713	ACCSSION:AZ792713
1452	19	0.7	19	1	ACCSSION:CF312403	1525	19	0.7	19	1	AZ841581	ACCSSION:AZ841581
C1453	19	0.7	19	1	ACCSSION:CF315299	1526	19	0.7	19	1	AZ861896	ACCSSION:AZ861896
C1454	19	0.7	19	1	ACCSSION:CF316480	C1527	19	0.7	19	1	AZ936798	ACCSSION:AZ936798
1455	19	0.7	19	1	ACCSSION:CF318788	1528	19	0.7	19	1	AZ985501	ACCSSION:AZ985501
1456	19	0.7	19	1	ACCSSION:CF329986	1529	19	0.7	19	1	BH000498	ACCSSION:BH000498
C1457	19	0.7	19	1	ACCSSION:CF332063	1530	19	0.7	19	1	CL680736	ACCSSION:CL680736
1458	19	0.7	19	1	ACCSSION:CF333507	1531	19	0.7	19	1	CL685439	ACCSSION:CL685439
1459	19	0.7	19	1	ACCSSION:CF333753	1532	19	0.7	19	1	CL693186	ACCSSION:CL693186
C1460	19	0.7	19	1	ACCSSION:CF334014	1533	19	0.7	19	1	CL693191	ACCSSION:CL693191
C1461	19	0.7	19	1	ACCSSION:CN545602	1534	19	0.7	19	1	AL038507	ACCSSION:AL038507
C1462	19	0.7	19	1	ACCSSION:CN545922	1535	19	0.7	19	1	AL038576	ACCSSION:AL038576
C1463	19	0.7	19	1	ACCSSION:CN545964	1536	19	0.7	19	1	AL038754	ACCSSION:AL038754
C1464	19	0.7	19	1	ACCSSION:CN546303	1537	19	0.7	19	1	AL038845	ACCSSION:AL038845
1465	19	0.7	19	1	ACCSSION:CN546303	1538	19	0.7	19	1	AL587759	ACCSSION:AL587759
C1466	19	0.7	19	1	ACCSSION:CN546303	1539	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1467	19	0.7	19	1	ACCSSION:CN546303	1540	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1468	19	0.7	19	1	ACCSSION:CN546303	1541	19	0.7	19	1	CF318278	ACCSSION:CF318278
1469	19	0.7	19	1	ACCSSION:CN546303	1542	19	0.7	19	1	CF318278	ACCSSION:CF318278
1470	19	0.7	19	1	ACCSSION:CN546303	1543	19	0.7	19	1	CF318278	ACCSSION:CF318278
1471	19	0.7	19	1	ACCSSION:CN546303	1544	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1472	19	0.7	19	1	ACCSSION:CN546303	1545	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1473	19	0.7	19	1	ACCSSION:CN546303	1546	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1474	19	0.7	19	1	ACCSSION:CN546303	1547	19	0.7	19	1	CF318278	ACCSSION:CF318278
1475	19	0.7	19	1	ACCSSION:CN546303	1548	19	0.7	19	1	CF318278	ACCSSION:CF318278
1476	19	0.7	19	1	ACCSSION:CN546303	1549	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1477	19	0.7	19	1	ACCSSION:CN546303	1550	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1478	19	0.7	19	1	ACCSSION:CN546303	1551	19	0.7	19	1	CF318278	ACCSSION:CF318278
1479	19	0.7	19	1	ACCSSION:CN546303	1552	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1480	19	0.7	19	1	ACCSSION:CN546303	1553	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1481	19	0.7	19	1	ACCSSION:CN546303	1554	19	0.7	19	1	CF318278	ACCSSION:CF318278
1482	19	0.7	19	1	ACCSSION:CN546303	1555	19	0.7	19	1	CF318278	ACCSSION:CF318278
1483	19	0.7	19	1	ACCSSION:CN546303	1556	19	0.7	19	1	CF318278	ACCSSION:CF318278
1484	19	0.7	19	1	ACCSSION:CN546303	1557	19	0.7	19	1	CF318278	ACCSSION:CF318278
1485	19	0.7	19	1	ACCSSION:CN546303	1558	19	0.7	19	1	CF318278	ACCSSION:CF318278
1486	19	0.7	19	1	ACCSSION:CN546303	1559	19	0.7	19	1	CF318278	ACCSSION:CF318278
1487	19	0.7	19	1	ACCSSION:CN546303	1560	19	0.7	19	1	CF318278	ACCSSION:CF318278
1488	19	0.7	19	1	ACCSSION:CN546303	1561	19	0.7	19	1	CF318278	ACCSSION:CF318278
1489	19	0.7	19	1	ACCSSION:CN546303	1562	19	0.7	19	1	CF318278	ACCSSION:CF318278
1490	19	0.7	19	1	ACCSSION:CN546303	1563	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1491	19	0.7	19	1	ACCSSION:CN546303	1564	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1492	19	0.7	19	1	ACCSSION:CN546303	1565	19	0.7	19	1	CF318278	ACCSSION:CF318278
C1493	19	0.7	19	1	ACCSSION:CN546303	1566	19	0.7	19	1	CF318278	ACCSSION:CF318278

1567	18.4	0.7	20	1	AZ579122	ACCESION:AZ579122	c1640	17.4	0.6	19	1	AZ645841	ACCESION:AZ645841
c1568	18.4	0.7	20	1	A2645312	ACCESION:A2645312	1641	17.4	0.6	19	1	AZ650252	ACCESION:A2650252
1569	18.4	0.7	20	1	A8221905	ACCESION:A8221905	c1642	17.4	0.6	19	1	AZ654747	ACCESION:A2654747
1570	18.4	0.7	20	1	A949997	ACCESION:A949997	1643	17.4	0.6	19	1	CL693177	ACCESION:CL693177
c1571	18.4	0.7	20	1	CL680297	ACCESION:CL680297	c1644	17.4	0.6	20	1	CF319428	ACCESION:CF319428
c1572	18.4	0.7	20	1	DX071064	ACCESION:DX071064	c1645	17.4	0.6	20	1	CF333052	ACCESION:CF333052
1573	18.4	0.7	20	1	DX071075	ACCESION:DX071075	c1646	17.4	0.6	20	1	DY228778	ACCESION:DY228778
c1574	18.4	0.7	21	1	BX558161	ACCESION:BX558161	c1647	17.4	0.6	21	1	ACCESSION:AZ308846	ACCESION:AZ308846
c1575	18.4	0.7	21	1	CF319625	ACCESION:CF319625	c1648	17	0.6	17	1	BQ590128	ACCESION:BQ590128
c1576	18.4	0.7	21	1	CF333393	ACCESION:CF333393	1649	17	0.6	17	1	BQ590687	ACCESION:BQ590687
c1577	18.4	0.7	21	1	DU829016	ACCESION:DU829016	c1650	17	0.6	17	1	BQ591177	ACCESION:BQ591177
1578	18.4	0.7	22	1	AL048750	ACCESION:AL048750	c1651	17	0.6	17	1	CF290854	ACCESION:CF290854
c1579	18.4	0.7	22	1	CT019890	ACCESION:CT019890	c1652	17	0.6	17	1	CF294668	ACCESION:CF294668
1580	18	0.7	18	1	AL038692	ACCESION:AL038692	c1653	17	0.6	17	1	CF295988	ACCESION:CF295988
c1581	18	0.7	18	1	BQ582676	ACCESION:BQ582676	c1654	17	0.6	17	1	CF298589	ACCESION:CF298589
c1582	18	0.7	18	1	BQ590027	ACCESION:BQ590027	c1655	17	0.6	17	1	CF310219	ACCESION:CF310219
c1583	18	0.7	18	1	CF277873	ACCESION:CF277873	c1656	17	0.6	17	1	CF334566	ACCESION:CF334566
c1584	18	0.7	18	1	CF297446	ACCESION:CF297446	c1657	17	0.6	17	1	CF336950	ACCESION:CF336950
c1585	18	0.7	18	1	CF299027	ACCESION:CF299027	c1658	17	0.6	17	1	CF309551	ACCESION:CF309551
c1586	18	0.7	18	1	CF299674	ACCESION:CF299674	c1659	17	0.6	17	1	CF301057	ACCESION:CF301057
c1587	18	0.7	18	1	CF301151	ACCESION:CF301151	c1660	17	0.6	18	1	CF320046	ACCESION:CF320046
c1588	18	0.7	18	1	CF301325	ACCESION:CF301325	c1661	17	0.6	18	1	CF320418	ACCESION:CF320418
c1589	18	0.7	18	1	CF301760	ACCESION:CF301760	1662	17	0.6	19	1	AZ853220	ACCESION:AZ853220
c1590	18	0.7	18	1	CF302409	ACCESION:CF302409	1663	17	0.6	20	1	CF298207	ACCESION:CF298207
c1591	18	0.7	18	1	DR073142	ACCESION:DR073142	1664	17	0.6	20	1	AZ818055	ACCESION:AZ818055
c1592	18	0.7	18	1	DR074121	ACCESION:DR074121	c1665	17	0.6	21	1	DR065210	ACCESION:DR065210
c1593	18	0.7	19	1	CF293167	ACCESION:CF293167	c1666	17	0.6	21	1	AZ943299	ACCESION:AZ943299
c1594	18	0.7	19	1	CF298396	ACCESION:CF298396	c1667	16.8	0.6	20	1	CF298018	ACCESION:CF298018
c1595	18	0.7	19	1	CF302456	ACCESION:CF302456	c1668	16.8	0.6	20	1	CF300961	ACCESION:CF300961
c1596	18	0.7	19	1	CF309821	ACCESION:CF309821	c1669	16.8	0.6	20	1	CF301101	ACCESION:CF301101
c1597	18	0.7	19	1	CF311778	ACCESION:CF311778	c1670	16.8	0.6	20	1	AW333777	ACCESION:AW333777
c1598	18	0.7	19	1	CF331361	ACCESION:CF331361	1671	16.8	0.6	20	1	DY223532	ACCESION:DY223532
c1599	18	0.7	19	1	CF335293	ACCESION:CF335293	c1672	16.8	0.6	20	1	AZ343730	ACCESION:AZ343730
c1600	18	0.7	19	1	CX002732	ACCESION:CX002732	1673	16.8	0.6	20	1	AZ633741	ACCESION:AZ633741
1601	18	0.7	19	1	AK002732	ACCESION:AK002732	c1674	16.8	0.6	21	1	CF319122	ACCESION:CF319122
1602	18	0.7	19	1	A2345795	ACCESION:A2345795	c1675	16.8	0.6	18	1	AJ725584	ACCESION:AJ725584
1603	18	0.7	19	1	A2650575	ACCESION:A2650575	1676	16.4	0.6	18	1	AL048754	ACCESION:AL048754
c1604	18	0.7	20	1	AJ666275	ACCESION:AJ666275	1677	16.4	0.6	18	1	BM658677	ACCESION:BM658677
c1605	18	0.7	20	1	AJ587727	ACCESION:AJ587727	c1678	16.4	0.6	18	1	CF300456	ACCESION:CF300456
c1606	18	0.7	20	1	CA853586	ACCESION:CA853586	c1679	16.4	0.6	18	1	CF309376	ACCESION:CF309376
c1607	18	0.7	20	1	CF282002	ACCESION:CF282002	c1680	16.4	0.6	18	1	CF329285	ACCESION:CF329285
c1608	18	0.7	20	1	CF320843	ACCESION:CF320843	c1681	16.4	0.6	18	1	CF329484	ACCESION:CF329484
c1609	18	0.7	20	1	A2345856	ACCESION:A2345856	c1682	16.4	0.6	18	1	CF329485	ACCESION:CF329485
c1610	18	0.7	20	1	A2370699	ACCESION:A2370699	1683	16.4	0.6	18	1	CF329485	ACCESION:CF329485
1611	18	0.7	21	1	AL048772	ACCESION:AL048772	1684	16.4	0.6	18	1	CR786637	ACCESION:CR786637
c1612	18	0.7	21	1	DN955603	ACCESION:DN955603	c1685	16.4	0.6	19	1	AJ666205	ACCESION:AJ666205
c1613	18	0.7	21	1	A2610868	ACCESION:A2610868	c1686	16.4	0.6	19	1	CF298472	ACCESION:CF298472
1614	18	0.7	21	1	A2764492	ACCESION:A2764492	c1687	16.4	0.6	19	1	CF326845	ACCESION:CF326845
c1615	18	0.7	22	1	CF328832	ACCESION:CF328832	1688	16.4	0.6	19	1	CF327587	ACCESION:CF327587
1616	18	0.7	22	1	A2843648	ACCESION:A2843648	1689	16.4	0.6	19	1	DT497638	ACCESION:DT497638
1617	18	0.7	22	1	TA231508Q	ACCESION:TA231508Q	1690	16.4	0.6	19	1	AZ360314	ACCESION:AZ360314
c1618	18	0.7	22	1	TR386H07Q	ACCESION:TR386H07Q	c1691	16.4	0.6	19	1	AZ447251	ACCESION:AZ447251
c1619	17.8	0.6	21	1	BX564412	ACCESION:BX564412	c1692	16	0.6	16	1	BQ590166	ACCESION:BQ590166
c1620	17.8	0.6	21	1	CF330439	ACCESION:CF330439	c1693	16	0.6	16	1	BQ590507	ACCESION:BQ590507
c1621	17.8	0.6	21	1	AW248782	ACCESION:AW248782	1694	16	0.6	16	1	BQ592600	ACCESION:BQ592600
1622	17.8	0.6	21	1	DV751812	ACCESION:DV751812	c1695	16	0.6	16	1	BQ592965	ACCESION:BQ592965
c1623	17.8	0.6	21	1	A5597932	ACCESION:A5597932	c1696	16	0.6	16	1	BQ595369	ACCESION:BQ595369
c1624	17.8	0.6	21	1	A2627840	ACCESION:A2627840	1697	16	0.6	16	1	BQ595717	ACCESION:BQ595717
c1625	17.8	0.6	21	1	A647578	ACCESION:A647578	c1698	16	0.6	16	1	CF279325	ACCESION:CF279325
1626	17.8	0.6	21	1	CL693188	ACCESION:CL693188	c1699	16	0.6	16	1	CF296130	ACCESION:CF296130
1627	17.8	0.6	21	1	DU834197	ACCESION:DU834197	c1700	16	0.6	16	1	CF311057	ACCESION:CF311057
c1628	17.8	0.6	22	1	DU831616	ACCESION:DU831616	c1701	16	0.6	16	1	CF314013	ACCESION:CF314013
c1629	17.8	0.6	22	1	DU833993	ACCESION:DU833993	c1702	16	0.6	16	1	CF314377	ACCESION:CF314377
c1630	17.4	0.6	19	1	CF291665	ACCESION:CF291665	c1703	16	0.6	16	1	CF315789	ACCESION:CF315789
c1631	17.4	0.6	19	1	CF291899	ACCESION:CF291899	c1704	16	0.6	16	1	CF316056	ACCESION:CF316056
c1632	17.4	0.6	19	1	CF292072	ACCESION:CF292072	c1705	16	0.6	16	1	CF317718	ACCESION:CF317718
c1633	17.4	0.6	19	1	CF292144	ACCESION:CF292144	c1706	16	0.6	16	1	CF320356	ACCESION:CF320356
1634	17.4	0.6	19	1	CF310688	ACCESION:CF310688	c1707	16	0.6	16	1	CF327722	ACCESION:CF327722
c1635	17.4	0.6	19	1	CF329136	ACCESION:CF329136	c1708	16	0.6	16	1	CF329320	ACCESION:CF329320
c1636	17.4	0.6	19	1	CF334610	ACCESION:CF334610	1709	16	0.6	16	1	CF333386	ACCESION:CF333386
c1637	17.4	0.6	19	1	AW248747	ACCESION:AW248747	1710	16	0.6	16	1	CR786853	ACCESION:CR786853
c1638	17.4	0.6	19	1	A2363907	ACCESION:A2363907	1711	16	0.6	16	1	DT498583	ACCESION:DT498583
c1639	17.4	0.6	19	1	A2513919	ACCESION:A2513919	c1712	16	0.6	17	1	BQ591181	ACCESION:BQ591181

```

c1713      16      0.6      17      1      CF295807      ACCESSION:CF295807
c1714      16      0.6      17      1      CF299639      ACCESSION:CF299639
c1715      16      0.6      17      1      CF302447      ACCESSION:CF302447
c1716      16      0.6      17      1      CF311499      ACCESSION:CF311499
c1717      16      0.6      17      1      CF313013      ACCESSION:CF313013
c1718      16      0.6      17      1      CF319075      ACCESSION:CF319075
c1719      16      0.6      18      1      CF298591      ACCESSION:CF298591
c1720      16      0.6      19      1      CF278272      ACCESSION:CF278272
c1721      16      0.6      19      1      CF308042      ACCESSION:CF308042
c1722      16      0.6      19      1      CF311668      ACCESSION:CF311668
c1723      16      0.6      19      1      AZ764517      ACCESSION:AZ764517
c1724      15.8      0.6      19      1      AJ663023      ACCESSION:AJ663023
c1725      15.8      0.6      19      1      CF298134      ACCESSION:CF298134
c1726      15.8      0.6      19      1      CF300236      ACCESSION:CF300236
c1727      15.8      0.6      19      1      CF309636      ACCESSION:CF309636
c1728      15.8      0.6      19      1      CF309858      ACCESSION:CF309858
c1729      15.8      0.6      19      1      CF329137      ACCESSION:CF329137
c1730      15.8      0.6      19      1      AZ345499      ACCESSION:AZ345499
c1731      15.8      0.6      19      1      AZ509929      ACCESSION:AZ509929
c1732      15.8      0.6      19      1      AZ611602      ACCESSION:AZ611602
c1733      15.8      0.6      19      1      AZ786336      ACCESSION:AZ786336

```

ALIGNMENTS

```

RESULT 1
BY799992      80 bp      mRNA      linear      EST 16-AUG-2005
LOCUS
DEFINITION
BY799992      Homo sapiens eye Homo sapiens cDNA clone
HemBye2033G10_072.abl 5', mRNA sequence.
ACCESSION
BY799992
VERSION
BY799992.1      GI:73472467
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1      (bases 1 to 80)
Choy, K., Wang, C., Ogura, A., Lau, T., Rogers, M., Ikeo, K.,
Gojobori, T., Lam, D. and Pang, C.
Comparative annotation of 15,809 ESTs identified from pooled early
gestation human eyes
Unpublished (2005)
JOURNAL
Contact: Kw Choy
COMMENT
National Institute of Genetics, Center for Information Biology and
DBJ
Yacallil, Mishima, 411-8540, Japan
Tel: 852-2632-3099
Email: richardchoy@cuhk.edu.hk
This sequence is assembled via IDEA. This clone was obtained from
National Institute of Genetics and Chinese University of HongKong.
Location/Qualifiers
1..80
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEmBye2033G10_072.abl"
/tissue_type="eye"
/clone_lib="Homo sapiens eye"

```

FEATURES

```

source
Query Match      2.9%; Score 78.4; DB 1; Length 80;
Best Local Similarity 98.8%; Pred. No. 0.52;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      869      ATCAGTAGATCATAGCAGTCATCGAGATCTTTGGCTGTGGTCTTATCGTACCGAG 928
          |||||
Db      1      ATCAGTAGATCATAGCAGTCATCGAGATCTTTGGCTGTGGTCTTATCGTACCGAG 60
          |||||
QY      929      AAAGACAAAATTCAGTGA 948
          |||||
Db      61      AAAGACAAAATTCAGTGA 80
          |||||

```

RESULT 2

```

AA587192/c
LOCUS
DEFINITION
AA587192      78 bp      mRNA      linear      EST 26-SEP-1997
nm78c02.s1      NCI CGAP Co9 Homo sapiens cDNA clone IMAGE:1089986 3',
similar to gb:S38729 LUPUS KU AUTOANTIGEN PROTEIN P70 (HUMAN);,
mRNA sequence.
ACCESSION
AA587192
VERSION
AA587192.1      GI:2398006
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1      (bases 1 to 78)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1006      Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
1..78
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1089986"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Co9"
/note="Organ: colon; Vector: p773D-PacI; 1st strand cDNA
was prepared from RER+ colon tumor, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is not normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo
(Soares4)."

```

FEATURES

```

source
Query Match      2.7%; Score 73.8; DB 1; Length 78;
Best Local Similarity 97.4%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2633      CCATGGTGATGGTGTAGCCCTCCACCTTGCTGTTCTTTACTTTACTGCTGAATAAAGA 2692
          |||||
Db      78      CCATGGTGATGGTGTAGCCCTCCCTCTTGGCTGTTCTTTACTTTACTGCTGAATAAAGA 19
          |||||
QY      2693      GCCCTAAGTTGTACTA 2709
          |||||
Db      18      GCCCTAAGTTGTACTA 2
          |||||
RESULT 3
AA079243/c
LOCUS
DEFINITION
AA079243      61 bp      mRNA      linear      EST 23-DEC-1997
zm70b11.s1      Stratagene neuroepithelium (#937231) Homo sapiens cDNA
clone IMAGE:530973 3', similar to gb:S38729 LUPUS KU AUTOANTIGEN
PROTEIN P70 (HUMAN);, mRNA sequence.
ACCESSION
AA079243
VERSION
AA079243.1      GI:1618135
KEYWORDS
EST.

```



```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP06361"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      1.8%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 32;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 139 AGACTCGAGACCAAGCTCTCTTCCTCGGAAGGAGGGCGGACCTCGCGTTT 188
      |||||
Db 1 AGACTCGAGACCAAGCTCTCTTCCTCGGAAGGAGGGCGGACCTCGCGTTT 50

RESULT 6
LOCUS AU103751
DEFINITION AU103751 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION HEP06548, mRNA sequence.
VERSION AU103751
KEYWORDS AU103751.1 GI:13553272
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP13405"
/clone_lib="Sugano Homo sapiens cDNA library"

Query Match      1.7%; Score 46.8; DB 1; Length 50;
Best Local Similarity 96.0%; Pred. No. 40;
Matches 48; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CCGTTATCCATTGTGTTGTTTCGCCAGCTAGCGCTGGCTCCCGCTT 55
Db 1 CCGTTATCCATTGTGTTGTTTCGCCAGCTAGCGCTGGCTCCCGCTT 50

RESULT 8
LOCUS T92783/c
DEFINITION T92783
ACCESSION T92783
VERSION T92783.1 GI:724696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 52)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le.M., Le.N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasaki,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

```


[illegible]

RESULT 14
CV732719/c
LOCUS
DEFINITION
FLO--07-F03.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-F03, mRNA sequence.

ACCESSION
CV732719
VERSION
CV732719.1 GI:55438841
KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 46)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..46
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-F03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.4%; Score 37.2; DB 1; Length 46;
Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2702 TTGTACTTAAAAA 1
Db 46 TTATAAAAAA 5

RESULT 15
CF329026/c
LOCUS
DEFINITION
NACL--04-D06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-D06, mRNA sequence.

ACCESSION
CF329026
VERSION
CF329026.1 GI:33806289
KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..37
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match
Best Local Similarity 1.3%; Score 37; DB 1; Length 37;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAAAAA 1
Db 37 CTAAAAA 1

RESULT 16
AL046183/c
LOCUS
DEFINITION
DKF2p434C127.s1 434 (synonym: htes3) Homo sapiens cDNA clone

ACCESSION
AL046183
VERSION
AL046183.1 GI:49682657
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 42)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..42
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p434C127"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site 1: NotI; Site 2: SalI"

Query Match
Best Local Similarity 1.3%; Score 37; DB 1; Length 42;
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTAAAAA 1
Db 41 GTNNNNAAAAA 2

RESULT 17
CF32388/c
LOCUS
DEFINITION
NACL--08-002.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-002, mRNA

sequence.
CF332388
CF332388.1 GI:33812996
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 44)
Song, S.I., Kim, J.K., Kim, Y.-K., Lee, T.H., Shin, Y.C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .44
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="NACL-08-O02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 37; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2707 CTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 44 CTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 18
CV730946/c
LOCUS
DEFINITION
FLO--04-L22.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-L22, mRNA
sequence.
CV730946
CV730946.1 GI:55435629
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 43)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="FLO--04-L22"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36.8; DB 1; Length 43;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2704 GTACTAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 GTAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 19
CF302212/c
LOCUS
DEFINITION
7LEAF--07-IL4.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-IL4, mRNA
sequence.
CF302212
CF302212.1 GI:33673973
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 44)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .44
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="7LEAF--07-IL4"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 36.8; DB 1; Length 44;
Best Local Similarity 95.0%; Pred. No. 1.6e+02;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2704 GTACTAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 GTAGAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 20
CF332152


```

Db      43 TTTAAAAA..... 44 bp mRNA linear EST 18-AUG-2003
CF331239 NACL--07-E14.b1 Rice callus plasmid cDNA library (NACL) Oryza
LOCUS sativa (japonica cultivar-group) cDNA clone NACL--07-E14, mRNA
DEFINITION
sequence.
ACCESSION CF331239.1 GI:33810702
VERSION /mol_type="mRNA"
KEYWORDS /cultivar="Nackdong"
SOURCE /db_xref="taxon:39947"
ORGANISM /clone="NACL--08-K14"
Oryza sativa (japonica cultivar-group) /tissue_type="callus"
Oryza sativa (japonica cultivar-group) /dev_stage="proliferated callus on 2N6 media for 30 days"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 44
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-K14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

FEATURES
source
Query Match 1.3%; Score 36.6; DB 1; Length 44;
Best Local Similarity 90.7%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2701 TTTGTACTAAAAA..... 45 bp mRNA linear EST 05-NOV-2004
LOCUS FLO--03-C10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-C10, mRNA
sequence.
ACCESSION CV729880
VERSION CV729880.1 GI:55433546
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-C10"
/tissue_type="flower"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

FEATURES
source
Query Match 1.3%; Score 36.6; DB 1; Length 45;
Best Local Similarity 90.7%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      44 TTTATAGATA..... 2743
QY 2701 TTTGTACTAAAAA..... 45 bp mRNA linear EST 05-NOV-2004
LOCUS FLO--03-C10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-C10, mRNA
sequence.
ACCESSION CV729880
VERSION CV729880.1 GI:55433546
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-C10"
/tissue_type="flower"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

FEATURES
source
Query Match 1.3%; Score 36.6; DB 1; Length 45;
Best Local Similarity 90.7%; Pred. No. 1.6e+02;
Matches 39; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      44 TCTATA..... 2
QY 2701 TTTGTACTAAAAA..... 45 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--08-K14.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--08-K14, mRNA
sequence.
ACCESSION CF332233
VERSION CF332233.1 GI:33812694
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 45)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

```


treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 1.3%; Score 36.4; DB 1; Length 44;
Best Local Similarity 97.4%; Pred. No. 1.7e+02;
Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2706 ACTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 4 AATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 41

RESULT 29
CF292085/c
LOCUS
DEFINITION
14ROOT--02-M10.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA sequence.
CF292085 GI:33661118
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-M10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
Query Match 1.3%; Score 36.2; DB 1; Length 42;
Best Local Similarity 92.7%; Pred. No. 1.7e+02;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 TATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 30
CV734468/c
LOCUS
DEFINITION
FLO--09-N17.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-N17, mRNA sequence.
CV734468 GI:55442297
EST.
ACCESSION
VERSION
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.

Query Match 1.3%; Score 36.2; DB 1; Length 42;
Best Local Similarity 92.7%; Pred. No. 1.7e+02;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 TATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 30
CV734468/c
LOCUS
DEFINITION
FLO--09-N17.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-N17, mRNA sequence.
CV734468 GI:55442297
EST.
ACCESSION
VERSION
KEYWORDS
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.

SOURCE ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES source

1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-N17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 36.2; DB 1; Length 42;
Best Local Similarity 92.7%; Pred. No. 1.7e+02;
Matches 38; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 TGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 31

CV734501/c

LOCUS

DEFINITION

FLO--09-O11.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-O11, mRNA sequence.

ACCESSION

CV734501

VERSION

CV734501.1

GI:55442364

EST.

ORIGIN

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 42)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..42

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO--09-O11"

```
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site1: EcoRI; Site2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
```

Query Match 1.3%; Score 36.2; DB 1; Length 42;
 Best Local Similarity 92.7%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 38; Conservative 0

Qy 2703 TGTACTAAAAA 2743
 |||
 41 TTTAAAAA 1

RESULT 32
 DY231327
 LOCUS EST02078 Bmp Bombyx mori cDNA Clone BmpG_G14_2005-10-17_WD-051017
 DEFINITION 5', mRNA sequence.
 ACCESSION DY231327
 VERSION DY231327.1 GI:86465455
 KEYWORDS Bombyx mori (domestic silkworm)
 SOURCE Bombyx mori

ORGANISM Bombyx mori
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 Bombycoidea; Bombycidae; Bombyx.
 1 (bases 1 to 44)
 Zhang, Y. Z., Xu, J., Chen, J., Wang, D., Nie, Z. M., Lv, Z. B., Jiang, C. Y.,
 Liu, L. L., Song, L., He, P. A., Chen, F. and Wu, X. F.

The full-length cDNA library construction of silkworm pupae (Bombyx mori) and large-scale sequencing
 Unpublished (2006)
 Contact: Yaozhao, Zhang

Biochemistry Laboratory, the college of life science
 Zhejiang Sci-Tech University
 2th Street, Xiaasha High Education area, Hangzhou City, 310018, P.
 R. China

Tel: 86 571 86843194
 Fax: 86 571 86843198
 Email: yaozhao@chinagen.com
 Seq primer: M13 Forward
 High quality sequence scop: 44
 POLYA=Yes.

FEATURES
 source

Location/Qualifiers
 1..44
 /organism="Bombyx mori"
 /mol_type="mRNA"
 /strain="Qingsong-Haoyue"
 /db_xref="taxon:7091"
 /clone="BmpG_G14_2005-10-17_WD-051017"
 /sex="male and female"
 /tissue_type="whole pupae body but for the skin"
 /dev_stage="metaphase"
 /clone_lib="Bmp"
 /note="Vector: pHelix; Site 1: Hind II; The synthesis of double-stranded cDNA from mRNA was based on the method described by Gubler and Hoffman. The obtained cDNA were ligated into the plasmid vector pHelix and subsequently the ligation product was transformed into E.coli competent cells TGI. At last, the recombinant clones were screened by blue-white plaques."

Query Match 1.3%; Score 36.2; DB 1; Length 44;
 Best Local Similarity 92.7%; Pred. No. 1.7e+02; Mismatches 38; Conservative 0; Indels 0; Gaps 0;

Qy 2703 TGTACTAAAAA 2743
 |||
 4 TATAGAAAAA 44

RESULT 33

AJ659250
 LOCUS AJ659250 KN277 Sus scrofa cDNA clone C0005215_D15, mRNA sequence.
 DEFINITION AJ659250
 ACCESSION AJ659250
 VERSION AJ659250.1 GI:49343381
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

1 (bases 1 to 37)
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)
 JOURNAL
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute

Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13p Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source
 1..37
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0005215_D15"
 /tissue_type="embryo"
 /clone_lib="KN277"
 /note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

Query Match 1.3%; Score 36; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 36; Conservative 0

Qy 2708 TAAAAA 2743
 |||
 1 TAAAAA 36

RESULT 34
 CF328866/c
 LOCUS CF328866
 DEFINITION CF328866.1 GI:33805974
 sativa (japonica cultivar-group) cDNA clone NACL--03-P15, mRNA sequence.

ACCESSION CF328866
 VERSION CF328866.1
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 37)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-03-P15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 36; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAA 2743

Db 36 TAAA 1

RESULT 35

CV731657/c

LOCUS

DEFINITION CV731657 37 bp mRNA linear EST 05-NOV-2004
sativa (japonica cultivar-group) cDNA clone FLO--05-M14, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-M14"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with XhoI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAA 2743
Db 36 TAAA 1

RESULT 36

CV730040/c

LOCUS

DEFINITION

CV730040 38 bp mRNA linear EST 05-NOV-2004
FLO--03-G05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--03-G05, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-G05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY 2708 TAAA 2743

Db 38 TAAA 3

RESULT 37

CF300591/c

LOCUS

DEFINITION

CF300591 39 bp mRNA linear EST 15-AUG-2003
7LEAF--05-C03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-C03, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF-05-C03"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 1.3%; Score 36; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAA 39 bp mRNA linear EST 04-NOV-2004
||||| 14Salt--04-N17.g1 Salt treated rice leaf lambda phage cDNA library
Db 36 TAAAAA 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
||||| 14Salt--04-N17, mRNA sequence.
CV726948
CV726948.1 GI:55414572
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-N17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2708 TAAAAA 39 bp mRNA linear EST 04-NOV-2004
||||| 14Salt--05-H06.g1 Salt treated rice leaf lambda phage cDNA library
Db 37 TAAAAA 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
||||| 14Salt--05-H06, mRNA sequence.

RESULT 39

CV727347/c

LOCUS

DEFINITION 14Salt--05-H06.g1 Salt treated rice leaf lambda phage cDNA library
14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-H06, mRNA sequence.

ACCESSION

CV727347

VERSION

CV727347.1

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 39)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..39

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-H06"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 36; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA 40 bp mRNA linear EST 15-AUG-2003

||||| ABF--03-N04.b1 ABF3-overexpressing transgenic rice plasmid cDNA

Db 39 TAAAAA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

||||| ABF--03-N04, mRNA sequence.

RESULT 40

CF309581/c

LOCUS

DEFINITION

ABF--03-N04.b1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--03-N04, mRNA sequence.

ACCESSION

CF309581

VERSION

CF309581.1

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 40)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .40
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--03-N04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.3%; Score 36; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

36 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 41

CV733657/c

LOCUS

FLO--08-K18.g1 Rice flower lambda phage cDNA library (FLO) Oryza

sativa (japonica cultivar-group) cDNA clone FLO--08-K18, mRNA

sequence.

CV733657

CV733657.1 GI:55440691

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 41)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .41

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO--08-K18"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

41 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 42

CV726108/c

LOCUS

DEFINITION

14Salt--03-J05.b1 Salt treated rice leaf lambda phage cDNA library

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--03-J05, mRNA sequence.

CV726108

CV726108.1 GI:55413732

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 43)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .43

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--03-J05"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lambda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

42 TAAAAA...AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 43

CV728159/c

LOCUS

CV728159

43 bp

mRNA

linear

EST 05-NOV-2004

```

DEFINITION 14Salt--06-L11.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
VERSION CV728159
KEYWORDS 14Salt--06-L11, mRNA sequence.
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-L11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 43 bp mRNA linear EST 05-NOV-2004
Db 41 TAAAAA... 6

RESULT 44
CV734232/c
LOCUS FLO--09-102.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--09-102, mRNA
sequence.
ACCESSION CV734232
VERSION CV734232.1 GI:55441811
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

```

```

Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-102"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 44 bp mRNA linear EST 04-NOV-2004
Db 43 TAAAAA... 8

RESULT 45
CV726790/c
LOCUS 14Salt--04-J20.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-J20, mRNA sequence.
ACCESSION CV726790
VERSION CV726790.1 GI:55414414
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 44)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. 44
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-J20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 36; DB 1; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAA... 44 bp mRNA linear EST 04-NOV-2004
Db 43 TAAAAA... 8

```

```

Db      44 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9
|||||
CF331757      45 bp      mRNA      linear      EST 18-AUG-2003
NACL--08-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-A04, mRNA
sequence.
CF331757
CF331757.1 GI:33811741
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-I01"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 36; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB      43 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
|||||

RESULT 48
CV729079/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-L18, mRNA
sequence.
ACCESSION
CV729079.1 GI:55432121
VERSION
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-L18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35.4; DB 1; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      41 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
|||||
CF331757      45 bp      mRNA      linear      EST 05-NOV-2004
FLO--09-I01.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-I01, mRNA
sequence.
CF331757
CF331757.1 GI:55441807
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-A04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 36; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB      41 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
|||||

RESULT 47
CV734230/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-I01, mRNA
sequence.
ACCESSION
CV734230.1 GI:55441807
VERSION
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 45)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .45
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-I01"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35.4; DB 1; Length 37;
Best Local Similarity 97.3%; Pred. No. 1.7e+02;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. .45

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-I01"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 36; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB

43 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 48

CV729079/c

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-L18, mRNA
sequence.

ACCESSION

CV729079.1

GI:55432121

VERSION

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO--01-L18"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35.4; DB 1; Length 37;

Best Local Similarity 97.3%; Pred. No. 1.7e+02;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-D04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 Query Match 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA 1
 Db 41 CCAAAAAA 5

RESULT 58
 CV732097/c
 LOCUS
 DEFINITION
 FLO--06-G18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G18, mRNA sequence.
 CV732097
 CV732097.1 GI:55437621
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 41)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. .41
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--06-G18"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into landa Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
 Query Match 1.3%; Score 35.4; DB 1; Length 41;
 Best Local Similarity 97.3%; Pred. No. 1.8e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAA 1
 Db 41 CCAAAAAA 5

RESULT 59
 CF302691/c
 LOCUS
 DEFINITION
 7LEAF--08-H12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--08-H12, mRNA sequence.
 CF302691
 CF302691.1 GI:33674452
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

QY 2707 CTAAAAA 1
 Db 43 CAAAAA 7

RESULT 60
 CV725096/c
 LOCUS
 DEFINITION
 14Salt--02-A01.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--02-A01, mRNA sequence.
 CV725096
 CV725096.1 GI:55412720
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

QY 2707 CTAAAAA 1
 Db 43 CAAAAA 7

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
 1..43
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /culivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt-02-A01"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35.4; DB 1; Length 43;
 Best Local Similarity 97.3%; Pred. No. 1.9e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAAGAAAAA 2743

Db 39 CCAAAAAA 3

RESULT 61

DV573571/c 43 bp mRNA linear EST 04-NOV-2005
 LOCUS 0058P0042B11.3 library 58 - normalized (50 mix pooled juveniles + adults) - male Taeniopygia guttata cDNA clone 0058P0042B11.3, similar to prohibitin, mRNA sequence.

ACCESSION DV573571

VERSION DV573571.1

KEYWORDS EST.

SOURCE Taeniopygia guttata

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.

REFERENCE

1 (bases 1 to 43)

Wada, K., Howard, J. T., McConnell, P., Lints, T., Rivas, M. V., Whitney, O., Horita, H., Patterson, M. A., White, S., Zhao, S., Sakaguchi, H., Hagiwara, M., Shiraki, T., Hirozane-Kishikawa, T., Skene, P., Hayashizaki, Y., Carninci, P., and Jarvis, E. D.

A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes

Unpublished (2005)

Other ESTs: 0058P0042Z.x0 B11

Contact: Kazuhiro Wada and Erich Jarvis

Erich D. Jarvis Lab

Duke University Medical Center - Department of Neurobiology

Box 3209 Bryan Research Building, Durham, NC 27710, USA

Tel: 919 681-1681

Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu

Plate: 0058P0042 row: B column: 11

POLYA=No.

FEATURES

source

1..43
 /organism="Taeniopygia guttata"
 /mol_type="mRNA"
 /db_xref="taxon:59729"
 /clone="0058P0042B11"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult and juvenile"
 /clone_lib="library 58 - normalized (50 mix pooled juveniles + adults) - male"
 /note="Organ: brain; Vector: pFLC-1; Site 1: EcoRI; Site 2: BamHI; The library was constructed as described by

Carninci, P. (2003) in DNA Microarrays: A Molecular Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.
 TAG_TISSUE=whole brain"

Query Match 1.3%; Score 35.4; DB 1; Length 43;
 Best Local Similarity 97.3%; Pred. No. 1.9e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAAGAAAAA 2743

Db 43 CCAAAAAA 7

RESULT 62

DV573572/c

LOCUS

DEFINITION DV573572 library 58 - normalized (50 mix pooled juveniles + adults) - male Taeniopygia guttata cDNA clone 0058P0042B11.5, similar to prohibitin, mRNA sequence.

ACCESSION DV573572

VERSION DV573572.1

KEYWORDS EST.

SOURCE Taeniopygia guttata

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.

REFERENCE

1 (bases 1 to 43)

Wada, K., Howard, J. T., McConnell, P., Lints, T., Rivas, M. V., Whitney, O., Horita, H., Patterson, M. A., White, S., Zhao, S., Sakaguchi, H., Hagiwara, M., Shiraki, T., Hirozane-Kishikawa, T., Skene, P., Hayashizaki, Y., Carninci, P., and Jarvis, E. D.

A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes

Unpublished (2005)

Other ESTs: 0058P0042Z.y0 B11

Contact: Kazuhiro Wada and Erich Jarvis

Erich D. Jarvis Lab

Duke University Medical Center - Department of Neurobiology

Box 3209 Bryan Research Building, Durham, NC 27710, USA

Tel: 919 681-1681

Email: wada@neuro.duke.edu and jarvis@neuro.duke.edu

Plate: 0058P0042 row: B column: 11

POLYA=No.

FEATURES

source

1..43
 /organism="Taeniopygia guttata"
 /mol_type="mRNA"
 /db_xref="taxon:59729"
 /clone="0058P0042B11"
 /sex="male"
 /tissue_type="brain"
 /dev_stage="adult and juvenile"
 /clone_lib="library 58 - normalized (50 mix pooled juveniles + adults) - male"
 /note="Organ: brain; Vector: pFLC-1; Site 1: EcoRI; Site 2: BamHI; The library was constructed as described by Carninci, P. (2003) in DNA Microarrays: A Molecular Cloning Manual, eds. Bowtell, D. & Sambrook, J. (Cold Spring Harbor, NY), pp. 647-670.
 TAG_TISSUE=whole brain
 TAG_SEQ=tcgagctctacacagtgacacacagaacca"

Query Match 1.3%; Score 35.4; DB 1; Length 43;
 Best Local Similarity 97.3%; Pred. No. 1.9e+02;
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAAGAAAAA 2743

Db 43 CCAAAAAA 7

RESULT 63

CF298596/c

LOCUS

DEFINITION

CF298596 44 bp mRNA linear EST 15-AUG-2003
7LEAF--02-A24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A24, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF298596.1 GI:33670357
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 44)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..44

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--02-A24"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35.4; DB 1; Length 44;

Best Local Similarity 97.3%; Pred. No. 1.9e+02;

Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 44 CAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 64

CN545689/c

LOCUS

DEFINITION

CN545689 43 bp mRNA linear EST 30-APR-2004
EST 17633 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00R004H05 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CN545689.1 GI:46910314
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 43)
Abbal, P., Agase, A., Agase, A., Agase, A., Agase, A., Agase, A., Agase, A.,
Couture, C., Dedalechamp, F., Delrot, S., Glissant, D., Grimpier, J.,
Hamdi, S., Romeu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche

Query Match 1.3%; Score 35.2; DB 1; Length 44;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 44;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

FEATURES

source

1..43

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00R004H05"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1:
SfiIA; Site 2: SfiIB; Oriented library"

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..43

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00R004H05"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1:
SfiIA; Site 2: SfiIB; Oriented library"

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Query Match 1.3%; Score 35.2; DB 1; Length 43;

Best Local Similarity 92.5%; Pred. No. 2e+02;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 40 GCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 65

CF334384/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

/dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 69
 CV725312/c
 LOCUS
 DEFINITION
 14Salt--02-F09.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-F09, mRNA sequence.

ACCESSION
 VERSION
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 Location/Qualifiers
 1..35

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-F09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 70
 CV725444/c
 LOCUS
 DEFINITION
 14Salt--02-I15.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-I15, mRNA sequence.

DEFINITION
 14Salt--02-I15.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-I15, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 Location/Qualifiers
 1..35

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-I15"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 71
 CV725518/c
 LOCUS
 DEFINITION
 14Salt--02-K09.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-K09, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

```

Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="14Salt--02-K09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 73
CV726506/c 35 bp mRNA linear EST 04-NOV-2004
LOCUS 14Salt--04-D02.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-D02, mRNA sequence.
ACCESSION CV726506
VERSION CV726506.1 GI:55414130
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1. .35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/db_xref="taxon:39947"
/clone="14Salt--04-D02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 74
CV727085/c 35 bp mRNA linear EST 04-NOV-2004
LOCUS 14Salt--05-A23.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-A23, mRNA sequence.
ACCESSION CV727085
VERSION CV727085.1 GI:55414709
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-A23"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
 |||||
 Db 35 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 75
 CV727326/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 04-NOV-2004
 14Salt--05-G17.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV727326
 CV727326.1 GI:55414950
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-G17"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"

/lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 76

CV728725/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 05-NOV-2004
 FLO--01-D10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--01-D10, mRNA
 sequence.
 CV728725
 CV728725.1 GI:55431423
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-D10"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 77

CV728984/c
 LOCUS
 DEFINITION 35 bp mRNA linear EST 05-NOV-2004
 FLO--01-J11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--01-J11, mRNA
 sequence.
 CV728984
 CV728984.1 GI:55431423
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 35)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..35
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-G17"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"

```

VERSION CV728984.1 GI:55431928
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-J11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 79
CV730453/c
LOCUS CV730453 35 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--04-A02.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-A02, mRNA
sequence.
ACCESSION CV730453
VERSION CV730453.1 GI:55434657
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
source
1..35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-A02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 80
CV730547/c
LOCUS CV730547 35 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--04-C08.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--04-C08, mRNA
sequence.

```



```

sativa (japonica cultivar-group) cDNA clone FLO--08-M15, mRNA
sequence.
ACCESSION CV733739
VERSION CV733739.1 GI:55440852
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..35
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="FLO--08-M15"
            /tissue_type="flower"
            /lab_host="E.coli SOLR"
            /clone_lib="Rice flower lambda phage cDNA library (FLO)"
            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87
CV734164/c
LOCUS FLO--09-G11.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--09-G11, mRNA
sequence.
ACCESSION CV734164
VERSION CV734164.1 GI:55441677
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..35
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="FLO--08-M15"
            /tissue_type="flower"
            /lab_host="E.coli SOLR"
            /clone_lib="Rice flower lambda phage cDNA library (FLO)"
            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 87
CV734164/c
LOCUS FLO--09-G11.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--09-G11, mRNA
sequence.
ACCESSION CV734164
VERSION CV734164.1 GI:55441677
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..35
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="FLO--09-G11"
            /tissue_type="flower"
            /lab_host="E.coli SOLR"
            /clone_lib="Rice flower lambda phage cDNA library (FLO)"
            /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
            XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
            end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 88
AZ623128/c
LOCUS AZ623128
DEFINITION 1M0460D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D02 R, genomic survey sequence.
ACCESSION AZ623128
VERSION AZ623128.1 GI:11745318
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
    source
        1..35
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="CS7BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0460D02"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were

```

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 89
 AZ803371/c
 LOCUS
 DEFINITION 2M0063C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0063C15 R, genomic survey sequence.

ACCESSION AZ803371
 VERSION AZ803371.1 GI:12955694
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 35)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0063 row: C column: 15

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 35.

FEATURES

Location/Qualifiers
 1..35
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0063C15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 90
 AJ791385/c

LOCUS
 DEFINITION AJ791385 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 018.2.08_j14, mRNA sequence.

ACCESSION AJ791385

VERSION AJ791385.1 GI:51061705

KEYWORDS EST.

SOURCE Antirrhinum majus (snapdragon)

ORGANISM Antirrhinum majus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 asterids; lamiales; Plantaginaceae; Antirrhineae;
 Antirrhinum.

1 (bases 1 to 36)

AUTHORS

Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
 Saedler,H. and Zachgo,S.

TITLE

Characterization of Antirrhinum Petal Development and
 Identification of Target Genes of the Class B MADS Box Gene
 DEFICIENS

JOURNAL Plant Cell 16 (12), 3197-3215 (2004)

PUBMED 15539471

COMMENT Contact: Schwarz-Sommer Z

Molekulare Pflanzen-genetik

MPI fuer zuechtungs-forschung

Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES

Location/Qualifiers

1..36
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="018.2.08_j14"
 /tissue_type="whole plant"
 /clone_lib="Antirrhinum majus whole plant"

Query Match 1.3%; Score 35; DB 1; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 91

AL587891/c

LOCUS

DEFINITION AL587891 BP Chicken Brain Library Gallus gallus cDNA clone
 RS064H03, mRNA sequence.

ACCESSION AL587891

VERSION AL587891.1 GI:13192925

KEYWORDS EST.

```

SOURCE
ORGANISM      Gallus gallus (chicken)
               Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
               Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 36)
AUTHORS      Murray, F.
TITLE        BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Contact: Frazer Murray
               Dept. Genomics and Bioinformatics
               Roslin Institute
               Roslin, Midlothian, EH25 9PS, UK
               Tel: +44 (0)131 527 4200
               Fax: +44 (0)131 440 0434
               Email: frazer.murray@bbsrc.ac.uk
               GCGGCGCTTTT TTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
               (*6854-
Seq primer: M13P.
               Location/Qualifiers
               1..36
               /organism="Gallus gallus"
               /mol_type="mRNA"
               /db_xref="taxon:9031"
               /clone="ROS064H03"
               /tissue_type="Brain"
               /dev_stage="Unknown"
               /lab_host="DH10B"
               /clone_lib="BP Chicken Brain Library"
               /notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
               unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
               5' TCACCTCGAG 3'; 3' adaptor sequence: 5'
               GCGGCGCTTTT TTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from
               Clontech (*6854-1)"

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 92
AM046410/c
LOCUS
DEFINITION      AM046410 Schistosoma mansoni lung schistosomulum Schistosoma
ACCESSION      AM046410
VERSION        AM046410.1 GI:75970489
KEYWORDS      EST.
SOURCE
ORGANISM      Schistosoma mansoni
               Schistosoma mansoni
               Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
               Strigeida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 36)
AUTHORS      Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
               Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
TITLE        Microarray analysis identifies genes preferentially expressed in
               the lung schistosomulum of Schistosoma mansoni
JOURNAL      Unpublished (2005)
COMMENT      Contact: Ivens AC
               Pathogen Microarrays Group
               Wellcome Trust Sanger Institute
               Hinxton, CB10 1SA, UNITED KINGDOM.
               Location/Qualifiers
               1..36
               /organism="Schistosoma mansoni"
               /mol_type="mRNA"
               /db_xref="taxon:6183"
               /clone="SmlC13d11.q1k"
               /dev_stage="lung schistosomulum"

FEATURES
source
               /clone_lib="Schistosoma mansoni lung schistosomulum"
               /note="country: Puerto Rico"

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 93
CF279874/c
LOCUS
DEFINITION      CF279874 -06-F10.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
               Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--06-F10,
               mRNA sequence.
ACCESSION      CF279874
VERSION        CF279874.1 GI:33657260
KEYWORDS      EST.
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 36)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
               Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Gyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@bio.myongji.ac.kr.
               Location/Qualifiers
               1..36
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="14ETL--06-F10"
               /tissue_type="leaf"
               /dev_stage="14 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice etiolated leaf plasmid cDNA library
               (14ETL)"
               /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 94
CF317028/c
LOCUS
DEFINITION      HD--06-J02.g1 OshDACL-overexpressing transgenic rice plasmid cDNA
               library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
               HD--06-J02, mRNA sequence.
ACCESSION      CF317028
VERSION        CF317028.1 GI:33688789
KEYWORDS      EST.
SOURCE
               Oryza sativa (japonica cultivar-group)

```

```

ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 36)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 321 6355
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..36
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="HD-06-J02"
              /tissue_type="callus"
              /dev_stage="proliferated callus on 2N6 media for 2 weeks"
              /lab_host="E.coli DH10B"
              /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
              cDNA library (HD)"
              /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
              treated with ABA(20um) for 1hr. Oligo-capped mRNA was
              reverse transcribed and then used for PCR. mRNA was
              derived from rice Histone Deacetylase overexpression
              line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 95
CF331913/c
LOCUS      CF331913.1 GI:33812047
DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 36)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..36
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="HD-06-J02"
              /tissue_type="callus"
              /dev_stage="proliferated callus on 2N6 media for 2 weeks"
              /lab_host="E.coli DH10B"
              /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
              cDNA library (HD)"
              /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
              treated with ABA(20um) for 1hr. Oligo-capped mRNA was
              reverse transcribed and then used for PCR. mRNA was
              derived from rice Histone Deacetylase overexpression
              line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 95
CF331913/c
LOCUS      CF331913.1 GI:33812047
DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 36)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..36
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"

```

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-D12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 96
CF331983/c
LOCUS      CF331983.1 GI:33812186
DEFINITION Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
            1 (bases 1 to 36)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 321 6355
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..36
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="NACL--08-F01"
              /tissue_type="callus"
              /dev_stage="proliferated callus on 2N6 media for 30 days"
              /lab_host="E.coli DH10B"
              /clone_lib="Rice callus plasmid cDNA library (NACL)"
              /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
              with oligoribonucleotides and then used as templates for
              RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 97
CF333863/c
LOCUS      CF333863

```

```

DEFINITION  JMT--02-022 b1 AtJMT-overexpressing transgenic rice plasmid cDNA
              library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-022, mRNA sequence.
CF333863
VERSION      CF333863.1 GI:33816032
KEYWORDS
SOURCE
ORGANISM     Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
              clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 36)
AUTHORS      Kim J.S., Jun K.M., Cheong, P.J., Kim M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Gyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
  source
    1..36
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="JMT--02-022"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="AtJMT-overexpressing transgenic rice plasmid
      cDNA library (JMT)"
      /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
      was reverse transcribed and then used for PCR. mRNA was
      prepared from Arabidopsis Jasmonate Carboxyl
      methyltransferase overexpression line."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 98
BE876160
LOCUS      BE876160
DEFINITION 601485659F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888015 5',
              mRNA sequence.
ACCESSION  BE876160
VERSION     BE876160.1 GI:10324936
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE    1 (bases 1 to 36)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs@mail.nih.gov
              Tissue Procurement: DCTD/DTF/Gazdar
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAN667 row: f column: 16
High quality sequence stop: 36.
Location/Qualifiers
  source
    1..36
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:388015"
      /tissue_type="large cell carcinoma, undifferentiated"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_69"
      /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
      Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
      Average insert size 1.1 kb. Library constructed by Life
      Technologies."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 99
CV724782/c
LOCUS      CV724782/c
DEFINITION 14Salt--01-119.g1 Salt treated rice leaf lambda phage cDNA library
              (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
              14Salt--01-119, mRNA sequence.
ACCESSION  CV724782
VERSION     CV724782.1 GI:55412406
KEYWORDS
SOURCE      Oryza sativa (japonica cultivar-group)
              Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
              clade; Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 36)
              Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Gyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
  source
    1..36
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="14Salt--01-119"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli SOLR"
      /clone_lib="Salt treated rice leaf lambda phage cDNA
      library (14Salt)"
      /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
      XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs.
      cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
      with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 100
CV725281/c
LOCUS 14Salt--02-E17.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-E17, mRNA sequence.
ACCESSION CV725281
VERSION CV725281.1 GI:55412905
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14Salt--02-E21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 102
CV725592/c
LOCUS 14Salt--02-M04.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-M04, mRNA sequence.
ACCESSION CV725592
VERSION CV725592.1 GI:55413216
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14Salt--02-E21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 101
CV725289/c
LOCUS 14Salt--02-E21.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-E21, mRNA sequence.
ACCESSION CV725289
VERSION CV725289.1 GI:55412913
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 36)

```

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14Salt--02-E21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 102
CV725592/c
LOCUS 14Salt--02-M04.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-M04, mRNA sequence.
ACCESSION CV725592
VERSION CV725592.1 GI:55413216
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 36)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14Salt--02-M04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"

```

```

/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 103
CV726151/c
LOCUS
DEFINITION
14Salt--03-K07.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-K07, mRNA sequence.
ACCESSION
CV726151 GI:55413775
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/library="(14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 104
CV726321/c
LOCUS
DEFINITION
14Salt--03-K08.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-K08, mRNA sequence.
ACCESSION
CV726321 GI:55413945
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/library="(14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 105
CV727111/c
LOCUS
DEFINITION
14Salt--05-B16.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-B16, mRNA sequence.
ACCESSION
CV727111 GI:55414735
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/library="(14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 106
CV727111/c
LOCUS
DEFINITION
14Salt--05-B16.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-B16, mRNA sequence.
ACCESSION
CV727111 GI:55414735
SOURCE
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-K07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/library="(14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

```

FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-B16"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 106
CV728675/c
LOCUS
DEFINITION
FLO--01-C05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C05, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-G18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 107
CV728870/c
LOCUS
DEFINITION
FLO--01-G18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-G18, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-G18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 108
CV729206/c
LOCUS
DEFINITION
FLO--01-021.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-021, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-C05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 36;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

```


Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-Q21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 109
CV730235/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--03-K22, mRNA
sequence.

ACCESSION
CV730235
VERSION
CV730235.1 GI:55434231
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-L09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 111
CV730953/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--04-M03, mRNA
sequence.

ACCESSION
CV730953
VERSION
CV730953.1 GI:55435643
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-04-M03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 112

CV732578/c
LOCUS
DEFINITION
FLO--07-B22.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-B22, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 36)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-07-B22"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 113

CV732659/c
LOCUS
DEFINITION
FLO--07-D18.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D18, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 36)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-D18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 114

CV733597/c
LOCUS
DEFINITION
FLO--08-J07.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-J07, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 36)

AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1..36
Location/Qualifiers
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="FLO-08-J07"
  /tissue_type="flower"
  /lab_host="E.coli SOLR"
  /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 115

CV734403/C

LOCUS FLO--09-M02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-M02, mRNA
sequence.
CV734403
CV734403.1 GI:55442165

ORIGIN Oryza sativa (japonica cultivar-group)
ORIGIN Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 36)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1..36
Location/Qualifiers
  /organism="Oryza sativa (japonica cultivar-group)"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:39947"
  /clone="FLO--09-M02"
  /tissue_type="flower"
  /lab_host="E.coli SOLR"
  /clone_lib="Rice flower lambda phage cDNA library (FLO)"
  /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 116

AZ470916/C

LOCUS 1M0285523F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clome UUGC1M0285E23 F, genomic survey sequence.

ACCESSION AZ470916

VERSION AZ470916.1

KEYWORDS GI:10629041

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 36)

Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0285 row: E column: 23

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 36.

Location/Qualifiers

1..36

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0285E23"

/sex="Male"

/lab_host="E. Coli strain Xli10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli Xli10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

1.3%; Score 35; DB 1; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 117
AZ628484/c
LOCUS
DEFINITION
  1M0480B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0480B08 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  GSS.
  AZ628484.1 GI:11750674
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 36)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0480 row: B column: 08
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 36.
  Location/Qualifiers
    1..36
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0480B08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
FEATURES
  source
    1..36

```

```

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 118
AZ793484/c
LOCUS
DEFINITION
  2M0046G15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0046G15 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
  GSS.
  AZ793484.1 GI:12938483
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 36)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0046 row: G column: 15
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 36.
  Location/Qualifiers
    1..36
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC2M0046G15"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
  musculus C57BL/6J (male) was obtained from the Jackson
  Laboratory Mouse DNA Resource
  (http://www.jax.org/resources/documents/dnares/). The DNA
  was hydrodynamically sheared by repeated passage through a
  0.005 inch orifice at constant velocity. The sheared DNA
  was blunt end-repaired with T4 DNA polymerase and T4
  polynucleotide kinase. Adaptor oligonucleotides were
  ligated to the blunt ends in high molar excess. The
  adaptor DNA was purified and size-selected for a 9.5 to
  10.5 kb range using preparative agarose gel
  electrophoresis. Vector DNA was prepared from a derivative
  of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
  inducible derivative of plasmid R1. The vector was ligated
  with adaptors complementary to the insert adaptors and
  purified. The sheared, adaptor mouse DNA was annealed to
  adaptor vector DNA, and transformed into
  chemically-competent E. coli XL10-Gold (Stratagene) cells
  and selected for ampicillin resistance."
FEATURES
  source
    1..36

```

```

Query Match      1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 119
AZ949866/c
LOCUS   2M0213H10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION
ACCESSION AZ949866
VERSION   AZ949866
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: H column: 10
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0213H10"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 120
AZ957867/c
LOCUS   2M0224G19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION
ACCESSION AZ957867
VERSION   AZ957867
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0224 row: G column: 19
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0224G19"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

```

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 121
LOCUS CZ914006 36 bp DNA linear GSS 08-AUG-2005
DEFINITION 4013005B08.2EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
ACCESSION CZ914006
VERSION CZ914006.1 GI:71930364
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 36)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: B column: 08
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site: 1: BamHI, Site: 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 122
LOCUS DU834235 36 bp DNA linear GSS 22-DEC-2005
DEFINITION KRS013L23F KRSr, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KRS013L23, genomic survey sequence.
ACCESSION DU834235
VERSION DU834235.1 GI:83870831

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 123
LOCUS DX046307/c 36 bp DNA linear GSS 10-JAN-2006
DEFINITION KRB047024F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KRB047024, genomic survey sequence.
ACCESSION DX046307
VERSION DX046307.1 GI:84740604
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone KRS013L23
Seq primer: T7
Class: BAC ends.
FEATURES
source
Location/Qualifiers
1..36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KRS013L23"
/lab_host="E. coli DH10B"
/clone_lib="KRSr, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site: 1: Sau3AI; Brassica rapa subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 123
LOCUS DX046307/c 36 bp DNA linear GSS 10-JAN-2006
DEFINITION KRB047024F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KRB047024, genomic survey sequence.
ACCESSION DX046307
VERSION DX046307.1 GI:84740604
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

```

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB047024
Seq primer: T7
Class: BAC ends.
Location/Qualifiers

FEATURES

source

```
1. .36
  /organism="Brassica rapa subsp. pekinensis"
  /mol_type="genomic DNA"
  /cultivar="Chifu"
  /sub_species="pekinensis"
  /db_xref="taxon:51351"
  /clone="KBrB047024"
  /lab_host="E.coli DH10B"
  /clone_lib="KBrB, Brassica rapa BamHI BAC library"
  /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
  pekinensis var. Chifu BAC library (KBrB BAC) is provided
  by Yong-Pyo Lim (CNU)."
```

Query Match 1.3%; Score 35; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 124

BG033620

LOCUS

DEFINITION 602301748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4403554 5',
mRNA sequence.

ACCESSION

BG033620

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10113 row: 0 column: 11
High quality sequence stop: 37.

FEATURES

source

```
1. .37
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:4403554"
  /tissue_type="mammary adenocarcinoma, cell line"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH MGC 87"
  /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;  
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.383 Kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH_MGC Library."
```

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 125

CF291818/c

LOCUS

DEFINITION

CF291818

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-G14"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 126

CF300002

LOCUS

DEFINITION

CF300002

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-G14"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-D21"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 127
CF300328
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-K23 g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-K23, mRNA sequence.
ACCESSION CF300328
VERSION CF300328.1 GI:33672089
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-K23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 128

CF301560
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-H14 g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-H14, mRNA sequence.
ACCESSION CF301560
VERSION CF301560.1 GI:33673321
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 37)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--06-H14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 129

CF301864/c
LOCUS 37 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-003.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-003, mRNA sequence.
ACCESSION CF301864
VERSION CF301864.1 GI:33673625
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 37)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--06-003"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 130

CF307971/c

LOCUS

DEFINITION ABF--01-J16.b1 ABF3-overexpressing transgenic rice plasmid cDNA
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--01-J16, mRNA sequence.

ACCESSION

CF307971

CF307971.1 GI:33679732

EST.

SOURCE**ORGANISM**

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE**AUTHORS**

1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE**JOURNAL****COMMENT**

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--01-J16"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 131

CF316114

LOCUS

DEFINITION HD--05-E13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--05-E13, mRNA sequence.

ACCESSION

CF316114

CF316114.1 GI:33687875

EST.

KEYWORDS**ORGANISM**

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE**AUTHORS**

1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE**JOURNAL****COMMENT**

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. 37
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--05-E13"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 132

CF321294

LOCUS

DEFINITION CF321294 37 bp mRNA linear EST 15-AUG-2003

```

DEFINITION HD--12-101.g1 OshDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION HD--12-101, mRNA sequence.
VERSION    CF321294
KEYWORDS   CF321294.1 GI:33693055
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 37)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES   Location/Qualifiers
            source
            1..37
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="HD--12-101"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."
            Query Match          1.3%; Score 35; DB 1; Length 37;
            Best Local Similarity 100.0%; Pred. No. 1.8e+02;
            Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 133
CF326975/c
LOCUS      CF326975.1 GI:33802205
DEFINITION NACL--01-E08.b1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--01-E08, mRNA
            sequence.
ACCESSION CF326975
VERSION    CF326975.1 GI:33802205
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 37)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea

```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..37
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="NACL--01-E08"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
Query Match          1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 134
CF333624/c
LOCUS      CF333624.1 GI:33815543
DEFINITION JMT--02-J14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
            JMT--02-J14, mRNA sequence.
ACCESSION CF333624
VERSION    CF333624.1 GI:33815543
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 37)
            Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..37
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="JMT--02-J14"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
    cDNA library (JMT)"
    /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
    was reverse transcribed and then used for PCR. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."
Query Match          1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 135
CF336769/c
LOCUS   CF336769 37 bp mRNA linear EST 18-AUG-2003
DEFINITION
JMT--06-P04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--06-P04, mRNA sequence.
ACCESSION
CF336769.1 GI:33821918
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 37)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--06-P04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 136
CV724637/c
LOCUS   CV724637 37 bp mRNA linear EST 04-NOV-2004
DEFINITION
14Salt--01-F06.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-F06, mRNA sequence.
ACCESSION
CV724637.1 GI:55412261
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 37)

```

```

AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-F06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db      37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 137
CV725878/c
LOCUS   CV725878 37 bp mRNA linear EST 04-NOV-2004
DEFINITION
14Salt--03-D12.gi Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-D12, mRNA sequence.
ACCESSION
CV725878.1 GI:55413502
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 37)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-D12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"

```



```

FEATURES
source
Location/Qualifiers
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-F08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 141
CV727448/c
LOCUS
DEFINITION
14Salt--05-J14.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-J14, mRNA sequence.
CV727448
CV727448.1 GI:55415072
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-J14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
source
Location/Qualifiers
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-J14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 142
CV727567/c
LOCUS
DEFINITION
14Salt--05-M08.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-M08, mRNA sequence.
CV727567
CV727567.1 GI:55415191
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..37
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360UM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 143
CV727819/c
LOCUS
DEFINITION
14Salt--06-C16.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-C16, mRNA sequence.
CV727819
CV727819.1 GI:55415443
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-C16"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 144
 CV728196/c
 LOCUS
 DEFINITION 14Salt--06-M10.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-M10, mRNA sequence.

ACCESSION CV728196 GI:55430492
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 37)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-M10"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 145
 CV728197/c
 LOCUS
 DEFINITION 14Salt--06-M11.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-M11, mRNA sequence.

ACCESSION CV728197 GI:55430493
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 37)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-M11"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 146
 CV730003/c
 LOCUS
 DEFINITION FLO--03-F09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--03-F09, mRNA sequence.

ACCESSION CV730003
 VERSION CV730003.1 GI:55433779
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 37)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--03-F09"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 147
 CV730176/c
 LOCUS
 DEFINITION FLO--03-J09.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--03-J09, mRNA
 sequence.

ACCESSION CV730176
 VERSION CV730176.1 GI:55434119
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--03-J09"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
 Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 148
 CV731472/c

LOCUS
 DEFINITION FLO--05-I10.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--05-I10, mRNA
 sequence.

ACCESSION CV731472
 VERSION CV731472.1 GI:55436672
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1. .37
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--05-I10"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 149
 AZ321759

LOCUS
 DEFINITION 1M0042P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0042P22 F, genomic survey sequence.

```

ACCESSION      AZ321759
VERSION        AZ321759.1  GI:10374820
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0042 row: P column: 22
               Seq primer: CGTTGTAACGACGCGCAGT
               Class: plasmid ends
               High quality sequence stop: 37.
               Location/Qualifiers
                 1. .37
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="UUGC1M0042P22"
                   /sex="Male"
                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                   /note="Vector: PWD42nv; Purified genomic DNA from M.
                   musculus C57BL/6J (male) was obtained from the Jackson
                   Laboratory Mouse DNA Resource
                   (http://www.jax.org/resources/documents/dnares/). The DNA
                   was hydrodynamically sheared by repeated passage through a
                   0.005 inch orifice at constant velocity. The sheared DNA
                   was blunt end-repaired with T4 DNA polymerase and T4
                   polynucleotide kinase. Adaptor oligonucleotides were
                   ligated to the blunt ends in high molar excess. The
                   adaptor DNA was purified and size-selected for a 9.5 to
                   10.5 kb range using preparative agarose gel
                   electrophoresis. Vector DNA was prepared from a derivative
                   of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                   inducible derivative of plasmid R1. The vector was ligated
                   with adaptors complementary to the insert adaptors and
                   purified. The sheared, adaptor mouse DNA was annealed to
                   adaptor vector DNA, and transformed into
                   chemically-competent E. coli XL10-Gold (Stratagene) cells
                   and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 150
AZ463801/c
LOCUS
DEFINITION      AZ463801 37 bp DNA linear GSS 04-OCT-2000
                  1M027E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC1M027E23 R, genomic survey sequence.

```

```

ACCESSION      AZ463801
VERSION        AZ463801.1  GI:10621926
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0272 row: E column: 23
               Seq primer: CACACAGGAACACGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 37.
               Location/Qualifiers
                 1. .37
                   /organism="Mus musculus"
                   /mol_type="genomic DNA"
                   /strain="C57BL/6J"
                   /db_xref="taxon:10090"
                   /clone="UUGC1M027E23"
                   /sex="Male"
                   /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                   /clone_lib="Mouse 10kb plasmid UUGC1M library"
                   /note="Vector: PWD42nv; Purified genomic DNA from M.
                   musculus C57BL/6J (male) was obtained from the Jackson
                   Laboratory Mouse DNA Resource
                   (http://www.jax.org/resources/documents/dnares/). The DNA
                   was hydrodynamically sheared by repeated passage through a
                   0.005 inch orifice at constant velocity. The sheared DNA
                   was blunt end-repaired with T4 DNA polymerase and T4
                   polynucleotide kinase. Adaptor oligonucleotides were
                   ligated to the blunt ends in high molar excess. The
                   adaptor DNA was purified and size-selected for a 9.5 to
                   10.5 kb range using preparative agarose gel
                   electrophoresis. Vector DNA was prepared from a derivative
                   of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                   inducible derivative of plasmid R1. The vector was ligated
                   with adaptors complementary to the insert adaptors and
                   purified. The sheared, adaptor mouse DNA was annealed to
                   adaptor vector DNA, and transformed into
                   chemically-competent E. coli XL10-Gold (Stratagene) cells
                   and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 151
AZ831214
LOCUS
DEFINITION      AZ831214 37 bp DNA linear GSS 20-FEB-2001
                  2M0110P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC2M0110P16 R, genomic survey sequence.

```



```

ACCESSION      AZ831214
VERSION        AZ831214.1  GI:13001122
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0110 row: P column: 16
               Seq primer: CACACAGGAACAGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 37.

FEATURES       source
               1..37
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0110P16"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number-
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 152
CZ914427/c
LOCUS          CZ914427          37 bp      DNA      linear      GSS 08-AUG-2005
DEFINITION    4013006H08.2EL_y1 4013 - RescueMu Grid O Zea mays genomic, genomic
               survey sequence.

AUTHORS        Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
               Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
               Hahn,J.H. and Park,B.S.

```

```

ACCESSION      CZ914427
VERSION        CZ914427.1  GI:71931035
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays

REFERENCE
AUTHORS        Walbot,V.
TITLE          Maize genomic sequences found using engineered RescueMu transposon
               Unpublished (2001)
JOURNAL        Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Possible ligation site of ends cut by 2 different endonucleases.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 4013006 row: H column: 08
               Class: transposon-tagged.

FEATURES       source
               1..37
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="mixed background W23/A188/B73/K55"
               /db_xref="taxon:4577"
               /tissue_type="leaf"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="4013 - RescueMu Grid O"
               /note="Organ: Leaf; Vector: RescueMu (engineered from
               pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
               RescueMu is a 4.9 kb, modified maize Mu transposon
               designed to allow plasmid rescue from total genomic DNA.
               Mu elements insert preferentially into transcription
               units. For more information on RescueMu, go to the web
               site 'http://www.mutransposon.org/project/RescueMu/'. Grid
               O was grown at Stanford in 2001. DNA was extracted from
               leaf strips, double digested using BamHI and BglII, and
               ligated to form circular plasmids. DH10B cells were
               transformed and then screened on LB plates with
               ampicillin."

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 153
DX071328/c
LOCUS          DX071328          37 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION    KBrB081A15P KBrB, Brassica rapa BamHI BAC library Brassica rapa
               subsp. pekinensis genomic clone KBrB081A15, genomic survey
               sequence.

ACCESSION      DX071328
VERSION        DX071328.1  GI:84765624
KEYWORDS       GSS.
SOURCE         Brassica rapa subsp. pekinensis
ORGANISM       Brassica rapa subsp. pekinensis

REFERENCE
AUTHORS        Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
               Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
               Hahn,J.H. and Park,B.S.

```

```

TITLE
JOURNAL
COMMENT
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbsomrda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB081A15
Seq primer: T7
Class: BAC ends.

FEATURES
    source
        1..37
            Location/Qualifiers
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrB081A15"
                /lab_host="E.coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."
```

```

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 154
LOCUS DX072665 37 bp DNA linear GSS 10-JAN-2006
DEFINITION KBrB082M17f KBrB, Brassica rapa BamHI BAC library Brassica rapa
ACCESSION subsp. pekinensis genomic clone KBrB082M17, genomic survey
VERSION DX072665.1 GI:84766961
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 37)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbsomrda.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB082M17
Seq primer: T7
Class: BAC ends.

FEATURES
    source
        1..37
            Location/Qualifiers
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrB082M17"
                /lab_host="E.coli DH10B"
                /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
                pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                by Yong-Pyo Lim (CNU)."
```

```

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 155
LOCUS DR102P24T/c 37 bp DNA linear GSS 21-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-102P24, genomic survey sequence.
ACCESSION AL977144
VERSION AL977144.1 GI:25173875
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 37)
Humphray, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 102P24. 102P24
is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
    source
        1..37
            Location/Qualifiers
                /organism="Danio rerio"
                /mol_type="genomic DNA"
                /db_xref="taxon:7955"
                /clone="DKEY-102P24"
                /tissue_type="Testis"
                /note="vector pindigoBAC-536"
```

```

Query Match      1.3%; Score 35; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 156
LOCUS DR102P2T 37 bp DNA linear GSS 21-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-102P2, genomic survey sequence.
ACCESSION AL985556
VERSION AL985556.1 GI:25173839
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 37)
Humphray, S.J., Huckle, E. and Hunt, S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
```

Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
 This sequence was generated from the T7 end of BAC 102P2. 102P2 is part of the Danokey BAC Library created by R. Plasterk and N.V. Keygene.
 Further details: http://www.sanger.ac.uk/Projects/D_reio/.

FEATURES

source

Location/Qualifiers
 1..37
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEY-102P2"
 /tissue_type="Testis"
 /notes="vector pindigobAC-536"

Query Match 1.3%; Score 35; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 157

CF291176/c

LOCUS
 DEFINITION
 14ROOT--01-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-I01, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ROOT--01-I01"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E. coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 158

CF301164/c

LOCUS

DEFINITION

38 bp mRNA linear EST.
 7LEAF--05-O13.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-O13, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--05-O13"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E. coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY

2709

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

2743

Db

38

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

4

RESULT 159

CF301819/c

LOCUS

DEFINITION

38 bp mRNA linear EST.
 7LEAF--06-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--06-N03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--01-I01"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E. coli DH10B"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 163
LOCUS CF329690 38 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-B17.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-B17, mRNA sequence.

ACCESSION CF329690.1 GI:33807593
VERSION CF329690
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-B17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 164
LOCUS CF329730/c 38 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-C15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--05-C15, mRNA sequence.

ACCESSION CF329730.1 GI:33807676
VERSION CF329730
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-C15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 165
LOCUS BF525501 38 bp mRNA linear EST 11-DEC-2000
DEFINITION 602069592P1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212527 5', mRNA sequence.

ACCESSION BF525501
VERSION BF525501.1 GI:11612862
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LAM9783 row: 9 column: 24
 High quality sequence stop: 38.

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo

1 (bases 1 to 38)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM9783 row: 9 column: 24

High quality sequence stop: 38.

FEATURES
 source

1..38

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4212527"

/tissue_type="glioblastoma with EGFR amplification"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Brn64"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.57 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 166
 BF526154

LOCUS BF526154 38 bp mRNA linear EST 11-DEC-2000

DEFINITION 602071057F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213910

5', mRNA sequence.

ACCESSION BF526154.1 GI:11613430

VERSION BF526154

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo

1 (bases 1 to 38)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

National Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM9787 row: a column: 15

High quality sequence stop: 38.

FEATURES
 source

1..38

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4213910"
 /tissue_type="glioblastoma with EGFR amplification"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Brn64"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.57 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.3%; Score 35; DB 1; Length 38;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 167

CV724657/c

LOCUS CV724657 38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--01-F18.g1 Salt treated rice leaf lambda phage cDNA library

14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--01-F18, mRNA sequence.

ACCESSION CV724657

VERSION CV724657.1 GI:55412281

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--01-F18"

/tissue_type="leaf"

/dev_host="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA

library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity

Matches

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 168

CV725198/c

LOCUS CV725198 38 bp mRNA linear EST 04-NOV-2004

DEFINITION 14Salt--02-C15.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725198 14Salt--02-C15, mRNA sequence.
 CV725198.1 GI:55412822
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source
 1..38
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-C15"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169
 CV725495/c
 LOCUS
 DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725495 14Salt--02-J20, mRNA sequence.
 CV725495.1 GI:55413119
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169
 CV725495/c
 LOCUS
 DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725495 14Salt--02-J20, mRNA sequence.
 CV725495.1 GI:55413119
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169
 CV725495/c
 LOCUS
 DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725495 14Salt--02-J20, mRNA sequence.
 CV725495.1 GI:55413119
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-J20"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 170
 CV726250/c
 LOCUS
 DEFINITION 14Salt--03-M16.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV726250 14Salt--03-M16, mRNA sequence.
 CV726250.1 GI:55413874
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 170
 CV726250/c
 LOCUS
 DEFINITION 14Salt--03-M16.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV726250 14Salt--03-M16, mRNA sequence.
 CV726250.1 GI:55413874
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169
 CV725495/c
 LOCUS
 DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725495 14Salt--02-J20, mRNA sequence.
 CV725495.1 GI:55413119
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 169
 CV725495/c
 LOCUS
 DEFINITION 14Salt--02-J20.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 CV725495 14Salt--02-J20, mRNA sequence.
 CV725495.1 GI:55413119
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 171
 CV726534/c 38 bp mRNA linear EST 04-NOV-2004
 LOCUS 14Salt--04-D18.g1 Salt treated rice leaf lambda phage cDNA library
 DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-D18, mRNA sequence.

ACCESSION CV726534
 VERSION CV726534.1 GI:55414158
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 38)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--04-D18"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 172
 CV726895/c 38 bp mRNA linear EST 04-NOV-2004
 LOCUS 14Salt--04-M09.g1 Salt treated rice leaf lambda phage cDNA library
 DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-M09, mRNA sequence.

ACCESSION CV726895
 VERSION CV726895.1 GI:55414519
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--04-M09"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 173
 CV726983/c 38 bp mRNA linear EST 04-NOV-2004
 LOCUS 14Salt--04-O14.g1 Salt treated rice leaf lambda phage cDNA library
 DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-O14, mRNA sequence.

ACCESSION CV726983
 VERSION CV726983.1 GI:55414607
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--04-D18"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 174
 CV726983/c 38 bp mRNA linear EST 04-NOV-2004
 LOCUS 14Salt--04-O14.g1 Salt treated rice leaf lambda phage cDNA library
 DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-O14, mRNA sequence.

ACCESSION CV726983
 VERSION CV726983.1 GI:55414607
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 38)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 source
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--04-O14"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 175
 CV726983/c 38 bp mRNA linear EST 04-NOV-2004
 LOCUS 14Salt--04-M09.g1 Salt treated rice leaf lambda phage cDNA library
 DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-M09, mRNA sequence.

ACCESSION CV726983
 VERSION CV726983.1 GI:55414519
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

/lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 174

CV727096/c

LOCUS

DEFINITION

CV727096 38 bp mRNA linear EST 04-NOV-2004
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA library

14Salt--05-B06, mRNA sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-B06"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 175

CV727478/c

LOCUS

DEFINITION

CV727478 38 bp mRNA linear EST 04-NOV-2004
 (14Salt--05-K07, mRNA sequence.

14Salt--05-B06, mRNA sequence.

ACCESSION

VERSION

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-K07, mRNA sequence.

CV727478

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-K07"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 176

CV727598/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 38)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..38

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-B06"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."Query Match 1.3%; Score 35; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-N02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 177
CV727921/c

LOCUS
DEFINITION 14Salt--06-F06.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV727921

VERSION 1.38
KEYWORDS
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-F06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 178
CV728176/c

LOCUS
DEFINITION 14Salt--06-L22.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV728176

VERSION 1.38
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1. 38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-L22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 179
CV728223/c

LOCUS
DEFINITION 14Salt--06-N02.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
CV728223

VERSION 1.38
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 38)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-N02"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 |||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 180
CV728809/c
LOCUS FLO--01-F07.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-F07, mRNA
 sequence.

ACCESSION CV728809
VERSION CV728809.1 GI:55431587
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-F07"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 |||
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 181
CV728835/c

LOCUS FLO--01-F21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--01-F21, mRNA
 sequence.

ACCESSION CV728835
VERSION CV728835.1 GI:55431639

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 1..38
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-F21"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 |||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 182
CV729857/c

LOCUS FLO--03-B18.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-B18, mRNA
 sequence.

ACCESSION CV729857
VERSION CV729857.1 GI:55433501

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

1. 38
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-B18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 193
CV731476/c
LOCUS FLO--05-I12.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-I12, mRNA sequence.
CV731476 38 bp mRNA linear EST 05-NOV-2004

ACCESSION CV731476.1 GI:55436680
VERSION Oryza sativa (japonica cultivar-group)
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 38)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

1. 38
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-I12"
/tissue_type="flower"
/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 184

DR064343
LOCUS ip76h05.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA sequence.
DEFINITION DR064343
ACCESSION DR064343.1 GI:66987911
VERSION EST.
KEYWORDS Ginkgo biloba (maidenhair tree)
SOURCE Ginkgo biloba
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE 1 (bases 1 to 38)
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Ballja, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
TITLE Expressed tag sequences from Ginkgo megasporophyll (NYBG)
JOURNAL Unpublished (2005)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source

1. 38
Location/Qualifiers
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="Female"
/clone_lib="Ginkgo megasporophyll (NYBG)"
/note="Organ: megasporophyll; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 185

DW337683/c
LOCUS EST-AR18G8 Sus scrofa mixed tissue cDNA library Sus scrofa cDNA clone AR18G8, mRNA sequence.
DEFINITION DW337683
ACCESSION DW337683.1 GI:84566064
VERSION EST.
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Cranita; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

```

REFERENCE
1. (bases 1 to 38)
Rink,A., Santschi,E.M. and Beattie,C.W.
Normalised cDNA libraries from a porcine model of orthopedic
implant-associated infection
Mamm. Genome 13 (4), 198-205 (2002)
11956763
JOURNAL
COMMENT
Contact: Rink, A
Animal Disease and Food Safety Laboratory
Nevada Department of Agriculture
350 Capitol Hill Avenue, Reno, NV 89502, USA
Tel: 775-688-1180 Ext. 232
Fax: 775-688-1198
Email: arink@govmail.state.nv.us
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGG'. row: G column: 8.
FEATURES
Location/Qualifiers
1..38
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="AR1808"
/tissue_type="mixed"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/clone_lib="Sus scrofa mixed tissue cDNA library"
/note="Vector: pBSK; Site 1: Eco RI; Site 2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCAGG'."
Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 186
A2785034/c 38 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
2M0028106R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0028106 R, genomic survey sequence.
ACCESSION
A2785034
VERSION
A2785034.1 GI:12921371
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Sus.
1. (bases 1 to 38)
Rink,A., Santschi,E.M. and Beattie,C.W.
Normalised cDNA libraries from a porcine model of orthopedic
implant-associated infection
Mamm. Genome 13 (4), 198-205 (2002)
11956763
JOURNAL
COMMENT
Contact: Rink, A
Animal Disease and Food Safety Laboratory
Nevada Department of Agriculture
350 Capitol Hill Avenue, Reno, NV 89502, USA
Tel: 775-688-1180 Ext. 232
Fax: 775-688-1198
Email: arink@govmail.state.nv.us
Tissues and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of Staphylococcus
aureus in a tibial transection, reduced and internally fixed with a
dynamic compression plate. NOTE: The sequences contain a 'cDNA
adapter' between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGG'. row: G column: 8.
FEATURES
Location/Qualifiers
1..38
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="crossbreed"
/db_xref="taxon:9823"
/clone="AR1808"
/tissue_type="mixed"
/cell_type="mixed"
/dev_stage="control, 5 month old castrated male"
/lab_host="SOLR"
/clone_lib="Sus scrofa mixed tissue cDNA library"
/note="Vector: pBSK; Site 1: Eco RI; Site 2: XhoI; Tissues
and cells are derived from a porcine model for
implant-associated infection using 1000 cfu of
Staphylococcus aureus in a tibial transection, reduced and
internally fixed with a dynamic compression plate. NOTE:
The sequences contain a 'cDNA adapter' between the EcoRI
site and the start of the EST. The adapter sequence is
'AATTCGGCAGG'."
Query Match 1.3%; Score 35; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 187
BG287495 39 bp mRNA linear EST 21-FEB-2001
LOCUS
DEFINITION
603284505F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4513609 5',
mRNA sequence.
ACCESSION
BG287495
VERSION
BG287495.1 GI:13041394
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 39)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: I column: 06
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
FEATURES
Location/Qualifiers
1..38
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028106"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAM10400 row: i column: 02
 High quality sequence stop: 36.
 Location/Qualifiers

FEATURES

1..39
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4513609"
 /tissue_type="transitional cell papilloma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_93"
 /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 188
 BI694035 39 bp mRNA linear EST 18-SEP-2001
 LOCUS 603342221F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5369956 5',
 DEFINITION mRNA sequence.

ACCESSION BI694035
 VERSION BI694035.1 GI:15656664

KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 39)
 NIH-MGC <http://mgs.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 TITLE Contact: Robert Strausberg, Ph.D.
 JOURNAL Email: cgapbs@mail.nih.gov
 COMMENT Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM11941 row: j column: 05
 High quality sequence stop: 39.
 Location/Qualifiers

FEATURES

1..39
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:5369956"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mam2"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 189

CF298508/c 39 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--01-O19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--01-O19, mRNA
 sequence.

ACCESSION CF298508
 VERSION CF298508.1 GI:33670269

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 39)
 Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,

Authors Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES

1..39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--01-O19"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 190

CF302356/c 39 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--07-M16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-M16, mRNA
 sequence.

ACCESSION CF302356
 VERSION CF302356.1 GI:33674117

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .39
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="7LEAF--07-M16"
   /tissue_type="leaf"
   /dev_stage="7 days after germination"
   /lab_host="E.coli DH10B"
   /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
   with oligoribonucleotides and then used as templates for
   RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 191
CF315736/c
LOCUS      Oryza sativa (japonica cultivar-group)
DEFINITION HD--04-M06.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--04-M06, mRNA sequence.
ACCESSION  CF315736
VERSION     1
KEYWORDS    Oryza sativa (japonica cultivar-group)
SOURCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 39)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .39
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="HD--04-M06"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
   library (HD)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 193
CF315736/c
LOCUS      Oryza sativa (japonica cultivar-group)
DEFINITION HD--12-I17.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--12-I17, mRNA sequence.
ACCESSION  CF315736
VERSION     1
KEYWORDS    Oryza sativa (japonica cultivar-group)
SOURCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 39)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .39
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="HD--12-I17"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 193
CF315732/c
LOCUS      Oryza sativa (japonica cultivar-group)
DEFINITION HD--06-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza

```

```

cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 192
CF3121323/c
LOCUS      Oryza sativa (japonica cultivar-group)
DEFINITION HD--12-I17.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--12-I17, mRNA sequence.
ACCESSION  CF3121323
VERSION     1
KEYWORDS    Oryza sativa (japonica cultivar-group)
SOURCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 39)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1. .39
   /organism="Oryza sativa (japonica cultivar-group)"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:39947"
   /clone="HD--12-I17"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 2 weeks"
   /lab_host="E.coli DH10B"
   /clone_lib="OshDACL1-overexpressing transgenic rice plasmid
   cDNA library (HD)"
   /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
   treated with ABA(20um) for 1hr. Oligo-capped mRNA was
   reverse transcribed and then used for PCR. mRNA was
   derived from rice Histone Deacetylase overexpression
   line."

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 193
CF312132/c
LOCUS      Oryza sativa (japonica cultivar-group)
DEFINITION HD--06-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza

```

sativa (japonica cultivar-group) cDNA clone NACL--06-J06, mRNA sequence.
 CF330732.1 GI:33809685
 EST.
 ORIGIN
 ORYZA SATIVA (japonica cultivar-group)
 ORYZA SATIVA (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzoideae; Oryza.
 1 (bases 1 to 39)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-J06"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 194
 BF032623
 LOCUS 601453114F1 NIH_MGC_66 39 bp mRNA linear EST 20-OCT-2000
 DEFINITION mRNA sequence.
 ACCESSION BF032623
 VERSION BF032623.1 GI:10740335
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 39)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9586 row: k column: 04

High quality sequence stop: 39.
 Location/Qualifiers
 1..39
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3857019"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_66"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 195
 BE891613
 LOCUS 601434505F1 NIH_MGC_72 39 bp mRNA linear EST 20-OCT-2000
 DEFINITION mRNA sequence.
 ACCESSION BE891613
 VERSION BE891613.1 GI:10351110
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 39)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM9749 row: j column: 01

High quality sequence stop: 39.
 Location/Qualifiers
 1..39
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3919584"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

FEATURES

source
 1..39
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3919584"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 196
CV724457/c
LOCUS
DEFINITION
CV724457 39 bp mRNA linear EST 04-NOV-2004
14Salt--01-A17.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-A17, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-A17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 197
CV724623/c
LOCUS
DEFINITION
CV724623 39 bp mRNA linear EST 04-NOV-2004
14Salt--01-E22.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-E22, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-E22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-E22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 198

CV725192/c

LOCUS

DEFINITION

CV725192 39 bp mRNA linear EST 04-NOV-2004

14Salt--02-C12.g1 Salt treated rice leaf lambda phage cDNA library

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

14Salt--02-C12, mRNA sequence.

ACCESSION

CV725192

VERSION

CV725192.1 GI:55412816

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..39

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--02-C12"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 199
CV725228/c
LOCUS
DEFINITION
14Salt--02-D09.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-D09, mRNA sequence.

ACCESSION CV725228.1 GI:55412852
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..39
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-D09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 200
CV725383/c
LOCUS
DEFINITION
14Salt--02-H03.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-H03, mRNA sequence.

ACCESSION CV725383.1 GI:55413007
VERSION
KEYWORDS

SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..39
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-H03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 201
CV725570/c
LOCUS
DEFINITION
14Salt--02-L15.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-L15, mRNA sequence.

ACCESSION CV725570.1 GI:55413194
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..39
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-L15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes=Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 202
CV726046/c
LOCUS
DEFINITION
14Salt--03-H15.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-H15, mRNA sequence.
ACCESSION
CV726046
VERSION
E01
KEYWORDS
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes=Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 204
CV726327/c
LOCUS
DEFINITION
14Salt--03-O11.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-O11, mRNA sequence.
ACCESSION
CV726327
VERSION
E01
KEYWORDS
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes=Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

```

RESULT 203
CV726057/c
LOCUS
DEFINITION
14Salt--03-H22.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-H22, mRNA sequence.
ACCESSION
CV726057
VERSION
E01
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-H22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes=Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 204
CV726327/c
LOCUS
DEFINITION
14Salt--03-O11.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-O11, mRNA sequence.
ACCESSION
CV726327
VERSION
E01
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-P04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 205

CV726361/c

LOCUS

DEFINITION

14Salt--03-P04.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P04, mRNA sequence.

ACCESSION

CV726361

VERSION

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-P04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 206

CV726728/c

LOCUS

DEFINITION

14Salt--04-I09.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-I09, mRNA sequence.

ACCESSION

CV726728

VERSION

EST

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 39)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-I09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 207

CV726866/c

LOCUS

DEFINITION

14Salt--04-L17.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-L17, mRNA sequence.

ACCESSION

CV726866

VERSION

EST

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 213
 CV727215/c
 LOCUS
 DEFINITION 39 bp mRNA linear EST 04-NOV-2004
 14Salt--05-E03.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt--05-E03, mRNA sequence.

ACCESSION CV727215 GI:55414839
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 39)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source
 1..39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-E03"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 214
 CV727351/c
 LOCUS
 DEFINITION 39 bp mRNA linear EST 04-NOV-2004
 14Salt--05-H08.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt--05-H08, mRNA sequence.

ACCESSION CV727351 GI:55414975
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 39)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source

1..39
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-H08"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 215
 CV727680/c
 LOCUS
 DEFINITION 39 bp mRNA linear EST 04-NOV-2004
 14Salt--05-P01.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-P01, mRNA sequence.

ACCESSION CV727680 GI:55415304
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 39)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source

1..39
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"

```

/clone="14Salt--05-P01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

```

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

```

```

RESULT 216
CV728240/c
LOCUS
DEFINITION
14Salt--06-N13.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-N13, mRNA sequence.

```

```

ACCESSION
CV728240
VERSION
CV728240.1 GI:55430541
KEYWORDS
SOURCE

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Erihartoideae; Oryzae; Oryza.

```

```

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-N13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

```

FEATURES
source

```

```

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

```

```

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

```

```

RESULT 217

```

```

CV728278/c
LOCUS
DEFINITION
14Salt--06-O12.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-O12, mRNA sequence.

```

```

ACCESSION
CV728278
VERSION
CV728278.1 GI:55430594
KEYWORDS
SOURCE

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Erihartoideae; Oryzae; Oryza.

```

```

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-O12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

```

FEATURES
source

```

```

Query Match      1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

```

```

RESULT 218
CV729217/c
LOCUS
DEFINITION
FLO--01-P02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-P02, mRNA
sequence.

```

```

ACCESSION
CV729217
VERSION
CV729217.1 GI:55432392
KEYWORDS
SOURCE

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Erihartoideae; Oryzae; Oryza.

```

```

REFERENCE
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

```

```

Contact: Nahm B.H.
of Bioscience and Bioinformatics, Myongji University

```



```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-P02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 219
CV730113/c
LOCUS
DEFINITION
FLO--03-H21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--03-H21, mRNA
sequence.
CV730113
VERSION
CV730113.1 GI:55433994
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 39)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-H21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 220
CV732729/c
LOCUS
DEFINITION
FLO--07-F09.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-F09, mRNA
sequence.
CV732729
VERSION
CV732729.1 GI:55438860
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 39)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-F09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 221
CV733026/c
LOCUS
DEFINITION
FLO--07-M05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-M05, mRNA
sequence.
CV733026
VERSION
CV733026.1 GI:55439436
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 39)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-H21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-M05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 222

CV733160/c
LOCUS
DEFINITION
FLO--07-P05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-P05, mRNA sequence.

ACCESSION CV733160

VERSION CV733160.1

GI:55439700

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 39)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-P05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 223

CV733431/c

LOCUS

DEFINITION

FLO--08-F12.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-F12, mRNA sequence.

ACCESSION CV733431

VERSION CV733431.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 39)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-F12"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 224

CV733935/c

LOCUS

DEFINITION

FLO--09-B06.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-B06, mRNA sequence.

ACCESSION CV733935

VERSION CV733935.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 39)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..39
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-R06"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 225

CV733973/c
LOCUS
DEFINITION
FLO--09-C05.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-C05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CV733973.1 GI:55441315
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 39)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1..39
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-C05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 226

AZ639088/c
LOCUS
DEFINITION
1M0499A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0499A20 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ639088.1 GI:11762488
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0499 row: A column: 20
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 39.

FEATURES

source

1..39
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0499A20"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2709	AA	2743
Db	39	AA	5
RESULT 227			
AL037510		40 bp	mRNA
LOCUS		linear	EST 06-JUL-2004
DEFINITION		DKFZp564E1872_r1_564 (synonym: hfb2) Homo sapiens cDNA clone	
ACCESSION		AL037510	
VERSION		AL037510.1	GI:49682008
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.	
TITLE		EST (Blum, et al.)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: MIPS	
FEATURES		MIPS	
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.			
Location/Qualifiers			
1. .40			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="DKFZp564E1872"			
/tissue_type="brain"			
/dev_stage="fetal"			
/lab_host="Xl-2blue"			
/clone_lib="564 (synonym: hfb2)"			
/note="Vector: pAMF1; Site_1: NotI; Site_2: SalI"			
Query Match		1.3%;	Score 35; DB 1; Length 40;
Best Local Similarity		100.0%;	Pred. No. 1.9e+02;
Matches		35; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2709	AA	2743
Db	5	AA	39
RESULT 228			
AL449576/c		40 bp	mRNA
LOCUS		linear	EST 15-NOV-2000
DEFINITION		AL449576 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA, mRNA	
ACCESSION		AL449576	
VERSION		AL449576.1	GI:11181211
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Stavrides, G.S., Huckle, E.J. and Deloukas, P.	
TITLE		Unpublished. Stavrides, G.S., Huckle, E.J. and Deloukas, P	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Stavrides GS	
The Sanger Centre			
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK			
Email: humquery@sanger.ac.uk			
Sanger Centre name : sccd3232.			
Location/Qualifiers			
1. .40			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
FEATURES			
source			

/map="20"			
/tissue_type="Testis"			
/clone_lib="Homo sapiens Testis (Stavrides GS)"			
/note="cDNA fragment isolated using a cDNA end rescue technique"			
Query Match		1.3%;	Score 35; DB 1; Length 40;
Best Local Similarity		100.0%;	Pred. No. 1.9e+02;
Matches		35; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2709	AA	2743
Db	40	AA	6
RESULT 229			
BGI66502		40 bp	mRNA
LOCUS		linear	EST 06-FEB-2001
DEFINITION		602339795F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4447702 5', mRNA sequence.	
ACCESSION		BGI66502	
VERSION		BGI66502.1	GI:12673205
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Robert Strausberg, Ph.D.	
Email: cgapbs-remail.nih.gov			
Tissue Procurement: ATCC			
cDNA Library Preparation: Life Technologies, Inc.			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Incyte Genomics, Inc.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
Plate: LLNL0228		row: n	column: 23
High quality sequence stop: 40.			
Location/Qualifiers			
1. .40			
/organism="Homo sapiens"			
/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="IMAGE:4447702"			
/tissue_type="hypernephroma, cell line"			
/lab_host="DH10B (phage-resistant)"			
/clone_lib="NIH_MGC_89"			
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."			
Query Match		1.3%;	Score 35; DB 1; Length 40;
Best Local Similarity		100.0%;	Pred. No. 1.9e+02;
Matches		35; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	2709	AA	2743
Db	1	AA	35
RESULT 230			
CF311814/c		40 bp	mRNA
LOCUS		linear	EST 15-AUG-2003
DEFINITION		ABF--07-D23.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone	
ABF--07-D23, mRNA sequence.			

```

ACCESSION      CF311814
VERSION        CF311814.1  GI:33683575
KEYWORDS
SOURCE
ORGANISM       Oryza sativa (japonica cultivar-group)
               Oryza sativa (japonica cultivar-group)
               Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-07-D23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 231
CF327027/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-P21, mRNA
               sequence.
ACCESSION      CF328199
VERSION        CF328199.1  GI:33804646
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-07-D23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 231
CF327027/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-F11, mRNA
               sequence.
ACCESSION      CF327027
VERSION        CF327027.1  GI:33802307
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

```

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-F11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 232
CF328199/c
LOCUS
DEFINITION     Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-P21, mRNA
               sequence.
ACCESSION      CF328199
VERSION        CF328199.1  GI:33804646
KEYWORDS
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
               clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-P21"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

```

```

RESULT 233
CF328306
LOCUS
DEFINITION
  NACL--03-C09.g1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa (japonica cultivar-group) cDNA clone NACL--03-C09, mRNA
  sequence.
ACCESSION
CF328306
VERSION
CF328306.1 GI:33804858
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="NACL--03-C09"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
Query Match
  1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 234
CF334545/c
LOCUS
DEFINITION
  JMT--03-002.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
  library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
  JMT--03-002, mRNA sequence.
ACCESSION
CF334545
VERSION
CF334545.1 GI:33817420
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="NACL--03-C09"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
Query Match
  1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 235
CV724551/c
LOCUS
DEFINITION
  14Salt--01-D05.b1 Salt treated rice leaf lambda phage cDNA library
  14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--01-D05, mRNA sequence.
ACCESSION
CV724551
VERSION
CV724551.1 GI:55412175
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--01-D05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: Bluescript SK(+); Site_1: EcoRI; Site_2:
    XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."

```

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="JMT--03-002"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
    cDNA library (JMT)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
    was reverse transcribed and then used for PCR. mRNA was
    prepared from Arabidopsis Jasmonate Carboxyl
    methyltransferase overexpression line."
Query Match
  1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 235
CV724551/c
LOCUS
DEFINITION
  14Salt--01-D05.b1 Salt treated rice leaf lambda phage cDNA library
  14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--01-D05, mRNA sequence.
ACCESSION
CV724551
VERSION
CV724551.1 GI:55412175
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzae; Oryza.
  1 (bases 1 to 40)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..40
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--01-D05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: Bluescript SK(+); Site_1: EcoRI; Site_2:
    XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."

```



```

/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

```

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 239
 CV727416/c
 LOCUS
 DEFINITION 14Salt--05-121.bl Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-121, mRNA sequence.

ACCESSION CV727416
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-121"
 /tissue type="leaf"
 /dev stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 240
 CV727587/c
 LOCUS
 DEFINITION 14Salt--06-C07.gi Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-C07, mRNA sequence.

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 240
 CV727587/c
 LOCUS
 DEFINITION 14Salt--06-C07.gi Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-C07, mRNA sequence.

LOCUS
 DEFINITION 14Salt--05-M20.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--05-M20, mRNA sequence.

ACCESSION CV727587
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-M20"
 /tissue type="leaf"
 /dev stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 241
 CV727805/c
 LOCUS
 DEFINITION 14Salt--06-C07.gi Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-C07, mRNA sequence.

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 241
 CV727805/c
 LOCUS
 DEFINITION 14Salt--06-C07.gi Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-C07, mRNA sequence.

ACCESSION CV727805
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 40)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

FEATURES
 source
 1..40
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--05-M20"
 /tissue type="leaf"
 /dev stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .40
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-C07"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 242

CV727843/c
 LOCUS
 DEFINITION
 14Salt--06-D06.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-D06, mRNA sequence.

ACCESSION CV727843.1 GI:55415467

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .40
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-D06"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 243

CV727858/c
 LOCUS
 DEFINITION
 14Salt--06-D16.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-D16, mRNA sequence.

ACCESSION CV727858.1 GI:55415482

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .40
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--06-D16"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 244

CV728325/c
 LOCUS
 DEFINITION
 14Salt--06-P15.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--06-P15, mRNA sequence.

ACCESSION CV728325.1 GI:55430670

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

Query Match

1.3%; Score 35; DB 1; Length 40;

```

REFERENCE
AUTHORS   clade: Ehrhartoideae; Oryzae; Oryza.
          1 (bases 1 to 40)
JOURNAL   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
COMMENT   Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source    Location/Qualifiers
          1..40
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:39947"
          /clone="14Salt--06-P15"
          /tissue_type="leaf"
          /dev_stage="14 days after germination"
          /lab_host="E.coli SOLR"
          /clone_lib="Salt treated rice leaf lambda phage cDNA
          library (14Salt)"
          /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
          XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
          cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
          with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
     |||||||
Db   40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 245
LOCUS   CV728655/c
DEFINITION FLO--01-B17.g1 Rice flower lambda phage cDNA library (FLO) Oryza
          sativa (japonica cultivar-group) cDNA clone FLO--01-B17, mRNA
          sequence.
ACCESSION CV728655
VERSION   CV728655.1 GI:55431284
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzae; Oryza.
          1 (bases 1 to 40)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source    Location/Qualifiers
          1..40
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:39947"
          /clone="FLO--01-B17"
          /tissue_type="flower"

```

```

          /lab_host="E.coli SOLR"
          /clone_lib="Rice flower lambda phage cDNA library (FLO)"
          /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
          XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
          end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
     |||||||
Db   40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 246
LOCUS   CV730371/c
DEFINITION FLO--03-005.b1 Rice flower lambda phage cDNA library (FLO) Oryza
          sativa (japonica cultivar-group) cDNA clone FLO--03-005, mRNA
          sequence.
ACCESSION CV730371
VERSION   CV730371.1 GI:55434492
KEYWORDS EST.
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzae; Oryza.
          1 (bases 1 to 40)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source    Location/Qualifiers
          1..40
          /organism="Oryza sativa (japonica cultivar-group)"
          /mol_type="mRNA"
          /cultivar="Nackdong"
          /db_xref="taxon:39947"
          /clone="FLO--03-005"
          /tissue_type="flower"
          /lab_host="E.coli SOLR"
          /clone_lib="Rice flower lambda phage cDNA library (FLO)"
          /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
          XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
          end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

Oy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
     |||||||
Db   40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 247
LOCUS   CV731031/c
DEFINITION FLO--04-N24.g1 Rice flower lambda phage cDNA library (FLO) Oryza
          sativa (japonica cultivar-group) cDNA clone FLO--04-N24, mRNA
          sequence.
ACCESSION CV731031
VERSION   CV731031.1 GI:55435791
KEYWORDS EST.

```

```

SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-N24"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 248
CV731319/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-E21, mRNA
sequence.
ACCESSION
CV731319.1 GI:55436371
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-E21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 248
CV731319/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-E21, mRNA
sequence.
ACCESSION
CV731319.1 GI:55436371
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-E21"

```

```

/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 249
CV731528/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-J15, mRNA
sequence.
ACCESSION
CV731528.1 GI:55436755
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-J15"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 250
CV732353/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-M17, mRNA
sequence.
ACCESSION
CV732353.1 GI:55438119

```

```

KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-06-M17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 251
CV732629/c
LOCUS
DEFINITION
FLO--07-D02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-D02, mRNA
sequence.
ACCESSION
CV732629
VERSION
CV732629.1 GI:55438664
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-D02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 251
CV732629/c
LOCUS
DEFINITION
FLO--07-D02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-D02, mRNA
sequence.
ACCESSION
CV732629
VERSION
CV732629.1 GI:55438664
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-D02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 253
CV733006/c
LOCUS
DEFINITION
FLO--07-L19.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-L19, mRNA
sequence.
ACCESSION
CV733006

```

```

/clone="FLO--07-D02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 252
CV732676/c
LOCUS
DEFINITION
FLO--07-E04.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-E04, mRNA
sequence.
ACCESSION
CV732676
VERSION
CV732676.1 GI:55438756
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 40)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
UNPUBLISHED (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-E04"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6
RESULT 253
CV733006/c
LOCUS
DEFINITION
FLO--07-L19.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-L19, mRNA
sequence.
ACCESSION
CV733006

```

[illegible]

```

ACCESSION CV733638
VERSION CV733638.1 GI:55440654
KEYWORDS EST.
SOURCE
ORGANISM
Orzyza sativa (japonica cultivar-group)
Orzyza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaeae; Oryza.
1 (bases 1 to 40)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-K08"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_libs="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 257
AZ831983
LOCUS AZ831983 40 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0112K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0112K02 F, genomic survey sequence.
ACCESSION AZ831983
VERSION AZ831983.1 GI:13001891
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 40)
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: K column: 02
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers
1. .40
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0112K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 258
DUB35034/c
LOCUS DUB35034 40 bp DNA linear GSS 22-DEC-2005
DEFINITION KBR5015N17F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBR5015N17, genomic survey
sequence.
ACCESSION DUB35034
VERSION DUB35034.1 GI:83871630
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 40)
REFERENCE
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBRs) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBR5015N17
Seq primer: T7

```

```

FEATURES
  source
    Class: BAC ends.
    Location/Qualifiers
      1..40
        /organism="Brassica rapa subsp. pekinensis"
        /mol_type="genomic DNA"
        /cultivar="Chiifu"
        /sub_species="pekinensis"
        /db_xref="taxon:51351"
        /clone="KBrS015N17"
        /lab_host="E. coli DH10B"
        /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
        ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
        available at NIMB."
      1..3%; Score 35; DB 1; Length 40;
      Best Local Similarity 100.0%; Pred. No. 1.9e+02;
      Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 259
AJ792759
LOCUS
DEFINITION
  AJ792759 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
  018.2.12.h22, mRNA sequence.
ACCESSION
  AJ792759
KEYWORDS
  EST.
SOURCE
  Antirrhinum majus (snapdragon)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  asterids; lamids; Lamiales; Plantaginaceae; Antirrhineae;
  Antirrhinum.
REFERENCE
  1 (bases 1 to 41)
  Saedler, H. and Zachgo, S.
  Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
  Characterization of Antirrhinum Petal Development and
  Identification of Target Genes of the Class B MADS Box Gene
  DEFICIENS
  Plant Cell 16 (12), 3197-3215 (2004)
  15539471
COMMENT
  Contact: Schwarz-Sommer Z
  Molekulare Pflanzen-genetik
  MPI fuer Zuechtungs-forschung
  Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
  source
    1..41
      /organism="Antirrhinum majus"
      /mol_type="mRNA"
      /db_xref="taxon:4151"
      /clone="018.2.12.h22"
      /tissue_type="whole plant"
      /clone_lib="Antirrhinum majus whole plant"
    1..3%; Score 35; DB 1; Length 41;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 260
CF291539/c
LOCUS
DEFINITION
  14ROOT--02-A03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
  sativa (japonica cultivar-group) cDNA clone 14ROOT--02-A03, mRNA

```

```

sequence.
CF291539
VERSION
  CF291539.1 GI:33660572
EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 41)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyonggi, Korea
  Tel: 82 31 321 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
  source
    1..41
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="14ROOT--02-A03"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."
    Query Match 1..3%; Score 35; DB 1; Length 41;
    Best Local Similarity 100.0%; Pred. No. 2e+02;
    Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 261
CF318677/c
LOCUS
DEFINITION
  CF318677 41 bp mRNA linear EST 15-AUG-2003
  HD--08-009.g1 OshD4C1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
  HD--08-009, mRNA sequence.
ACCESSION
  CF318677
VERSION
  CF318677.1 GI:33690438
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 41)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyonggi, Korea
  Tel: 82 31 321 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
  source
    1..41

```

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-08-O09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 262
CF320203/c
LOCUS
DEFINITION
HD--10-P19.b1 OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-P19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 264
CF320203/c
LOCUS
DEFINITION
HD--10-P19.b1 OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-P19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 263
CF330464/c
LOCUS
DEFINITION
NACL--06-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-D01, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-D01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 264
CF334638/c
LOCUS
DEFINITION
JMT--04-A03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--04-A03, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs

```


Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
 1. .41
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--04-A03"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="ACJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred.No.2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 265
 CV725868/c

LOCUS
 DEFINITION CV725868 41 bp mRNA linear EST 04-NOV-2004
 (14Salt)-03-D07.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt--03-D07, mRNA sequence.

ACCESSION
 VERSION CV725868.1 GI:55413492
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .41
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--03-D07"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 266
CV725993/c

LOCUS CV725993 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-G10.b1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-G10, mRNA sequence.

ACCESSION CV725993
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..41
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-G10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 267
CV726255/c

LOCUS CV726255 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-M18.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-M18, mRNA sequence.

ACCESSION CV726255
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

```

KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt-03-M18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
RESULT 268
CV726393/c
LOCUS 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-P21.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P21, mRNA sequence.
ACCESSION CV726393
VERSION 1 GI:55414017
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt-03-M18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7
RESULT 268
CV726393/c
LOCUS 41 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--03-P21.g1 Salt treated rice leaf lambda phage cDNA library
(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--03-P21, mRNA sequence.
ACCESSION CV726393
VERSION 1 GI:55414017
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt-04-N03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

```

CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-D24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 272
CV727412/c
LOCUS
DEFINITION
41 bp mRNA linear EST 04-NOV-2004
14Salt--05-118.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-118, mRNA sequence.

ACCESSION
CV727412.1 GI:55415036
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-P08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 271
CV727210/c
LOCUS
DEFINITION
41 bp mRNA linear EST 04-NOV-2004
14Salt--05-D24.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-D24, mRNA sequence.

ACCESSION
CV727210
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-P08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 271
CV727210/c
LOCUS
DEFINITION
41 bp mRNA linear EST 04-NOV-2004
14Salt--05-D24.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-D24, mRNA sequence.

ACCESSION
CV727210
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-P08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 271
CV727210/c
LOCUS
DEFINITION
41 bp mRNA linear EST 04-NOV-2004
14Salt--05-D24.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-D24, mRNA sequence.

ACCESSION
CV727210
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-P08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 271
CV727210/c
LOCUS
DEFINITION
41 bp mRNA linear EST 04-NOV-2004
14Salt--05-D24.g1 Salt treated rice leaf lambda phage cDNA library
14Salt--05-D24, mRNA sequence.

ACCESSION
CV727210
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@

cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 273
CV727841/c
LOCUS
DEFINITION 14Salt--06-D05.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-D05, mRNA sequence.

ACCESSION CV727841 GI:55415465
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-D05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 274
CV728055/c
LOCUS
DEFINITION 14Salt--06-I18.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-I18, mRNA sequence.

ACCESSION CV728055 GI:55430231
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--06-I18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 275
CV728228/c
LOCUS
DEFINITION 14Salt--06-N05.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--06-N05, mRNA sequence.

ACCESSION CV728228 GI:55430529
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 41)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

CV731668/c	LOCUS	CV731668	41 bp	mRNA	linear	EST 05-NOV-2004
LOCUS	DEFINITION	FLO--05-M20.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-M20, mRNA sequence.				
ACCESSION	VERSION	CV731668				
KEYWORDS	SOURCE	CV731668.1	GI:55436958			
ORGANISM	REFERENCE	Oryza sativa (japonica cultivar-group)				
	AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
	TITLE	Large-scale Sequencing Analysis of Rice ESTs				
	JOURNAL	Unpublished (2003)				
	COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University				
	Yongin, Kyeonggi, Korea					
	Tel: 82 31 330 6193					
	Fax: 82 31 321 6355					
	Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.					
FEATURES	source	1. 41				
		/organism="Oryza sativa (japonica cultivar-group)"				
		/mol_type="mRNA"				
		/cultivar="Nackdong"				
		/db_xref="taxon:39947"				
		/clone="FLO--05-M20"				
		/tissue_type="flower"				
		/lab_host="E.coli SOLR"				
		/clone_lib="Rice flower lambda phage cDNA library (FLO)"				
		/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."				
	Query Match	1.3%;	Score 35;	DB 1;	Length 41;	
	Best Local Similarity	100.0%;	Pred. No. 2e+02;			
	Matches	35;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
QY		2709	AAA	2743		
Db		41	AAA	7		
RESULT 281	LOCUS	CV732073	41 bp	mRNA	linear	EST 05-NOV-2004
LOCUS	DEFINITION	FLO--06-G04.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-G04, mRNA sequence.				
ACCESSION	VERSION	CV732073				
KEYWORDS	SOURCE	CV732073.1	GI:55437579			
ORGANISM	REFERENCE	Oryza sativa (japonica cultivar-group)				
	AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
	TITLE	Large-scale Sequencing Analysis of Rice ESTs				
	JOURNAL	Unpublished (2003)				
	COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University				
	Yongin, Kyeonggi, Korea					
	Tel: 82 31 330 6193					
	Fax: 82 31 321 6355					
	Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.					
FEATURES	source	1. 41				
		/organism="Oryza sativa (japonica cultivar-group)"				
		/mol_type="mRNA"				
		/cultivar="Nackdong"				
		/db_xref="taxon:39947"				
		/clone="FLO--05-H10"				
		/tissue_type="flower"				
		/lab_host="E.coli SOLR"				
		/clone_lib="Rice flower lambda phage cDNA library (FLO)"				
		/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."				
	Query Match	1.3%;	Score 35;	DB 1;	Length 41;	
	Best Local Similarity	100.0%;	Pred. No. 2e+02;			
	Matches	35;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
QY		2709	AAA	2743		
Db		41	AAA	7		
RESULT 280	LOCUS	CV731427/c	41 bp	mRNA	linear	EST 05-NOV-2004
LOCUS	DEFINITION	FLO--05-H10.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--05-H10, mRNA sequence.				
ACCESSION	VERSION	CV731427				
KEYWORDS	SOURCE	CV731427.1	GI:55436952			
ORGANISM	REFERENCE	Oryza sativa (japonica cultivar-group)				
	AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.				
	TITLE	Large-scale Sequencing Analysis of Rice ESTs				
	JOURNAL	Unpublished (2003)				
	COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University				
	Yongin, Kyeonggi, Korea					
	Tel: 82 31 330 6193					
	Fax: 82 31 321 6355					
	Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.					
FEATURES	source	1. 41				
		/organism="Oryza sativa (japonica cultivar-group)"				
		/mol_type="mRNA"				

```

FEATURES
source
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--06-G04"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 282
CV733839/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--08-O22, mRNA
sequence.
CV733839
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-J18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 284
CV733839/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--08-O22, mRNA
sequence.
CV733839
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-O22"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

```

```

RESULT 283
CV734304/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--09-J18, mRNA
sequence.
CV734304
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-J18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 284
CV735066
LOCUS
DEFINITION
2M0007101F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0007101 F, genomic survey sequence.
CV735066
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0007 row: I column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

source

```
1. .41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007101"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 285
AZ827008
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ827008 41 bp DNA linear GSS 20-FEB-2001
2M0103107F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0103107 F, genomic survey sequence.

ACCESSION AZ827008.1 GI:12996916
VERSION GSS.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: I column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

source

```
1. .41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103107"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 286
DU834001/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

DU834001 41 bp DNA linear GSS 22-DEC-2005
KBR5013D19F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBR5013D19, genomic survey
sequence.

ACCESSION DU834001.1 GI:83870597
VERSION DU834001
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa esp. pekinensis Sau3AI BAC clone
 KBrS013D19
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1. .41
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS013D19"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
 available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 287

DU834619 41 bp DNA linear GSS 22-DEC-2005
 LOCUS KBrS014M09F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrS014M09, genomic survey
 sequence.

ACCESSION DU834619.1 GI:83871215
 VERSION
 KEYWORDS
 SOURCE

ORGANISM Brassica rapa subsp. pekinensis
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J. H. and Park,B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa esp. pekinensis Sau3AI BAC clone
 KBrS014M09

Seq primer: T7

Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1. .41
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS014M09"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /notes="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is

available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 288

DU835000/c 41 bp DNA linear GSS 22-DEC-2005
 LOCUS KBrS015L21F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrS015L21, genomic survey
 sequence.

ACCESSION DU835000
 VERSION DU835000.1 GI:83871596
 KEYWORDS
 SOURCE

ORGANISM Brassica rapa subsp. pekinensis
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids 1; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J. H. and Park,B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS015L21

Seq primer: T7

Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1. .41
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS015L21"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
 available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 41;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 289

DX049410/c 41 bp DNA linear GSS 10-JAN-2006
 LOCUS KBrB052A12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrB052A12, genomic survey
 sequence.

ACCESSION DX049410
 VERSION DX049410.1 GI:84743707

```

KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 41)
AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL
Unpublished (2005)
COMMENT
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB052A12
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..41
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB052A12"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (GNU)."

Query Match 1.3%; Score 35; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 290
AJ691919
LOCUS
DEFINITION
AJ691919 KN261 Bos taurus cDNA clone KN261-025_M11, mRNA sequence.
ACCESSION
AJ691919
VERSION
AJ691919.1 GI:49424527
KEYWORDS
EST.
SOURCE
Bos taurus (cattle)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 42)
REFERENCE
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 5', Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

FEATURES
source
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..42
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-025_M11"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII (SK+); Site_1: EcoRI; Site_2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 291
BG292448
LOCUS
DEFINITION
602386574P1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4515403 5',
mRNA sequence.
ACCESSION
BG292448
VERSION
BG292448.1 GI:13051253
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 42)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10405 row: c column: 20
High quality sequence stop: 42.
Location/Qualifiers
1..42
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4515403"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_93"
/notes="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

```



```

treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 295
CF3320056
LOCUS
DEFINITION
HD--10-M17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--10-M17, mRNA sequence.
CF3320056
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--10-M17"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 296
CF332408/c
LOCUS
DEFINITION
NACL--08-O12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-O12, mRNA
sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 42)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-O12"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 1.3%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 297
BF343329
LOCUS
DEFINITION
60201593F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151542
5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 42)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9416 row: j column: 23
High quality sequence stop: 39.
Location/Qualifiers

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 42)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9416 row: j column: 23
High quality sequence stop: 39.
Location/Qualifiers

```

```

source      1. .42
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:4151542"
            /tissue_type="glioblastoma with EGFR amplification"
            /lab_hosts="DH10B (T1 phage-resistant)"
            /clone_lib="NCI_CGAP_Brn64"
            /note="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 1.57 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 298
AW334133/c
LOCUS      42 bp mRNA linear EST 31-JAN-2000
DEFINITION S30H7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AW334133
VERSION     AW334133.1 GI:6830490
KEYWORDS   EST.
SOURCE     Pneumocystis carinii
            ORGANISM
            Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE  1 (bases 1 to 42)
AUTHORS   Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
TITLE     Expressed sequence tags from Pneumocystis carinii
JOURNAL   Unpublished (2000)
COMMENT   Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.

FEATURES
source      1. .42
            /organism="Pneumocystis carinii"
            /mol_type="mRNA"
            /db_xref="taxon:4754"
            /lab_host="E. coli"
            /clone_lib="AGS-1"
            /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
            P. carinii organisms (3x10e9) from a single rat (99-1-6,
            sacrificed on 3/17/99) at Cincinnati VA facilities.
            Trizol extracted RNA. Oligo dT priming, standard
            conditions described by vendor, Stratagene. Further
            details see www.uky.edu/Project/Pneumocystis/"

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 299
CV062024
LOCUS      42 bp mRNA linear EST 24-AUG-2004
DEFINITION BNEL75e2 Barley EST endospore library Hordeum vulgare subsp.

vulgare cDNA clone BNEL75e2 5' similar to Unknown Function, mRNA
sequence.
CV062024
VERSION    CV062024.1 GI:51525163
KEYWORDS   EST.
SOURCE     Hordeum vulgare subsp. vulgare
            ORGANISM
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales;
            Poaceae; BEP
            clade; Poideae; Triticeae; Hordeum.
            1 (bases 1 to 42)
            Ali,S. Holloway,B. and Taylor,W.C.
            Normalisation of cereal endospore EST libraries for structural and
            functional genomic analysis
            Plant Mol. Biol. Rep. 18, 123-132 (2000)
            Contact: Bill Taylor
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry,
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
            Seq primer: M13 reverse primer
            High quality sequence stop: 42.
            Location/Qualifiers
            1. .42
            /organism="Hordeum vulgare subsp. vulgare"
            /mol_type="mRNA"
            /cultivar="Himalaya"
            /sub_species="vulgare"
            /db_xref="taxon:112509"
            /clone="BNEL75e2"
            /tissue_type="endospore"
            /dev_stage="developing endospore tissue 10, 12, 15 dpa
            (days post anthesis)"
            /lab_host="DH10B (Life Technology)"
            /clone_lib="Barley EST endospore library"
            /note="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
            was prepared from endospore tissues of the Barley cultivar
            Himalaya. cDNA was synthesised from pooled 10, 12, and 15
            dpa endospore using Not I-oligo(dT)18 primer/adaptor
            (Pharmacia Biotech), and then ligated to the Sal I-Not I
            site of ZipLox vector (Life Technology) after adding a
            Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
            Ali and Bill Taylor."

Query Match      1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 300
CV725428/c
LOCUS      42 bp mRNA linear EST 04-NOV-2004
DEFINITION 14Salt--02-I06.b1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-I06, mRNA sequence.
            CV725428
            CV725428.1 GI:55413052
            EST.
            Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales;
            Poaceae; BPP
            clade; Ehrhartoideae; Oryzae; Oryza.
            1 (bases 1 to 42)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nohm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs

```

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

```
1..42
/morganism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-106"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cdna library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
```

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 301
 CV726363/c
 LOCUS 42 bp mRNA linear EST 04-NOV-2004
 DEFINITION 14Salt--03-P05.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CV726363
 VERSION 1 GI:55413987
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

```
1..42
/morganism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-P05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cdna library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
```

XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 302
 CV726372/c
 LOCUS 42 bp mRNA linear EST 04-NOV-2004
 DEFINITION 14Salt--03-P10.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION CV726372
 VERSION 1 GI:55413996
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers

```
1..42
/morganism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-P10"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cdna library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
```

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||
 Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 303
 CV728634/c
 LOCUS 42 bp mRNA linear EST 05-NOV-2004
 DEFINITION FLO--01-B05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-B05, mRNA

sequence.
 ACCESSION CV728634
 VERSION CV728634.1 GI:55431251

```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--01-805"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 304
CV728806/c
LOCUS
DEFINITION
  FLO--01-F05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--01-F05, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--01-F05"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 306
CV728806/c
LOCUS
DEFINITION
  FLO--01-F05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--01-F05, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"

```

```

/clone="FLO--01-F05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 305
CV729215/c
LOCUS
DEFINITION
  FLO--01-P01.g1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--01-P01, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--01-P01"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 306
CV729267/c
LOCUS
DEFINITION
  FLO--02-A05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--02-A05, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--01-P01"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match
Best Local Similarity 100.0%; Score 35; DB 1; Length 42;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 306
CV729267/c
LOCUS
DEFINITION
  FLO--02-A05.g1 Rice flower lambda phage cDNA library (FLO) Oryza
  sativa (japonica cultivar-group) cDNA clone FLO--02-A05, mRNA
  sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
  Unpublished (2003)
COMMENT

FEATURES
source
  1. .42
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"

```



```

ACCESSION CV732835
VERSION CV732835.1 GI:55439068
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
sequence.
ACCESSION CV732860.1 GI:55439116
VERSION CV732860
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
sequence.
ACCESSION CV732860.1 GI:55439116
VERSION CV732860
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
sequence.
ACCESSION CV732860.1 GI:55439116
VERSION CV732860
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
sequence.
ACCESSION CV732860.1 GI:55439116
VERSION CV732860
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-110, mRNA
sequence.
ACCESSION CV732860.1 GI:55439116
VERSION CV732860
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..42
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-H20"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ory 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 310
CV732860/c
LOCUS CV732860
DEFINITION FLO--07-110.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone
```

```

sequence.
CV733323
VERSION CV733323.1 GI:55440025
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 321 6193
          Fax: 82 31 321 6355
          Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
          source
          Location/Qualifiers
            1..42
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="FLO--08-D02"
              /tissue_type="flower"
              /lab_host="E.coli SOLR"
              /clone_lib="Rice flower lambda phage cDNA library (FLO)"
              /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
              XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
              end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 313
LOCUS CV733544/c
DEFINITION FLO--08-I03.b1 Rice flower lambda phage cDNA library (FLO) Oryza
          sativa (japonica cultivar-group) cDNA clone FLO--08-I03, mRNA
          sequence.
ACCESSION CV733544
VERSION CV733544.1 GI:55440468
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 321 6193
          Fax: 82 31 321 6355
          Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
          source
          Location/Qualifiers
            1..42
              /organism="Oryza sativa (japonica cultivar-group)"

```

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-I03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 314
LOCUS CV733603/c
DEFINITION FLO--08-J11.b1 Rice flower lambda phage cDNA library (FLO) Oryza
          sativa (japonica cultivar-group) cDNA clone FLO--08-J11, mRNA
          sequence.
ACCESSION CV733603
VERSION CV733603.1 GI:55440585
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 42)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 321 6193
          Fax: 82 31 321 6355
          Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
          source
          Location/Qualifiers
            1..42
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="FLO--08-J11"
              /tissue_type="flower"
              /lab_host="E.coli SOLR"
              /clone_lib="Rice flower lambda phage cDNA library (FLO)"
              /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
              XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
              end with EcoRI and 3' end with XhoI site."
Query Match 1.3%; Score 35; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8

RESULT 315
LOCUS CV733690/c
DEFINITION FLO--08-L13.b1 Rice flower lambda phage cDNA library (FLO) Oryza

```


DEFINITION PDUTs2028G11 Porcine testis cDNA library II Sus scrofa cDNA clone
ACCESSION PDUTs2028G11 5', mRNA sequence.
VERSION CX058845
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 42)
AUTHORS Lee,W.C., Lin,E.-C., Huang,M.C., Chiou,S.H., Sun,H.S., Huang,S.Y.,
 Chuang,C.K., Chen,M.Y., Liu,M.L., Hsu,M.C., Yang,K.T., Fan,Y.H.,
 Lin,J.H., Liu,C.C., Huang,C.H., Chen,Y.C. and Lin,D.T.
TITLE Porcine testis EST project
JOURNAL Unpublished (2005)
COMMENT Lab of Genetic & breeding
 Department of Animal Science, National Chung-Hsing University
 250 Kuo-Kuang Road, Taichung 402, Taiwan, R.O.C.
 Tel: 886 4 22860265
 Fax: 886 4 22870613(ext.)239
 Email: mchuang@mail.nchu.edu.tw
 The EST project for testis from Duroc was granted by Council of
 Agriculture, Taiwan. Material with normal function was tested and
 heat stress experiments of animals were conducted by Divisions of
 Biotechnology and Animal Resources, Animal Technology Institute
 Taiwan (AIT). Library was constructed and EST clones were
 sequenced by Graduate Institutes of Veterinary Microbiology and
 Department of Animal Science, National Chung-Hsing University.
 Bioinformatic work was conducted by a network from AIT, National
 Cheng-Kung University, and Chung-Hua University. The sequences were
 stored in a database 'Tropical Pig Bioinformatic Center'. Bases
 called and alt trimmed with phred v0.020425.c. Vector identified
 and masked by cross match. Sequences were cleaned of vector,
 adaptors and repetitions.
 Plate: 28 row: G column: 11
 Seq primer: T7 promoter primer
 High quality sequence stop: 42
 POLYA=No.

FEATURES

source
 1. .42
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /strain="Duroc"
 /db_xref="taxon:9823"
 /clone="PDUTs2028G11"
 /sex="male"
 /dev_stage="adult, 1 year of age, heat stressed"
 /lab_host="PH10B (Life Technologies)"
 /clone_lib="Porcine testis cDNA library II"
 /note="Organ: testis; Vector: pSPORT1; Site_1: NotI;
 Site_2: SalI; Material with normal function was tested and
 heat stress experiments of animals were conducted by
 Divisions of Biotechnology and Animal Resources, Animal
 Technology Institute Taiwan (AIT). First strand cDNA was
 primed with a NotI-oligo(dT) primer and 2nd strand cDNA
 was synthesized by using nick translational replacement of
 the mRNA. Double-strand cDNA was added with SalI adapter,
 then digested with NotI and cloned into the NotI and SalI
 sites of pSPORT1 vector."

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 5 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39
 |||||

RESULT 319
 DUB35485/c

LOCUS DUB35485
DEFINITION KBrS016M05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrS016M05, genomic survey
 sequence.
ACCESSION DUB35485
VERSION DUB35485.1 GI:83872081
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 42)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa sep. pekinensis Sau3AI BAC clone
 KBrS016M05
 Seq primer: M13 Reverse
 Class: BAC ends.
FEATURES Location/Qualifiers
 source
 1. .42
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS016M05"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
 sep pekinensis var. Chifu BAC library (KBrS BAC) is
 available at NIAB."

Query Match 1.3%; Score 35; DB 1; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 42 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 8
 |||||

RESULT 320

AJ923543
LOCUS AJ923543
DEFINITION AJ923543 Theileria annulata piroplasm Theileria annulata cDNA clone
 TAC21c10_plka, mRNA sequence.
ACCESSION AJ923543
VERSION AJ923543.1 GI:67493891
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
 Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 Theileria.

REFERENCE 1 (bases 1 to 43)

AUTHORS Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
 Kerhornou,A., Aslett,M., Bishop,R., Bouchier,C., Cochet,M.,
 Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Fosker,N.,
 Gardner,M., Gobie,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
 Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,P.,
 Nene,V., O'Neill,S., Price,C., Quail,M.A., Rabinowitsch,E.,
 Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
 Squares,R., Tivey,A., Walker,A.R., Woodward,J.,

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11541 row: a column: 09
High quality sequence stop: 43.
Location/Qualifiers

FEATURES

Source

1..43
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5215376"
/tissue_type="leukocyte"
/lab_host="DH108"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 324
CF302744/c
LOCUS

DEFINITION
CF302744 43 bp mRNA linear EST 15-AUG-2003
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-I23, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF302744 GI:33674505
CF302744 43 bp mRNA linear EST 15-AUG-2003
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-I23, mRNA sequence.
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--08-I23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 325
CF334344

LOCUS
DEFINITION
CF334344 43 bp mRNA linear EST 18-AUG-2003
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-J17, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF334344 GI:33817016
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 43)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-J17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT	326
CV0621138	
LOCUS	CV0621138
DEFINITION	BNEL76g12 Barley EST endosperm library Hordeum vulgare subsp. vulgare cDNA clone BNEL76g12 5' similar to Unknown Function, mRNA sequence.
ACCESSION	CV0621138
VERSION	CV0621138.1 GI:51525277
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Hordeum.
AUTHORS	1. (bases 1 to 43)
TITLE	Ali,S, Holloway,B. and Taylor,W.C. Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
JOURNAL	Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT	Contact: Bill Taylor Commonwealth Scientific and Industrial Research Organisation Division of Plant Industry. CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia Tel.: 61 2 6246 5223 Fax: 61 2 6246 5000 Email: Bill.Taylor@csiro.au Seq primer: M13 reverse primer High quality sequence stop: 43.

[illegible]

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 43)

AUTHORS
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.

TITLE
Large-scale Sequencing Analysis of Rice ESTs

COMMENT
Unpublished (2003)

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14SALT-01-C21"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14SALT)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs
cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match	1.3%; Score 35; DB 1; Length 43;
Best local Similarity	100.0%; Pred. No. 2e+02;
Matches	35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db	 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9
RESULT 328	
CV724959/c	
LOCUS	CV724959 43 bp mRNA linear EST 04-NOV-2004
DEFINITION	(14Salt)-O1-M23.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone
ACCESSION	CV724959
VERSION	CV724959.1 GI:55412583
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group)
ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartioideae; Oryzoae; Oryza.
REFERENCE	1. (bases 1 to 43) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003) Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	1.. 43 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:39947" /clone="14Salt--01-M23"

```

/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 329
CV724969/c
LOCUS
DEFINITION
14Salt--01-N04.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-N04, mRNA sequence.
ACCESSION
CV724969
VERSION
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-A20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 331
CV725506/c
LOCUS
DEFINITION
14Salt--02-K02.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-K02, mRNA sequence.
ACCESSION
CV725506
VERSION
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-N04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db  43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 330
CV725127/c
LOCUS
DEFINITION
14Salt--02-A20.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--02-A20, mRNA sequence.
ACCESSION
CV725127
VERSION
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-A20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```


Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1. .43
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-K02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AA 2743
|||||
Db 43 AA 9

RESULT 332

CV725680/c

LOCUS
DEFINITION
14Salt--02-005.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone
14Salt--02-005, mRNA sequence.

ACCESSION
CV725680

VERSION
CV725680.1 GI:55413304

KEYWORDS
EST.

SOURCE
Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
1. .43
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-005"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 333

CV725720/c

LOCUS

DEFINITION

14Salt--02-P03.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone

14Salt--02-P03, mRNA sequence.

ACCESSION

CV725720

VERSION

CV725720.1 GI:55413344

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .43

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--02-P03"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 334

CV725822/c

LOCUS

DEFINITION

14Salt--03-C05.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) CDNA clone

14Salt--03-C05, mRNA sequence.

ACCESSION

CV725822

VERSION

CV725822.1 GI:55413446

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

1 (bases 1 to 43)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .43

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--02-005"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

clade; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..43
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--03-C05"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 335
 CV726349/c
 LOCUS
 DEFINITION 14Salt--03-022.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--03-022, mRNA sequence.

ACCESSION CV726349
 VERSION CV726349.1 GI:55413973

KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..43
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--03-022"
 /tissue_type="leaf"

/dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 336

CV726694/c

LOCUS

DEFINITION 14Salt--04-H13.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-H13, mRNA sequence.

ACCESSION CV726694

VERSION CV726694.1 GI:55414318

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 43)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..43
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--04-H13"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 337

CV726751/c

LOCUS

DEFINITION 14Salt--04-H13.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--04-H13, mRNA sequence.

ACCESSION CV726751

VERSION CV726751.1 GI:55414318

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

```

DEFINITION 14Salt--04-I22.g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-I22, mRNA sequence.
CV726751 1 GI:55414375
FEATURES             source
  ACCESSION
  VERSION
  KEYWORDS
  SOURCE
  ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 43)
REFERENCE
  AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE      Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL    Unpublished (2003)
  COMMENT    Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
  1..43
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--04-I22"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."
  Query Match      1.3%; Score 35; DB 1; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

  RESULT 338
  CV727328/c
  LOCUS
  DEFINITION
  14Salt--05-G19.g1 Salt treated rice leaf lambda phage cDNA library
  (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--05-G19, mRNA sequence.
  CV727328 1 GI:55414952
  FEATURES             source
    ACCESSION
    VERSION
    KEYWORDS
    SOURCE
    ORGANISM
      Oryza sativa (japonica cultivar-group)
      Oryza sativa (japonica cultivar-group)
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
      clade; Ehrhartoideae; Oryzaceae; Oryza.
    1 (bases 1 to 43)
    REFERENCE
      AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
      TITLE      Large-scale Sequencing Analysis of Rice ESTs
      JOURNAL    Unpublished (2003)
      COMMENT    Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
  Query Match      1.3%; Score 35; DB 1; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

  RESULT 338
  CV727328/c
  LOCUS
  DEFINITION
  14Salt--05-G19.g1 Salt treated rice leaf lambda phage cDNA library
  (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--05-G19, mRNA sequence.
  CV727328 1 GI:55414952
  FEATURES             source
    ACCESSION
    VERSION
    KEYWORDS
    SOURCE
    ORGANISM
      Oryza sativa (japonica cultivar-group)
      Oryza sativa (japonica cultivar-group)
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
      clade; Ehrhartoideae; Oryzaceae; Oryza.
    1 (bases 1 to 43)
    REFERENCE
      AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
      TITLE      Large-scale Sequencing Analysis of Rice ESTs
      JOURNAL    Unpublished (2003)
      COMMENT    Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
  Query Match      1.3%; Score 35; DB 1; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..43
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--05-G19"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."
  Query Match      1.3%; Score 35; DB 1; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2e+02;
  Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

  RESULT 339
  CV727684/c
  LOCUS
  DEFINITION
  14Salt--05-P03.g1 Salt treated rice leaf lambda phage cDNA library
  (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
  14Salt--05-P03, mRNA sequence.
  CV727684 1 GI:55415308
  FEATURES             source
    ACCESSION
    VERSION
    KEYWORDS
    SOURCE
    ORGANISM
      Oryza sativa (japonica cultivar-group)
      Oryza sativa (japonica cultivar-group)
      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
      clade; Ehrhartoideae; Oryzaceae; Oryza.
    1 (bases 1 to 43)
    REFERENCE
      AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
      TITLE      Large-scale Sequencing Analysis of Rice ESTs
      JOURNAL    Unpublished (2003)
      COMMENT    Contact: Nahm B.H.
                 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                 of Bioscience and Bioinformatics, Myongji University
                 Yongin, Kyeonggi, Korea
                 Tel: 82 31 330 6193
                 Fax: 82 31 321 6355
                 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
  1..43
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14Salt--05-P03"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="Salt treated rice leaf lambda phage cDNA
    library (14Salt)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
    cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
    with EcoRI and 3' end with XhoI site."
  Query Match      1.3%; Score 35; DB 1; Length 43;
  Best Local Similarity 100.0%; Pred. No. 2e+02;

```

```

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 340
CV728681/c LOCUS
DEFINITION FLO--01-C09.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C09, mRNA sequence.
ACCESSION CV728681.1 GI:55431334
VERSION CV728681
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-C09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 341
CV728686/c LOCUS
DEFINITION FLO--01-C11.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-C11, mRNA sequence.
ACCESSION CV728686.1 GI:55431344
VERSION CV728686
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-C11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 342
CV728737/c LOCUS
DEFINITION FLO--01-D16.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-D16, mRNA sequence.
ACCESSION CV728737.1 GI:55431446
VERSION CV728737
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-D16"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;

```

```

Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 35; Conservative 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 343
CV728887/c
LOCUS
DEFINITION
FLO--01-H03.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-H03, mRNA
sequence.
CV728887 43 bp mRNA linear EST 05-NOV-2004
FLO--01-H03.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-H03, mRNA
sequence.
CV728887.1 GI:55431741
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-H03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

REFERENCE
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-H03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 345
CV729158/c
LOCUS
DEFINITION
FLO--01-N17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158 43 bp mRNA linear EST 05-NOV-2004
FLO--01-N17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158.1 GI:55432276
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-H03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

REFERENCE
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-H03"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 344
CV729000/c
LOCUS
DEFINITION
FLO--01-J22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
sequence.
CV729000 43 bp mRNA linear EST 05-NOV-2004
FLO--01-J22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
sequence.
CV729000.1 GI:55431960
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-N17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

REFERENCE
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

```

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-J22"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 345
CV729158/c
LOCUS
DEFINITION
FLO--01-N17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158 43 bp mRNA linear EST 05-NOV-2004
FLO--01-N17.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-N17, mRNA
sequence.
CV729158.1 GI:55432276
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-N17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

REFERENCE
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-N17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 344
CV729000/c
LOCUS
DEFINITION
FLO--01-J22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
sequence.
CV729000 43 bp mRNA linear EST 05-NOV-2004
FLO--01-J22.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--01-J22, mRNA
sequence.
CV729000.1 GI:55431960
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-N17"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

REFERENCE
1 (bases 1 to 43)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

```

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Db

RESULT 346
CV729970/c
LOCUS FLO--03-E14.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--03-E14, mRNA
sequence.
ACCESSION CV729970
VERSION FLO--03-E14.b1 GI:55433717
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--03-E14"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Db

RESULT 347
CV730586/c
LOCUS FLO--04-D05.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--04-D05, mRNA
sequence.
ACCESSION CV730586
VERSION FLO--04-D05.b1 GI:55434920
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)

```

```

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-D05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
      43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

Db

RESULT 348
CV730813/c
LOCUS FLO--04-I21.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--04-I21, mRNA
sequence.
ACCESSION CV730813
VERSION FLO--04-I21.b1 GI:55435364
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-I21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

```

```

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 349
CV731060/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--04-016, mRNA
CV731060
CV731060.1 GI:55435848
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--04-016"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 351
CV732091/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--06-G15, mRNA
sequence.
CV732091
CV732091.1 GI:55437609
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--06-G15"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
    |||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 350
CV731475/c
LOCUS
DEFINITION
sativa (japonica cultivar-group) cDNA clone FLO--05-I11, mRNA
sequence.
CV731475
CV731475.1 GI:55436678
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 43)
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--05-I11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

```

end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 352
CV732291/c

LOCUS CV732291 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--06-L08.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--06-L08, mRNA sequence.

ACCESSION CV732291
VERSION
KEYWORDS
SOURCE EST. GI:55437995

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--06-L08"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 353
CV732533/c

LOCUS CV732533 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-A19.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-A19, mRNA sequence.

ACCESSION CV732533
VERSION
KEYWORDS
SOURCE EST. GI:55438473

ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-A19"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 354
CV732664/c

LOCUS CV732664 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-D21.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D21, mRNA sequence.

ACCESSION CV732664
VERSION CV732664.1 GI:55438733

KEYWORDS
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-D21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 354
CV732664/c

LOCUS CV732664 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-D21.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D21, mRNA sequence.

ACCESSION CV732664
VERSION CV732664.1 GI:55438733

KEYWORDS
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-D21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 354
CV732664/c

LOCUS CV732664 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-D21.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-D21, mRNA sequence.

ACCESSION CV732664
VERSION CV732664.1 GI:55438733

KEYWORDS
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

XhoI: cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 355
CV733072/c
LOCUS
DEFINITION
FLO--07-N05.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-N05, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-N05"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 356
CV733143/c
LOCUS
DEFINITION
FLO--07-021.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--07-021, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--07-021"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 357
CV733227/c

LOCUS
DEFINITION
FLO--08-A18.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-A18, mRNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1. .43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-A18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 358

CV733316/C
LOCUS CV733316.1 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--08-C21.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--08-C21, mRNA sequence.

ACCESSION CV733316 GI:55440010
VERSION CV733316
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Oryza sativa (japonica cultivar-group)
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 43)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaem@bio.com, bhnaem@bio.myongji.ac.kr.

FEATURES

source
1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-C21"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 359

CV734334/C
LOCUS CV734334.1 43 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--09-K09.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-K09, mRNA sequence.

ACCESSION CV734334 GI:55442029
VERSION CV734334
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE

AUTHORS

JOURNAL

COMMENT

FEATURES

source

1..43
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-K09"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
DB 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 360

CV736048/C
LOCUS CV736048.1 43 bp mRNA linear EST 03-DEC-2004

DEFINITION iv31f05.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris CDNA, mRNA sequence.

ACCESSION CX002408 GI:56273824
VERSION CX002408
KEYWORDS EST.

SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 43)

AUTHORS Balijs, V.S., Nascimento, L.U. and McCombie, W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)

JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.

FEATURES

source

1..43
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1:

EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 361

AZ355703/c

LOCUS

DEFINITION AZ355703 43 bp DNA linear GSS 02-OCT-2000
IM0095D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0095D02 R, genomic survey sequence.

ACCESSION

AZ355703

VERSION

GSS.

KEYWORDS

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 43)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0095 row: D column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 43.

FEATURES

source

1..43

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0095D02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.3%; Score 35; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 43 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 362

CR762707

LOCUS

DEFINITION CR762707 40 bp mRNA linear EST 23-SEP-2004
DKFZp469F0617_r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DKFZp469F0617 5', mRNA sequence.

ACCESSION

CR762707

VERSION

EST.

KEYWORDS

SOURCE

Pongo pygmaeus (orangutan)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Pongo.

REFERENCE

1 (bases 1 to 40)

AUTHORS

Ansorge,W., Krieger,S., Regiert,T., Rittmuller,C., Schwager,B.,

Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and

Wiemann,S.

TITLE

Pongo pygmaeus mRNA (Ansorge,W., Krieger,S., Regiert,T., et al.)

JOURNAL

Unpublished (2004)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact

RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469F0617

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

1..40

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp469F0617"

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="469 (synonym: pkid1)"

/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 1.3%; Score 34.8; DB 1; Length 40;

Best Local Similarity 94.7%; Pred. No. 2e+02;

Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

Db 2 ACCACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 39

RESULT 363

CV066153

LOCUS

DEFINITION

CV066153

WNEI30e11 Wheat EST endosperm library Triticum aestivum cDNA clone

WNEI30e11 5' similar to Unknown Function, mRNA sequence.

ACCESSION

CV066153

VERSION

CV066153.1 GI:51529330

```

KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 43)
AUTHORS
Ali, S., Holloway, B. and Taylor, W.C.
TITLE
Normalisation of cereal endosperm EST libraries for structural and
functional genomic analysis
JOURNAL
Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 43.
Location/Qualifiers
1..43
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNEJ30e11"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days
post anthesis)"
/lab_host="PH108 (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: _ZipLox; Site_1: Sal I; Site_2: Not I; mRNA
was prepared from endosperm tissues of the wheat cultivar
Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa
endosperm using Not I-oligo(dT)18 primer/adaptor
(Pharmacia Biotech), and then ligated to the Sal I-Not I
site of ZipLox vector (Life Technology) after adding a
Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
Ali and Bill Taylor."

Query Match 1.3%; Score 34.8; DB 1; Length 43;
Best Local Similarity 94.7%; Pred. No. 2.1e+02;
Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2704 GTACTTAAAAA 36 bp mRNA linear EST 04-NOV-2004
||||| 14Salt--02-M17.g1 Salt treated rice leaf lambda phage cDNA library
||||| (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
||||| 14Salt--02-M17, mRNA sequence.
Db 1 GTAAATTA 38

RESULT 364
CV725617/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 36)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--02-M17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match 1.3%; Score 34.4; DB 1; Length 36;
Best Local Similarity 97.2%; Pred. No. 2e+02;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAA 41 bp mRNA linear EST 03-FEB-2006
||||| DY231388 Bmp Bombyx mori cDNA clone BmpK_K44_2005-10-30_WD-051030
||||| S, mRNA sequence.
Db 36 TC 2743

RESULT 365
DY231388
LOCUS
DEFINITION
DY231388 Bmp Bombyx mori cDNA clone BmpK_K44_2005-10-30_WD-051030
ACCESSION
DY231388
VERSION
DY231388.1 GI:86465516
KEYWORDS
EST.
SOURCE
Bombyx mori (domestic silkworm)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
REFERENCE
1 (bases 1 to 41)
AUTHORS
Zhang, Y.Z., Xu, J., Chen, J., Wang, D., Nie, Z.M., Lv, Z.B., Jiang, C.Y.,
Liu, L.L., Song, L., He, P.A., Chen, F. and Wu, X.F.
TITLE
The full-length cDNA library construction of silkworm pupae (Bombyx
mori) and large-scale sequencing
JOURNAL
Unpublished (2006)
COMMENT
Contact: Yaohao, Zhang
Biochemistry Laboratory, the college of life science
Zhejiang Sci-Tech University
2th Street, Xiaoha High Education area, Hangzhou City, 310018, P.
R. China
Tel: 86 571 86843194
Fax: 86 571 86843198
Email: yaohao@chinagen.com
Seq primer: M13 Forward
High quality sequence stop: 41
POLYA=Yes.
Location/Qualifiers
1..41
/organism="Bombyx mori"
/mol_type="mRNA"
/strain="Qingsong-Haoyue"
/db_xref="taxon:7091"
/clone="BmpK_K44_2005-10-30_WD-051030"
/sex="male and female"
/tissue_type="whole pupae body but for the skin"
/clone_lib="Bmp"
/notes="vector: pHelix; Site_1: Hind II; The synthesis of
double-stranded cDNA from mRNA was based on the method
described by Gubler and Hoffman. The obtained cDNA were

```

ligated into the plasmid vector pHelix and subsequently the ligation product was transformed into E.coli competent cells TGI. At last, the recombinant clones were screened by blue-white plaques."

Query Match 1.3%; Score 34.4; DB 1; Length 41;
Best Local Similarity 97.2%; Pred. No. 2.1e+02;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAACAAAAA 34 bp mRNA linear EST 22-OCT-2004
||||| 2743
Db 5 TAAACAAAAA 40

RESULT 366

CJ038300
LOCUS
DEFINITION CJ038300 full-length enriched swine cDNA library, adult uterus Sus
scrofa cDNA clone UTR01C110090 5', mRNA sequence.

ACCESSION CJ038300

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE

AUTHORS Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N. and Awata, T.

TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries

JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)

PUBMED 14681463

COMMENT

Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES

source

1..34
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="UTR01C110090"
/tissue_type="uterus"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult uterus"

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAACAAAAA 34 bp mRNA linear EST 04-NOV-2004
||||| 2741

Db 1 TAAACAAAAA 34

RESULT 367

CJ038300
LOCUS
DEFINITION CJ038300 full-length enriched swine cDNA library, adult uterus Sus
scrofa cDNA clone UTR01C110090 5', mRNA sequence.

ACCESSION CJ038300

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE

AUTHORS Unishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
Okumura, N., Hamasima, N. and Awata, T.

TITLE PEDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries

JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)

PUBMED 14681463

COMMENT

Contact: Hirohide Unishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

(14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--01-A16, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..34
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-A16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA
library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs.
cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 100.0%; Pred. No. 2e+02; DB 1; Length 34;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 2742

Db 34 AAAAAAAAAA 1

RESULT 368

LOCUS

DEFINITION

CV726231 34 bp mRNA linear EST 04-NOV-2004
14Salt--03-M05.b1 Salt treated rice leaf lambda phage cDNA library
14Salt--03-M05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-M05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 369

CV726784/c
LOCUS
DEFINITION
14Salt--04-J17.bi Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--04-J17, mRNA sequence.
ACCESSION
CV726784.1 GI:55414408
VERSION
CV726784.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-J17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 370

CV727320/c
LOCUS
DEFINITION
14Salt--05-G14.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
14Salt--05-G14, mRNA sequence.
ACCESSION
CV727320
VERSION
CV727320.1 GI:55414944
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--05-G14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 371

CV729064/c
LOCUS
DEFINITION
FLO--01-L10.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-L10, mRNA sequence.
ACCESSION
CV729064.1 GI:55432090
VERSION
CV729064.1
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES

source

1. .34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-01-L10"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 372

CV730592/c

LOCUS FLO-04-D09.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO-04-D09, mRNA
sequence.

ACCESSION CV730592

VERSION CV730592.1 GI:55434932

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .34

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO-04-D09"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Indels 0; Gaps 0;
Matches 34; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 373

CV730644/c

LOCUS FLO-04-E17.g1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO-04-E17, mRNA
sequence.

ACCESSION CV730644

VERSION CV730644.1 GI:55435034

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 34)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .34

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="FLO-04-E17"

/tissue_type="flower"

/lab_host="E.coli SOLR"

/clone_lib="Rice flower lambda phage cDNA library (FLO)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with EcoRI and 3' end with XhoI site."

Query Match

Best Local Similarity 1.2%; Score 34; DB 1; Length 34;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742

Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 374

CV731182/c

LOCUS FLO-05-B16.b1 Rice flower lambda phage cDNA library (FLO) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone FLO-05-B16, mRNA
sequence.

ACCESSION CV731182

VERSION CV731182.1 GI:55436088

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

```

REFERENCE
AUTHORS      1 (bases 1 to 34)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 321 6355
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
    1..34
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO-05-B16"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
    end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 375
LOCUS      CV734338
DEFINITION FLO--09-K11.g1 Rice flower lambda phage cDNA library (FLO) Oryza
            sativa (japonica cultivar-group) cDNA clone FLO--09-K11, mRNA
            sequence.
ACCESSION  CV734338
VERSION     CV734338.1 GI:55442037
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS      1 (bases 1 to 34)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 321 6355
              Fax: 82 31 321 6355
              Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
    1..34
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="FLO--09-K11"
    /tissue_type="flower"
    /lab_host="E.coli SOLR"
    /clone_lib="Rice flower lambda phage cDNA library (FLO)"
    /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
    XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

```

```

end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
DB 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 376
LOCUS      AZ465350
DEFINITION lM0275012F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0275012 F, genomic survey sequence.
ACCESSION  AZ465350
VERSION     AZ465350.1 GI:10623475
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      1 (bases 1 to 34)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0275 row: 0 column: 12
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 34.

FEATURES
source
    1..34
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0275012"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells

```


and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 377
AZ501040
LOCUS
DEFINITION
IM0339P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0339P09 R, genomic survey sequence.
ACCESSION
AZ501040
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 34)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0339 row: P column: 09
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

FEATURES
source
High quality sequence stop: 34.
Location/Qualifiers
1..34

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0339P09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 378
AZ809643
LOCUS
DEFINITION
2M0073C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073C14 R, genomic survey sequence.
ACCESSION
AZ809643
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 34)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: C column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

FEATURES
source
High quality sequence stop: 34.
Location/Qualifiers
1..34

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 379
DU835285
LOCUS
DEFINITION KBrS016F23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016F23, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DU835285 34 bp DNA linear GSS 22-DEC-2005
DU835285.1 GI:83871881
GSS.
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS016F23

Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..34
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016F23"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAF."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 380
DX037933
LOCUS
DEFINITION DX037933 34 bp DNA linear GSS 10-JAN-2006
KBrB036016R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB036016, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DX037933 34 bp DNA linear GSS 10-JAN-2006
DX037933.1 GI:84732230

KEYWORDS
SOURCE
ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS

1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB036016

Seq primer: M13 Reverse

Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..34
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB036016"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 34; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 381
CV730365/C
LOCUS

DEFINITION CV730365 35 bp mRNA linear EST 05-NOV-2004
FLO-03-001.b1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO-03-001, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CV730365
CV730365.1 GI:55434480
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

1 (bases 1 to 35)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE
JOURNAL
COMMENT

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES


```

FEATURES
source
Class: BAC ends.
Location/Qualifiers
1. .41
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB047E15"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note=vector: pUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)".

```

11074000

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Erythraea; Euphorbia; Euphorbiaceae; Euphorbia; Euphorbia

AUTHORS Habermann B., Bebin A.G., Herklotz, S., Volkmer M., Eckelt, K.,
 Pehlke K., Epperlein, H.H., Schackert, H.K., Wiebe G. and Tanaka E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
 expressed sequence tags from embryonic and regenerating blastema
 cDNA libraries

JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
 Tanaka Lab
 Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden
 Pflotenhauerstrasse 108, 01307 Dresden, Germany
 Tel: 0049 351 210 2620
 Fax: 0049 351 210 1489
 Email: tanaka@mpi-cbg.de
 Plate: BL284A row: 08 column: H
 Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES
 source
 1..35
 Location/Qualifiers
 /organism="Ambystoma mexicanum"
 /mol_type="mRNA"
 /db_xref="taxon:8296"
 /tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
 /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
 Unnormalized cDNA plasmid library prepared by Invitrogen.
 Size fractionated mRNA was polydT primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LTB=6DAXBL"

FEATURES
 source
 1..35
 Location/Qualifiers
 /organism="Ambystoma mexicanum"
 /mol_type="mRNA"
 /db_xref="taxon:8296"
 /tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
 /note="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
 Unnormalized cDNA plasmid library prepared by Invitrogen.
 Size fractionated mRNA was polydT primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LTB=6DAXBL"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 35 AAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 391
LOCUS DN955388
DEFINITION it87b05.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
 sequence.
ACCESSION DN955388
VERSION DN955388.1 GI:63027526
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
 1 (bases 1 to 35)
AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Balija, V., Martensen, R.A., McCombie, R.W.,
 Benfey, P., Coruzzi, G. and Stevenson, D.
 Expressed tag sequences from Gnetum female cone (NYBG)

TITLE Unpublished (2003)
JOURNAL Contact: W. Richard McCombie
COMMENT Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES
 source
 1..35
 Location/Qualifiers
 /organism="Gnetum gnemon"
 /mol_type="mRNA"
 /db_xref="taxon:3382"
 /sex="female"
 /clone_lib="Gnetum female cone (NYBG)"

/note="Organ: mature, unfertilized reproductive strobili;
 Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
 Completed 02/11/02, submitted for sequencing 02/12/02.
 Library: Stratagene ZAP Express cDNA Synthesis Kit. The
 library was size-fractionated to enrich for large inserts.
 Sample: NYBG accession number #436/84"

Query Match 1.2%; Score 33.4; DB 1; Length 35;
Best Local Similarity 97.1%; Pred. No. 2.2e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 392
LOCUS BE894682
DEFINITION 601435925F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920911 5',
 mRNA sequence.
ACCESSION BE894682
VERSION BE894682.1 GI:10357319
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
REFERENCE 1 (bases 1 to 36)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC/DCTP/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1AM9753 row: a column: 08
 High quality sequence stop: 30.

FEATURES
 source
 1..36
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3920911"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 393
LOCUS CV724804/C
DEFINITION CV724804 14Salt--01-J08.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--01-J08, mRNA sequence.

```

CV724804
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Class: transposon-tagged.
Location/Qualifiers
1. .36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 36 AAAAAAAAAAACCAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 395
DUB30895/c
LOCUS
DEFINITION
KBR-S007101F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS007101, genomic survey sequence.
ACCESSION DUB30895.1 GI:83867491
VERSION DUB30895
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS007101
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS007101"
/lab_host="E. coli DH10B"

FEATURES
source
1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-J08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli S01R"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
DB 35 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 394
CZ912531/c
LOCUS
DEFINITION
CZ912531.1EL.Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic survey sequence.
ACCESSION CZ912531
VERSION CZ912531.1 GI:71927929
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 36)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence.
Plate: 4012010 row: G column: 11

CV724804
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Class: transposon-tagged.
Location/Qualifiers
1. .36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
DB 36 AAAAAAAAAAACCAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 395
DUB30895/c
LOCUS
DEFINITION
KBR-S007101F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS007101, genomic survey sequence.
ACCESSION DUB30895.1 GI:83867491
VERSION DUB30895
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 36)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS007101
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS007101"
/lab_host="E. coli DH10B"

FEATURES
source
1. .36
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-J08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli S01R"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
DB 35 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 394
CZ912531/c
LOCUS
DEFINITION
CZ912531.1EL.Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic survey sequence.
ACCESSION CZ912531
VERSION CZ912531.1 GI:71927929
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 36)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence.
Plate: 4012010 row: G column: 11

```

```

/clone lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIAB."

Query Match      1.2%; Score 33.4; DB 1; Length 36;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 396
AL048768
LOCUS              37 bp mRNA linear EST 04-SEP-2003
DEFINITION      DKFZp566M083.r1.566 (synonym: hfk2) Homo sapiens cDNA clone
ACCESSION      DKFZp566M083 mRNA sequence.
VERSION      AL048768
KEYWORDS      AL048768.1 GI:4727839
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 37)
AUTHORS      Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE      EST (Koehrer, et al.)
JOURNAL      Unpublished (1999)
COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
    source
        1..37
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp566M083"
            /tissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="Xl-2blue"
            /clone_lib="566 (synonym: hfk2)"
            /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAA 35

RESULT 397
CV732356/c
LOCUS              37 bp mRNA linear EST 05-NOV-2004
DEFINITION      FLO--06-M19.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--06-M19, mRNA
sequence.
ACCESSION      CV732356
VERSION      CV732356.1 GI:55438125
KEYWORDS      EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 37)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs

```

```

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
    source
        1..37
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="FLO--06-M19"
            /tissue_type="flower"
            /lab_host="E.coli SOLR"
            /clone_lib="Rice flower lambda phage cDNA library (FLO)"
            /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 35 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 398
AZ824309/c
LOCUS              37 bp DNA linear GSS 20-FEB-2001
DEFINITION      2M0098017R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0098017 R, genomic survey sequence.
ACCESSION      AZ824309
VERSION      AZ824309.1 GI:12994217
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 37)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: O column: 17
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 37.
    Location/Qualifiers
        1..37
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0098017"
            /sex="Male"

```


/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PMD42nv; Purified genomic DNA from M.
musculorum C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMW42 (GII4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 399
DX062077 37 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB068M24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB068M24, genomic survey
sequence.

ACCESSION DX062077.1 GI:84756373
VERSION DX062077.1
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 37)

REFERENCE Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team

National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB068M24
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..37
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB068M24"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp

pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 33.4; DB 1; Length 37;
Best Local Similarity 97.1%; Pred. No. 2.3e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 400
CF302184/c 38 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-H22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-H22, mRNA
sequence.

ACCESSION CF302184
VERSION CF302184.1 GI:33673945
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 38)

REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION
OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY
YONGIN, KYEONGGI, KOREA
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-H22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 38;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
|||||
Db 35 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 401
CF316791 38 bp mRNA linear EST 15-AUG-2003
LOCUS HD--06-D18.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-D18, mRNA sequence.

ACCESSION CF316791
VERSION CF316791.1 GI:33688552
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Eriartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 38)

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..38
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-D18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pcR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match

Best Local Similarity 1.2%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 35

RESULT 402

AW333985/c

LOCUS

AW333985 S28H9 AGS-1 Pneumocystis carinii cDNA 3', mRNA linear EST 31-JAN-2000

DEFINITION

AW333985 S28H9 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION

AW333985.1 GI:68303342

VERSION

KEYWORDS

SOURCE

ORGANISM

Pneumocystis carinii

Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

Pneumocystidaceae; Pneumocystis.

1 (bases 1 to 38)

Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,

Edman, J.C., Kovacs, J. and Cushion, M.

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky

101 Morgan Building, University of Kentucky, Lexington, KY

40506-0225, USA

Tel: 606 257 2161

Fax: 606 257 1717

Email: staben@pop.uky.edu.

Location/Qualifiers

1..38

/organism="Pneumocystis carinii"

/mol_type="mRNA"

/db_xref="taxon:4754"

/lab_host="E. coli"

/clone_lib="AGS-1"

/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dt priming. VA standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

Query Match

Best Local Similarity 1.2%; Score 33.4; DB 1; Length 38;

Matches

34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAA 4

RESULT 403

DR074451

LOCUS

DR074451 ik94d04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION

DR074451 ik94d04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

ACCESSION

DR074451 ik94d04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

VERSION

DR074451.1 GI:67052436

KEYWORDS

EST.

SOURCE

Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 38)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Original 3 prime EST has been reverse completed to be in 5 prime

direction

Seq primer: -21M13UnivRev.

Location/Qualifiers

1..38

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="male"

/clone_lib="Ginkgo male leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:

Eco RI; Stratagene ZAP Express cDNA Synthesis kit. The

library was size-fractionated to enrich for large

inserts."

Query Match

Best Local Similarity 1.2%; Score 33.4; DB 1; Length 38;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db

1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 404

AZ589726/c

LOCUS

AZ589726 AZ589726 38 bp DNA linear GSS 13-DEC-2000

DEFINITION

1M0398124R Mouse 10kb plasmid UGCLM library Mus musculus genomic

clone UGCLM0398124 R, genomic survey sequence.

ACCESSION

AZ589726

VERSION

AZ589726.1 GI:11711916

KEYWORDS

GSS.

SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0398 row: I column: 24
Seq primer: CACACAGGAACACGATGACC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES
source
1..38
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0398124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. Musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 405
LOCUS
DEFINITION
CF319510 HD--10-A16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-A16, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin,yeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..38
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB066N13"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 406
LOCUS
DEFINITION
CF319510 HD--10-A16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-A16, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin,yeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..38
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0398124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. Musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 405
LOCUS
DEFINITION
DX060574 KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB066N13, genomic survey sequence.
ACCESSION
VERSION
DX060574.1 GI:84754870

KEYWORDS
SOURCE
ORGANISM
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 38)

REFERENCE
AUTHORS
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrB066N13
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..38
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB066N13"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 406
LOCUS
DEFINITION
CF319510 HD--10-A16.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--10-A16, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin,yeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..38
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0398124"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. Musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gl|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 38;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 38 AAAAAAAAAAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 405
LOCUS
DEFINITION
DX060574 KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB066N13, genomic survey sequence.
ACCESSION
VERSION
DX060574.1 GI:84754870

```

source
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-10-A16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 39;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 407
CO786273/c
LOCUS
DEFINITION
CO786273
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ambystoma mexicanum (axolotl)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 39)
Habermaann.B., Bebin.A.G., Herklotz.S., Volkmer.M., Eckelt.K.,
Pehlike.K., Epperlein.H.H., Schackert.H.K., Wiebe.G. and Tanaka.E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Protenhauerstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL285D row: 07 column: F
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
Location/Qualifiers
1. .39
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"
/tissue_type="Tail Blastema"
/clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;
Unnormalized cDNA plasmid library prepared by Invitrogen.
Size fractionated mRNA was polydT primed and cloned into
NotI-SalI site of pCMVSPORT6. Bacterial host is
EMDH10B-TONA. Average insert size is 1.67 kb.
TAG_LIB=6DaxBL"

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 39;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

source
1. .39
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR10D12"
/clone_lib="RPCI-98"
/notes="end : TET3"

Query Match
Best Local Similarity 97.1%; Score 33.4; DB 1; Length 39;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 39 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 409
AL638703/c
LOCUS
DEFINITION
AL638703
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus tropicalis (western clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 40)
TITLE        Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
JOURNAL      Sanger Xenopus tropicalis EST project 2001 (10_2001)
COMMENT      Unpublished (2001)
              Contact: Huckle E
              Sanger Institute
              Hinxton, Cambridgeshire, CB10 1SA, UK
              Email: tropesanger.ac.uk
              Sanger Xenopus tropicalis EST project 2001
              TROPICALIS_SEQUENCE ID: L1E5g04.sp6
              Sequencing primer: SP6
              This sequence is from a Xenopus Gene Collection (XGC) library
              constructed by Aaron M. Zorn.
              Location/Qualifiers
FEATURES
source       1..40
              /organism="Xenopus tropicalis"
              /mol_type="mRNA"
              /db_xref="taxon:8364"
              /clone="L1E5g04"
              /dev_stage="egg"
              /lab_host="Escherichia coli XL1-blue"
              /clone_lib="XGC-egg"
              /notes="Vector: pCSI07; Site 1: EcoRI; Site 2: NotI; cDNA
              was oligo dT primed from Sug of poly A+ RNA from egg.
              EcoRI-NotI cut cDNA was then ligated into pCSI07 with
              EcoRI at the 5' end and NotI at the 3' end"
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 410
LOCUS      CF336399.1 GI:33821186
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone
              library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
              JMT--06-H01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
              library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
              JMT--06-H01, mRNA sequence.
ACCESSION   CF336399
VERSION     CF336399.1 GI:33821186
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
              clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
FEATURES
source       1..40
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:39947"
              /clone="JMT--06-H01"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH10B"
              /clone_lib="AtJMT-overexpressing transgenic rice plasmid

```

```

cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 35 ACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 411
LOCUS      DV082973
DEFINITION 327-384-37_O10_KS Nematostella vectensis normalized cDNA library
              sequence.
ACCESSION   DV082973
VERSION     DV082973.1 GI:82864366
KEYWORDS    EST.
SOURCE      Nematostella vectensis
ORGANISM    Nematostella vectensis
              Eukaryota; Metazoa; Chnidaria; Anthozoa; Hexacorallia; Actiniaria;
              Edwardsiidae; Nematostella.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Technau,U., Rudd,S., Maxwell,P., Gordon,P.M.K., Saina,M.,
              Grasso,L.C., Hayward,D.C., Sensen,C.W., Saint,R., Holstein,T.W.,
              Ball,E.E. and Miller,D.J.
              Maintenance of ancestral complexity and non-metazoan genes in two
              basal cnidarians
              Trends Genet. (2005) In press
              Contact: Ulrich Technau
              Sars Centre for Marine Molecular Biology
              High Technology Building, Thormohlenstgt. 5 5008 Bergen, Norway
              Tel: +47-55584340
              Email: ulrich.technau@sars.uib.no
              Plate: 37 row: 10 column: 0
              Seq primer: KS.
              Location/Qualifiers
FEATURES
source       1..40
              /organism="Nematostella vectensis"
              /mol_type="mRNA"
              /db_xref="taxon:45351"
              /clone="327-384-37_O10_KS"
              /sex="hermaphrodite"
              /tissue_type="whole embryos"
              /dev_stage="mixed stages from unfertilized eggs to primary
              polyyps"
              /clone_lib="Nematostella vectensis normalized cDNA library
              327"
              /notes="Vector: pBluescript II SK(+); Site 1: NotI; Site 2:
              EcoRI; Normalized oligo dT primed cDNA library using poly
              A+ RNA from mixed embryonic stages of Nematostella
              vectensis. Cloned directionally into pBluescript II SK(+).
              Ligated in NotI, EcoRI"
Query Match      1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 412
LOCUS      DX076358/c
DEFINITION KBrB087J22F KBrB, Brassica rapa BamHI BAC library Brassica rapa

```

```

subsp. pekinensis genomic clone KBrB087J22, genomic survey
sequence.
DX076358.1 GI:84770654
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
1 (bases 1 to 40)
/organism="Brassicales; Brassicaceae; Brassica."
REFERENCE
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
Unpublished (2005)
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB087J22
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..40
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB087J22"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: PCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (GNU)."

Query Match 1.2%; Score 33.4; DB 1; Length 40;
Best Local Similarity 97.1%; Pred. No. 2.4e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 413
CF300448/c
LOCUS CF300448.1 41 bp mRNA linear EST 15-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N15, mRNA
sequence.
ACCESSION CF300448
VERSION CF300448.1 GI:33672209
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 40 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 413
CF300448/c
LOCUS CF300448.1 41 bp mRNA linear EST 15-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N15, mRNA
sequence.
ACCESSION CF300448
VERSION CF300448.1 GI:33672209
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 414
CF302032/c
LOCUS CF302032.1 41 bp mRNA linear EST 15-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C22, mRNA
sequence.
ACCESSION CF302032
VERSION CF302032.1 GI:33673793
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 41)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-C22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

```

Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbsi@ms.stcn.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers

FEATURES
source

1..41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBCAAC09"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 91.9%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA 2743
DB 4 CTCACAAAAA 40

RESULT 417
CV731029/c
LOCUS
DEFINITION
FLO--04-N23.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--04-N23, mRNA sequence.
CV731029
CV731029.1 GI:55435787
EST
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 41)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@ggbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5', mRNA sequence.
ACCESSION
AV742106
VERSION
AV742106.1 GI:10859687
EST
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5', mRNA sequence.
ACCESSION
AV742106
VERSION
AV742106.1 GI:10859687
EST
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5', mRNA sequence.
ACCESSION
AV742106
VERSION
AV742106.1 GI:10859687
EST
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5', mRNA sequence.
ACCESSION
AV742106
VERSION
AV742106.1 GI:10859687
EST
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5', mRNA sequence.
ACCESSION
AV742106
VERSION
AV742106.1 GI:10859687
EST
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
Homo sapiens CB library cDNA clones
Unpublished (2000)
Contact: Zhu Chen

FEATURES
source

1..41
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="CLD1--01-105"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2743
DB 37 AAAAAA 3

RESULT 416
AV742106
LOCUS
DEFINITION
AV742106 CB Homo sapiens cDNA clone CECAAC09 5

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAAGAGAAAAAAAAAAAA 7

RESULT 418
 DX049794/c 41 bp DNA linear GSS 10-JAN-2006
 LOCUS KRB052116f KBrB, Brassica rapa BamHI BAC library Brassica rapa
 DEFINITION subsp. pekinensis genomic clone KBrB052116, genomic survey
 sequence.

ACCESSION DX049794 GI:84744091
 VERSION DX049794
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 41)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J.H. and Park,B.S.
 TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
 JOURNAL Unpublished (2003)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr

KBrB052116
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..41
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB052116"
 /lab_host="E.coli DH10B"
 /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 1.2%; Score 33.4; DB 1; Length 41;
 Best Local Similarity 97.1%; Pred. No. 2.5e+02;
 Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
 |||||
 Db 41 AAAAAAAAAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAA 7

RESULT 419
 AL038652 38 bp mRNA linear EST 06-JUL-2004
 LOCUS DKFZP566I1946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
 DEFINITION DKFZP566I1946_mRNA sequence.

ACCESSION AL038652
 VERSION AL038652
 KEYWORDS EST.
 SOURCE AL038652.1 GI:49682177
 Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 38)
 AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
 Wiemann,S.
 TITLE EST (Ottenwaelder, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
 FEATURES
 source
 1..38
 /location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp566I1946"
 /tissue_type="kidney"
 /dev_stage="fetal"
 /lab_host="X1-2blue"
 /clone_lib="566 (synonym: hfkd2)"
 /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.2%; Score 33.2; DB 1; Length 38;
 Best Local Similarity 92.1%; Pred. No. 2.4e+02;
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||||
 Db 1 TGGACAAAAAAAAAAAAAAAAAGAAAAAAAAAAAAA 38

RESULT 420
 CF328529/c 39 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--03-H18.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--03-H18, mRNA
 sequence.

ACCESSION CF328529
 VERSION CF328529.1 GI:33805303
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 39)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of BioScience and Bioinformatics, Myongji University
 Yongin,yeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
 source
 1..39
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--03-H18"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.2%; Score 33.2; DB 1; Length 39;
 Best Local Similarity 92.1%; Pred. No. 2.5e+02;


```

Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2701 TTGTGTAACAAAAA 33 bp mRNA linear EST 14-AUG-2003
    ||| | 14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
    ||| | sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B21, mRNA
    ||| | sequence.
Db 38 TTTTTCGAAAAA 33 bp mRNA linear EST 14-AUG-2003
    ||| | 14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
    ||| | sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B21, mRNA
    ||| | sequence.

RESULT 421
CF291613/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-B21, mRNA
sequence.
ACCESSION
CF291613.1 GI:33660646
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ROOT--02-B21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAA 33 bp mRNA linear EST 18-AUG-2003
    ||| | NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
    ||| | sativa (japonica cultivar-group) cDNA clone NACL--01-E04, mRNA
    ||| | sequence.
Db 33 AAAAAA 33 bp mRNA linear EST 18-AUG-2003
    ||| | NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
    ||| | sativa (japonica cultivar-group) cDNA clone NACL--01-E04, mRNA
    ||| | sequence.

RESULT 423
CF326967/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E04, mRNA
sequence.
ACCESSION
CF326967.1 GI:33802189
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ROOT--02-B21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAA 33 bp mRNA linear EST 15-AUG-2003
    ||| | ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA
    ||| | library Oryza sativa (japonica cultivar-group) cDNA clone
    ||| | ABF--06-F23, mRNA sequence.
Db 33 AAAAAA 33 bp mRNA linear EST 15-AUG-2003
    ||| | ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA
    ||| | library Oryza sativa (japonica cultivar-group) cDNA clone
    ||| | ABF--06-F23, mRNA sequence.

RESULT 422
CF311229/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone ABF--06-F23, mRNA
sequence.
ACCESSION
CF311229.1 GI:33682990
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="ABF--06-F23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

Query Match

1.2%; Score 33; DB 1; Length 33;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAA 2741

Db 33 AAAAAA 1

RESULT 423

CF326967/c

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-E04, mRNA

sequence.

ACCESSION

CF326967.1 GI:33802189

VERSION

EST.

KEYWORDS

Oryza sativa (japonica cultivar-group)

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

1 (bases 1 to 33)

AUTHORS

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..33

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/db_xref="taxon:39947"

/clone="NACL--01-E04"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-G18"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 427
 CV725203/c
 LOCUS
 DEFINITION
 14Salt--02-C18.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-C18, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 33)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-C18"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428
 CV725846/c
 LOCUS
 DEFINITION
 14Salt--03-C19.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--03-C19, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 33)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..33
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--03-C19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA
 library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
 cDNA was inserted into lambda Uni-ZAP XR vector at 5' end
 with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
 |||
 Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 429
 CV725871/c
 LOCUS
 DEFINITION
 14Salt--03-D09.b1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--03-D09, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 33)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

```

1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-D09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
      |||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 430

CV725959/c

LOCUS

DEFINITION

14Salt--03-F12.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV725959

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

```

1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-F12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

```

with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
      |||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 431

CV726801/c

LOCUS

DEFINITION

14Salt--04-K03.g1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV726801

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

```

1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--04-K03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
      |||||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 432

CV726984/c

LOCUS

DEFINITION

14Salt--04-O15.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION

CV726984

VERSION

KEYWORDS

SOURCE

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.


```

ACCESSION CV732853
VERSION CV732853.1 GI:55439103
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 33)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-07-M18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: ECORI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 436
LOCUS CV733051/c 33 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--07-M18.g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--07-M18, mRNA
sequence.
ACCESSION CV733051 GI:55439486
VERSION CV733051
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 33)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-07-M18"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: ECORI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 437
LOCUS CV734457/c 33 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--09-N11.b1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--09-N11, mRNA
sequence.
ACCESSION CV734457 GI:55442275
VERSION CV734457
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade: Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 33)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-N11"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: ECORI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 438
LOCUS CX013914 33 bp mRNA linear EST 06-DEC-2004
DEFINITION CX013914 Whole Heart Library (DOGESTS) Canis familiaris cDNA,
mRNA sequence.

```

```

ACCESSION      CX013914
VERSION         CX013914.1  GI:56396325
KEYWORDS        EST.
SOURCE          Canis familiaris (dog)
ORGANISM        Canis familiaris
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                Canis.
REFERENCE       1 (bases 1 to 33)
AUTHORS         Balija, V.S., Nascimento, L.U. and McCombie, W.R.
TITLE           ESTs from Canis familiaris whole heart (dog)
JOURNAL         Unpublished (2004)
COMMENT        Contact: W. Richard McCombie
                Lita Amberg-Hazen Genome Sequencing Center
                Cold Spring Harbor Laboratory
                PO Box 100, Cold Spring Harbor, NY 11724, USA
                Tel: 516 367 8884
                Fax: 516 367 8874
                Email: mcombie@cshl.org.
FEATURES       Location/Qualifiers
                source
                1..33
                /organism="Canis familiaris"
                /mol_type="mRNA"
                /db_xref="taxon:9615"
                /sex="Unknown"
                /dev_stage="3 month old normal canine"
                /lab_host="Xl10 Gold"
                /clone_lib="Whole Heart Library (DOESTS)"
                /notes="Organ: Heart; Vector: pBluescript II SK; Site 1:
                EcoRI; Site 2: XhoI; Library constructed using pBluescript
                XR kit from Stratagene. Cloned cDNA was size selected
                between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
                Medical Genetics, School of Veterinary Medicine,
                University of Pennsylvania, 3800 Spruce Street,
                Philadelphia, PA 19104-6051"
                Query Match      1.2%; Score 33; DB 1; Length 33;
                Best Local Similarity 100.0%; Pred. No. 2.3e+02;
                Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
    |||||||
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 439
AZ486795/c
LOCUS       AZ486795
DEFINITION  1M0315P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315P22 F, genomic survey sequence.
ACCESSION   AZ486795
VERSION     AZ486795.1  GI:10653918
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177

AZ486795
LOCUS       AZ486795
DEFINITION  1M0315P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315P22 F, genomic survey sequence.
ACCESSION   AZ486795
VERSION     AZ486795.1  GI:10653918
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177

CX013914
VERSION     CX013914.1  GI:56396325
KEYWORDS        EST.
SOURCE          Canis familiaris (dog)
ORGANISM        Canis familiaris
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                Canis.
REFERENCE       1 (bases 1 to 33)
AUTHORS         Balija, V.S., Nascimento, L.U. and McCombie, W.R.
TITLE           ESTs from Canis familiaris whole heart (dog)
JOURNAL         Unpublished (2004)
COMMENT        Contact: W. Richard McCombie
                Lita Amberg-Hazen Genome Sequencing Center
                Cold Spring Harbor Laboratory
                PO Box 100, Cold Spring Harbor, NY 11724, USA
                Tel: 516 367 8884
                Fax: 516 367 8874
                Email: mcombie@cshl.org.
FEATURES       Location/Qualifiers
                source
                1..33
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0315P22"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWB42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid RI. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
                Query Match      1.2%; Score 33; DB 1; Length 33;
                Best Local Similarity 100.0%; Pred. No. 2.3e+02;
                Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
    |||||||
Db  33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 440
AZ627839/c
LOCUS       AZ627839
DEFINITION  1M0474B02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474B02 F, genomic survey sequence.
ACCESSION   AZ627839
VERSION     AZ627839.1  GI:11750125
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177

```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0474 row: B column: 02
 Seq primer: CGTTGTAACACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 33.

FEATURES

source

```

1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0474B02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      1.2%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 441

CZ917348

LOCUS

DEFINITION CZ917348 33 bp DNA linear GSS 08-AUG-2005 survey sequence.

ACCESSION

CZ917348

VERSION

CZ917348.1

KEYWORDS

GSS.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 33)

Walbot,V.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4021005 row: C column: 07
 Class: transposon-tagged.

FEATURES

source

Location/Qualifiers

1. .33

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_hosts="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."


```

High quality sequence stop: 31.
Location/Qualifiers
1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3855737"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
Query Match 1.2%; Score 33; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 446
LOCUS CV734277/c 34 bp mRNA linear EST 05-NOV-2004
DEFINITION FLO--09-J02.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--09-J02, mRNA sequence.
ACCESSION CV734277
VERSION CV734277.1 GI:55441908
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 34)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..34
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--09-J02"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."
Query Match 1.2%; Score 33; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

High quality sequence stop: 31.
Location/Qualifiers
1..34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3855737"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
Query Match 1.2%; Score 33; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 447
LOCUS BI761940 36 bp mRNA linear EST 25-SEP-2001
DEFINITION 603048772F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189224 5', mRNA sequence.
ACCESSION BI761940
VERSION BI761940.1 GI:15753518
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 36)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1472 row: 0 column: 17
High quality sequence stop: 36.
Location/Qualifiers
1..36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189224"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 clones, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
Query Match 1.2%; Score 33; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 448
LOCUS AJ792257 38 bp mRNA linear EST 08-DEC-2004
DEFINITION AJ792257 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018.2.11.a08, mRNA sequence.
ACCESSION AJ792257
VERSION AJ792257.1 GI:51107585
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
1 (bases 1 to 38)
Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,

```

Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
source
1. .38
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_2_11_a08"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

Query Match 1.2%; Score 33; DB 1; Length 38;
Best Local Similarity 94.3%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

RESULT 449
CV064759
LOCUS
DEFINITION
WNE1498 Wheat EST endosperm library Triticum aestivum cDNA clone
WNE1498 5' similar to Unknown Function, mRNA sequence.
CV064759
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Triticum aestivum (bread wheat)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Ali,S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 38.
Location/Qualifiers
source
1. .38
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNE1498"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 6, 8, 10 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/notes="Vector: Ziplox; Site.1: Sal I; Site.2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of Ziplox vector (Life Technology) after adding a

Sal I-Xho I adapter (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.2%; Score 33; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 33

RESULT 450
CF327755/c
LOCUS
DEFINITION
CF327755 39 bp mRNA linear EST 18-AUG-2003
NACL--02-F23.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F23, mRNA sequence.
CF327755
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
source
1. .39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-F23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 33; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 451
CF292043/c
LOCUS
DEFINITION
CF292043 37 bp mRNA linear EST 14-AUG-2003
14ROOT--02-L12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-L12, mRNA sequence.
CF292043
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 37)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-L12"

/tissue_type="root"

/dev_stage="14 days after germination"

/clone_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 94.4%; Score 32.8; DB 1; Length 37;

Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2705 TACTAAAAA..... 34 bp mRNA linear EST 15-AUG-2003

Db 36 TAATCA..... 34 bp mRNA linear EST 15-AUG-2003

RESULT 452

CF302250/c

LOCUS

DEFINITION

sativa (japonica cultivar-group) cDNA clone 7LEAF--07-J10, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..34

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--07-J10"

/tissue_type="leaf"

FEATURES

source

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.2%; Score 32.4; DB 1; Length 34;

Best Local Similarity 97.1%; Pred. No. 2.5e+02;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTA..... 34 bp mRNA linear EST 15-AUG-2003

Db 34 CCA..... 34 bp mRNA linear EST 15-AUG-2003

RESULT 453

CF315464/c

LOCUS

DEFINITION

HD--04-G09.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--04-G09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 34)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..34

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--04-G09"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

1.2%; Score 32.4; DB 1; Length 34;

Best Local Similarity 97.1%; Pred. No. 2.5e+02;

Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAA..... 34 bp DNA linear GSS 08-AUG-2005

Db 34 AAAAA..... 34 bp DNA linear GSS 08-AUG-2005

RESULT 454

C2906552/c

LOCUS

DEFINITION

4011001D06.1EL_y2 4011 - RescueMu Grid J Zea mays genomic,

genomic

```

survey sequence.
ACCESSION      CZ906552
VERSION        CZ906552.1  GI:71917315
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 34)
AUTHORS       Walbot,V.
TITLE         Maize genomic sequences found using engineered RescueMu transposon
JOURNAL       Unpublished (2001)
COMMENT       Contact: Walbot V
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Very probable ligation site of ends cut by single endonuclease.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 4011001 row: D column: 06
               Class: transposon-tagged.
               Location/Qualifiers
               1..34
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="mixed background W23/A188/B73/K55"
               /db_xref="taxon:4577"
               /tissue_type="leaf"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="4011 - RescueMu Grid J"
               /notes="Organ: leaf; Vector: RescueMu (engineered from
               pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
               RescueMu is a 4.9 kb, modified maize Mu transposon
               designed to allow plasmid rescue from total genomic DNA.
               Mu elements insert preferentially into transcription
               units. For more information on RescueMu, go to the web
               site 'http://www.mutransposon.org/project/RescueMu/'. Grid
               J was grown at UCSD in 2000. DNA was extracted from leaf
               strips, double digested using BamHI and BglII, and ligated
               to form circular plasmids. DH10B cells were transformed
               and then screened on LB plates with ampicillin."

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 455
DX054666/c
LOCUS
DEFINITION
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 34)
Yang, T.J., Kwon, S.J., Kim, J.A, Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
PARK, J.Y., LIM, M.H., KIM, H.I., CHOI, B.S., SEOL, Y.J., PARK, D.S.,
HAHN, J.H. and PARK, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrB058P12
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..34
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB058P12"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa subsp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

```

/db_xref="taxon:51351"
/clone="KB-B063K14"
/lab_host="E.coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pkinsensis var. Chifu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (GNU)."

```

```

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      |||||||
Db 34 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 457
DR41A4T
LOCUS      34 bp      DNA      linear      GSS 22-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-41A4, genomic survey sequence.
ACCESSION  AL980969
VERSION     AL980969.1 GI:25182658
KEYWORDS   GSS.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio

```

```

REFERENCE
AUTHORS    Humphray, S.J., Huckle, E. and Hunt, S.E.
TITLE      Direct Submission
JOURNAL    Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
COMMENT    This sequence was generated from the T7 end of BAC 41A4. 41A4 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

```

```

FEATURES
source
1..34
Location/Qualifiers
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-41A4"
/tissue_type="Testis"
/notes="Vector pIndigoBAC-536"

```

```

Query Match      1.2%; Score 32.4; DB 1; Length 34;
Best Local Similarity 97.1%; Pred. No. 2.5e+02;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
      |||||||
Db 1 AAAAAAAAAAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

```

```

RESULT 458
AM047864/c
LOCUS      36 bp      mRNA      linear      EST 20-SEP-2005
DEFINITION AM047864 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC18b04.q1k, mRNA sequence.
ACCESSION  AM047864
VERSION     AM047864.1 GI:75967439
KEYWORDS   EST.
SOURCE     Schistosoma mansoni
ORGANISM   Schistosoma mansoni

```

```

REFERENCE
AUTHORS    Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigedid; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 36)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in

```

```

the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC18b04.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="Country: Puerto Rico"

```

FEATURES

```

source
1..36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC18b04.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="Country: Puerto Rico"

```

```

Query Match      1.2%; Score 32.4; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.6e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      |||||||
Db 36 AAAAAAAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAA 2

```

```

RESULT 459
CNS45543/c
LOCUS      38 bp      mRNA      linear      EST 30-APR-2004
DEFINITION EST 17487 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003C10 3', mRNA sequence.
ACCESSION  CNS45543
VERSION     CNS45543.1 GI:46910168
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera

```

```

REFERENCE
AUTHORS    Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1..38
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="B3CS00RL003C10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiA; Site_2: SfiIB; Oriented library"

```

FEATURES

source

```

1..38
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="B3CS00RL003C10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiA; Site_2: SfiIB; Oriented library"

```

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT


```

RESULT 463
BQ591342/c
LOCUS
DEFINITION
E012713-024-017-G20-T7 MP12-ADIS-024-storage root Beta vulgaris
CDNA clone 024-017-G20 3-PRIME, mRNA sequence.
ACCESSION
BQ591342
VERSION
BQ591342.1 GI:26120925
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 40)
AUTHORS
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
PUBMED
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissaha@mp1z-koeln.mpg.de
Insert Length: 40 Std Error: 0.00
Plate: 17 row: G column: 20
Seq primer: T7; GTAATACGACTCACTATAGGCG.
FEATURES
source
1..40
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188777"
/db_xref="taxon:161934"
/clone="024-017-G20"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: PCWVSORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 1.2%; Score 32.2; DB 1; Length 40;
Best Local Similarity 91.9%; Pred. No. 2.9e+02;
Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2707 CTAAGAAAAA 2743
1 |
40 CCAAAAAAAGCAATATAAAAAA 4
Db

RESULT 464
AJ923479
LOCUS
DEFINITION
AJ923479 Theileria annulata piroplasm Theileria annulata cDNA clone
TAC31d08_pkla, mRNA sequence.
ACCESSION
AJ923479
VERSION
AJ923479.1 GI:67493826
KEYWORDS
EST.
SOURCE
Theileria annulata
ORGANISM
Eukaryota; Apicomplexa; Piroplasmida; Theileriidae;
Theileria
1 (bases 1 to 32)
Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kethornou,A., Aletti,M., Bishop,R., Bouchier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,F.,
Nene,V., O'Neil,S., Price,C., Quail,M.A., Rabinowitch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,
Dobbelaeere,D.A.B., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shiels,B., Tait,A., Barrell,B. and Hall,N.
The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
Unpublished (2005)
JOURNAL
Contact: Pain A
COMMENT
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
Location/Qualifiers
1..32
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (Clone D7)"
/db_xref="taxon:5874"
/clone="TAC31d08_pkla"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/notes="Country: Turkey;Ankara"
Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAA 2740
1 |
Db 1 AAAAAA 32

RESULT 465
AM044529/c
LOCUS
DEFINITION
AM044529 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC1le12.q1k, mRNA sequence.
ACCESSION
AM044529
VERSION
AM044529.1 GI:75966821
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 32)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
JOURNAL
Contact: Ivens AC
COMMENT
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC1le12.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"

```



```

/note="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 466
AM044934
LOCUS
DEFINITION
AM044934 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC13D02.q1k, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL
Unpublished (2005)
COMMENT
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxtion, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC13D02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 467
AM045405
LOCUS
DEFINITION
AM045405 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC13C05.q1k, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL
Unpublished (2005)
COMMENT
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxtion, CB10 1SA, UNITED KINGDOM.

```

```

Hinxtion, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC13C05.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 468
CF291773/c
LOCUS
DEFINITION
CF291773 32 bp mRNA linear EST 14-AUG-2003
14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-F12, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Naim,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.
FEATURES
source
1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-F12"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 469
CF299386/c
LOCUS
DEFINITION
CF299386 32 bp mRNA linear EST 15-AUG-2003

```

DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-G07, mRNA sequence.

ACCESSION CF299386 GI:33671147

VERSION CF299386.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-G07"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

|||||

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 470

CF309233

LOCUS ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABF--03-F14, mRNA sequence.

ACCESSION CF309233

VERSION CF309233.1

KEYWORDS CF309233.1 GI:33680994

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--03-F14"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 471

CF309345/c

LOCUS ABP--03-I03.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

DEFINITION ABP--03-I03, mRNA sequence.

ACCESSION CF309345

VERSION CF309345.1

KEYWORDS CF309345.1 GI:33681106

SOURCE EST.

ORGANISM Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--03-I03"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;


```

/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 475
 CF331270/c
 LOCUS
 DEFINITION
 NACL--07-F08.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--07-F08, mRNA
 sequence.

ACCESSION
 VERSION
 CF331270.1 GI:33810751

KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
 1 (bases 1 to 32)

AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

JOURNAL
 COMMENT
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1. .32

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="NACL-07-F08"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
 AW327277
 LOCUS
 DEFINITION
 dq01d07.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
 sequence.

ACCESSION
 AW327277

VERSION
 KEYWORDS
 SOURCE
 ORGANISM

```

AW327277.1 GI:6797772
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 32)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio-llnl.gov/bbrp/image/image.html
Plate: LCM0028 row: G column: 13
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers

```

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

```

1. .32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2846628"
/tissue_type="T cell leukemia"
/cell_line="MGC2"
/clone_lib="NIH MGC 2"
/note="Organ: Blood; Vector: pOTB7a; Library prepared by
Edge Biosystems."

```

FEATURES
 source

1. .32

```

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 477

CV724815/c

LOCUS
 DEFINITION
 14Salt--01-J14.g1 Salt treated rice leaf lambda phage cDNA library
 (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--01-J14, mRNA sequence.

ACCESSION
 CV724815

CV724815.1 GI:55412439

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 32)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--01-J14"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

CV725190 32 bp mRNA linear EST 04-NOV-2004
 14Salt--02-C11.g1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-C11, mRNA sequence.

ACCESSION CV725190.1 GI:55412814
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 32)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-C11"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 479
 CV725571/c
 LOCUS
 DEFINITION

CV725571 32 bp mRNA linear EST 04-NOV-2004
 14Salt--02-L16.b1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--02-L16, mRNA sequence.

ACCESSION CV725571
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 32)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
 1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14Salt--02-L16"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli SOLR"
 /clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 480
 CV726012/c
 LOCUS
 DEFINITION

CV726012 32 bp mRNA linear EST 04-NOV-2004
 14Salt--03-G20.b1 Salt treated rice leaf lambda phage cDNA library
 14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
 14Salt--03-G20, mRNA sequence.

ACCESSION CV726012
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzae; Oryza.
 1 (bases 1 to 32)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--03-G20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 481

CV726385/c

LOCUS

DEFINITION 14Salt--03-P17.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--03-P17, mRNA sequence.

ACCESSION

CV726385

VERSION

CV726385.1

GI:55414009

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 32)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--03-P17"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end

with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 482

CV727659/c

LOCUS

DEFINITION 14Salt--05-014.b1 Salt treated rice leaf lambda phage cDNA library (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone 14Salt--05-014, mRNA sequence.

ACCESSION

CV727659

VERSION

CV727659.1

GI:55415283

EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 32)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..32

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14Salt--05-014"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match

1.2%; Score 32; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 483

CV728625/c

LOCUS

DEFINITION FLO--01-A24.g1 Rice flower lambda phage cDNA library (FLO) Oryza sativa (japonica cultivar-group) cDNA clone FLO--01-A24, mRNA sequence.

ACCESSION

CV728625

VERSION

CV728625.1

GI:55431234

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-A24"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 484
 CV729255/c
 LOCUS
 DEFINITION FLO--01-P21.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--01-P21, mRNA
 sequence.
 CV729255
 CV729255.1 GI:55432467
 EST.

ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-P21"
 /tissue_type="flower"

/lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 485
 CV732146/c

LOCUS
 DEFINITION FLO--06-H23.b1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--06-H23, mRNA
 sequence.
 CV732146
 CV732146.1 GI:55437717
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 32)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--06-H23"
 /tissue_type="flower"
 /lab_host="E.coli SOLR"
 /clone_lib="Rice flower lambda phage cDNA library (FLO)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 486
 CV732586/c

LOCUS
 DEFINITION FLO--07-C02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--07-C02, mRNA
 sequence.
 CV732586
 CV732586.1 GI:55438578
 EST.

FEATURES
 source

1..32
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="FLO--01-P21"
 /tissue_type="flower"

Query Match 1.2%; Score 32; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 |||
 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 486
 CV732586/c
 LOCUS
 DEFINITION FLO--07-C02.g1 Rice flower lambda phage cDNA library (FLO) Oryza
 sativa (japonica cultivar-group) cDNA clone FLO--07-C02, mRNA
 sequence.
 CV732586
 CV732586.1 GI:55438578
 EST.

SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cui var="Nackdong"
/db_xref="taxon:39947"
/clone="FLO-07-C02"
/tissue type="flower"
/lab host="E.coli SOLR"
/clone lib="Rice flower lambda phage cDNA library (FLO)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 487
AZ459536/c
LOCUS
DEFINITION
LM0264M16F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0264M16 F, genomic survey sequence.
ACCESSION
AZ459536
VERSION
AZ459536.1 GI:10617577
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: M column: 16
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

FEATURES
source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 488
AZ470832
LOCUS
DEFINITION
LM0285F14F Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0285F14 F, genomic survey sequence.
ACCESSION
AZ470832
VERSION
AZ470832.1 GI:10628957
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: F column: 14
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 32.
Location/Qualifiers
1. .32

FEATURES
Source

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0285F14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 489
AZ611890/C

LOCUS
DEFINITION
1M0438E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0438E02 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)
```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0438 row: E column: 02
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 32.
Location/Qualifiers
1. .32

FEATURES
Source

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0438E02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 490
AZ778018

LOCUS
DEFINITION
2M0012020R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0012020 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

```
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 32)
```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0012 row: O column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

```

High quality sequence stop: 32.
FEATURES             Location/Qualifiers
     source            1..32
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUC2M0012020"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 491
DU835386      32 bp      DNA      linear      GSS 22-DEC-2005
LOCUS      KBRs016J03P KBRs, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBRs016J03, genomic survey sequence.
ACCESSION      DU835386.1 GI:83871982
VERSION      DU835386
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 32)
AUTHORS      Yang, I.-J., Kwon, S.-J., Kim, J.-A., Kim, J.-S., Lim, K.-B., Jin, M., Park, J.-Y., Lim, M.-H., Kim, H.-I., Choi, B.-S., Seol, Y.-J., Park, D.-S., Hahn, J. H. and Park, B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBRs) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
               Brassica Genomics Team
               National Institute of Agricultural Biotechnology
               225 Seodun-Dong, Suwon, 441-707, Korea
               Tel.: +82-31-299-1670
               Fax: +82-31-299-1672
               Email: pbeom@da.90.kr
               BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBRs016J03
               Seq primer: T7
               Class: BAC ends.
FEATURES             Location/Qualifiers
     source            1..32

```

```

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRs016J03"
/lab_host="E. coli DH10B"
/clone_lib="KBRs, Brassica rapa Sau3AI BAC library"
/notes="vector: pCUGIBAC1; Site 1; Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBRs BAC) is available at NIAB."

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 492
DR85L21T      32 bp      DNA      linear      GSS 22-NOV-2002
LOCUS      Danio rerio genomic clone DKEY-85L21, genomic survey sequence.
ACCESSION      AL986044
VERSION      AL986044.1 GI:25187956
KEYWORDS      GSS.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE      1 (bases 1 to 32)
AUTHORS      Humphray, S.J., Huckle, E. and Hunt, S.E.
TITLE      Direct Submission
JOURNAL      Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
COMMENT      This sequence was generated from the T7 end of BAC 85L21. 85L21 is part of the Dariokey BAC Library created by R. Plasterk and N.V. Keygene.
               Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES             Location/Qualifiers
     source            1..32
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="DKEY-85L21"
                     /tissue_type="Testis"
                     /note="vector pIndigoBAC-536"

Query Match      1.2%; Score 32; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 493
AL587609/c     33 bp      mRNA      linear      EST 02-MAR-2001
LOCUS      AL587609 BP Chicken Brain Library Gallus gallus cdna clone
DEFINITION      ROS059G05, mRNA sequence.
ACCESSION      AL587609
VERSION      AL587609.1 GI:13192643
KEYWORDS      EST.
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
               Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Phasianinae; Gallus.
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn
(*6854-
Seq primer: M13F.

FEATURES
source

1. .33
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059G05"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH108"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetechn (*6854-1)"

Query Match 1.2%; Score 32; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 494
BU431798/c
LOCUS
DEFINITION

601655890R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855694 3', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU431798 33 bp mRNA linear EST 09-SEP-2002
BU431798
BU431798.1 GI:22770280
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LICM570 row: c column: 23
High quality sequence stop: 31.
Location/Qualifiers
1. .33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

1. .33
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:3855694"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies. "

Query Match 1.2%; Score 32; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 495
AZ345610
LOCUS
DEFINITION

1M0080C24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080C24 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ345610 34 bp DNA linear GSS 29-SEP-2000
AZ345610
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
1. .34
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080C24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electroporation. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 32; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 3 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34

RESULT 496

BF338797 35 bp mRNA linear EST 22-NOV-2000
LOCUS 602036229F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184167
DEFINITION 5', mRNA sequence.

ACCESSION BF338797
VERSION BF338797
KEYWORDS EST.
SOURCE GI:11285216
ORGANISM Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 35)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9501 row: j column: 08
High quality sequence stop: 30.

FEATURES

source
Location/Qualifiers

1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184167"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 497

DR073823 35 bp mRNA linear EST 08-JUN-2005
LOCUS ik86e02.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION

1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184167"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn64"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 497

DR073823 35 bp mRNA linear EST 08-JUN-2005
LOCUS ik86e02.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION

sequence.
ACCESSION DR073823
VERSION DR073823.1 GI:67051746
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 35)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
Location/Qualifiers

1..35
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

FEATURES

source
Location/Qualifiers

1..35
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 4 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 35

Query Match 1.2%; Score 32; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

/dev stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.2%; Score 32; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 499
CV7237373/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone root--04-J23, mRNA
sequence.

ACCESSION
CV723737.1 GI:55411361
VERSION
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 40)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="root--04-J23"
/tissue_type="root"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage cDNA library (root)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 32; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9

RESULT 500
BQ590703/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 024-018-B02-3-PRIME, mRNA sequence.

ACCESSION
BQ590703
VERSION
EST.
KEYWORDS
Beta vulgaris
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..40
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="root--04-J23"
/tissue_type="root"
/dev stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Rice root lambda phage cDNA library (root)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match      1.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.8e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 501
CV724720/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 024-018-B02-3-PRIME, mRNA sequence.

ACCESSION
CV724720.1 GI:55412344
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="taxon:161934"
/clone="024-018-B02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. Library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 35)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 35 Std Error: 0.00
Plate: 18 row: B column: 02
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
Location/Qualifiers
1..35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="taxon:161934"
/clone="024-018-B02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. Library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.8e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 501
CV724720/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 024-018-B02-3-PRIME, mRNA sequence.

ACCESSION
CV724720.1 GI:55412344
VERSION
EST.
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 35)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..35
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="taxon:161934"
/clone="024-018-B02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. Library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1. .35
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14Salt--01-H08"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="Salt treated rice leaf lambda phage cDNA library (14Salt)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site."

```

Query Match 1.2%; Score 31.8; DB 1; Length 35;
Best Local Similarity 94.3%; Pred. No. 2.8e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 2704 GTACTTAAAAA 1
DB 35 GCAGCTGAAAAA 1

```

RESULT 502

AZ945733/c
LOCUS 2M0207B13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0207B13 F, genomic survey sequence.

ACCESSION AZ945733
VERSION AZ945733.1 GI:13812542
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 36)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES
source
1. .36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0207B13"
/sex="Female"

Insert Length: 10000 Std Error: 0.00
Plate: 0207 row: B column: 13
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 36.
Location/Qualifiers

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.2%; Score 31.8; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.9e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 2709 AAAAAA 1
DB 36 AAAAAA 2

```

RESULT 503

CZ919025
LOCUS 4021011F02.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
DEFINITION survey sequence.

ACCESSION CZ919025
VERSION CZ919025.1 GI:71939140
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 36)
Walbot, V.

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021011 row: F column: 02
Class: transposon-tagged.
Location/Qualifiers

FEATURES

source

```

1. .36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA."

```

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.2%; Score 31.8; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 2.9e+02;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA 35

RESULT 504

CF299167/c

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-B09, mRNA

CF299167

EST.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep

Clade; Ehrhartoideae; Oryzoae; Oryza.

1 (bases 1 to 37)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..37

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-B09"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 1.2%; Score 31.8; DB 1; Length 37;

Best Local Similarity 94.3%; Pred. No. 2.9e+02;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

|||||

Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 505

DN988546/c

LOCUS

DEFINITION

ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.abl linear EST 17-MAY-2005

subtracted cold acclimated cDNA library Cynodon dactylon

DN988546

38 bp mRNA

EST 17-MAY-2005

ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.abl

ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.abl, mRNA sequence.

DN988546

DN988546.1 GI:66248373

EST.

Cynodon dactylon (Bermuda grass)

Cynodon dactylon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Chloridoideae; Cynodonteae; Cynodon.

1 (bases 1 to 38)

Melnaise,K., Elavarthi,S. and Guenzi,A.C.

Identification of differentially expressed genes associated with

cold acclimation using suppression subtraction hybridization (SSH)

and cDNA microarrays

Unpublished (2005)

Contact: Guenzi AC

Dep. of Plant and Soil Sciences

Oklahoma State University

368 Agriculture Hall, Stillwater, OK 74078-6028, USA

Tel: 405-744-6028

Fax: 405 744 6039

Email: acg@mail.pss.okstate.edu

PCR Primers

FORWARD: M13 forward

BACKWARD: M13 Reverse

Seq primer: M13 Forward.

Location/Qualifiers

1..38

/organism="Cynodon dactylon"

/mol_type="mRNA"

/cultivar="Zebra"

/db_xref="taxon:28909"

/clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_G05.abl"

/tissue_type="crown"

/lab_host="E. coli"

/clone_lib="Bermudagrass line Zebra subtracted cold

acclimated cDNA library"

/note="Vector: Qiagen's pDrive; Messenger RNA was

extracted from control and cold acclimated bermudagrass

crown tissue at 2 and 28 days after acclimation and cDNA

library was constructed following Clontech PCR- select

cDNA subtraction procedure."

Query Match 1.2%; Score 31.8; DB 1; Length 38;

Best Local Similarity 94.3%; Pred. No. 2.9e+02;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

|||||

Db 36 ATTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 506

TAIL6F09P/c

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 116f09, forward sequence,

genomic survey sequence.

39 bp DNA linear GSS 13-DEC-2000

AL462533

GI:11832371

GSS.

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 39)

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajadream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhi@sanger.ac.uk


```

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade: Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..37
Location/Qualifiers
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-D24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 31.4; DB 1; Length 37;
Best Local Similarity 97.0%; Pred. No. 3.1e+02;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA 5

RESULT 510
CA853500/c
LOCUS
DEFINITION
39 bp mRNA linear EST 01-AUG-2003
B09A01.5', mRNA sequence.
ACCESSION
CA853500
VERSION
CA853500.1 GI:33390293
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 39)
Alkharouf, N., Khan, R. and Matthews, B.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Genome 47 (2), 380-388 (2004)
15060591
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
Location/Qualifiers
1..39

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade: Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 37)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..37
Location/Qualifiers
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-D24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.1%; Score 31.4; DB 1; Length 37;
Best Local Similarity 97.0%; Pred. No. 3.1e+02;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
|||||
DB 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA 5

RESULT 511
CF321807/c
LOCUS
DEFINITION
38 bp mRNA linear EST 15-AUG-2003
HD--13-D01.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--13-D01, mRNA sequence.
ACCESSION
CF321807
VERSION
CF321807.1 GI:33693568
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade: Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 38)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..38
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--13-D01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 31.2; DB 1; Length 38;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
DB 36 TTCCAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAA 1

FEATURES
source
1..38
Location/Qualifiers
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--13-D01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.1%; Score 31.2; DB 1; Length 38;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
DB 36 TTCCAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 512
CF308197/c 39 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--01-018.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-018, mRNA sequence.
ACCESSION CF308197
VERSION CF308197.1 GI:33679958
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 39)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel.: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..39
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-018"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 1.1%; Score 31.2; DB 1; Length 39;
Best Local Similarity 91.7%; Pred. No. 3.2e+02;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2708 TAAAGAAAAA 1
Db 37 TAAAGAAAAAATCCCAAAAAAAAAAAAAAAAAAAAAA 2743

RESULT 513
AJ659810 31 bp mRNA linear EST 28-JUN-2004
LOCUS AJ659810 KN277 Sus scrofa cDNA clone C0005217_I13, mRNA sequence.
DEFINITION AJ659810
ACCESSION AJ659810
VERSION AJ659810.1 GI:49343941
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus
REFERENCE 1 (bases 1 to 31)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
CONTACT: Anderson SI

RESULT 514
AJ693992 31 bp mRNA linear EST 29-JUN-2004
LOCUS AJ693992 KN261 Bos taurus cDNA clone KN261-042_M08, mRNA sequence.
DEFINITION AJ693992
ACCESSION AJ693992
VERSION AJ693992.1 GI:49427411
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 31)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
CONTACT: Anderson SI

FEATURES
Location/Qualifiers
1..31
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-042_M08"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

```

```

Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.arkgenomics.org.
FEATURES
Location/Qualifiers
1..31
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005217_I13"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."
Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 1
Db 1 AAAAAAAAAA 2739

RESULT 514
AJ693992 31 bp mRNA linear EST 29-JUN-2004
LOCUS AJ693992 KN261 Bos taurus cDNA clone KN261-042_M08, mRNA sequence.
DEFINITION AJ693992
ACCESSION AJ693992
VERSION AJ693992.1 GI:49427411
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 31)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
CONTACT: Anderson SI

Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
Location/Qualifiers
1..31
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-042_M08"
/tissue_type="ovary"
/clone_lib="KN261"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."

```

```

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 515
AM044121 31 bp mRNA linear EST 11-AUG-2005
LOCUS AM044121 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone Smlc1lf01.q1k, mRNA sequence.
ACCESSION AM044121
VERSION 1 GI:72293459
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE Strigeidida; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
TITLE Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.,
JOURNAL Microarray analysis identifies genes preferentially expressed in
COMMENT the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1. .31
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="Smlc1lf01.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="country: Puerto Rico"

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 516
BX569502/c 31 bp mRNA linear EST 14-OCT-2003
LOCUS BX569502/c Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse9a03.pic, mRNA sequence.
ACCESSION BX569502
VERSION 1 GI:33437420
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 31)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit

```

```

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1. .31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse9a03.pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 517
CF278807 31 bp mRNA linear EST 14-AUG-2003
LOCUS CF278807 14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-N15,
mRNA sequence.
ACCESSION CF278807
VERSION 1 GI:33656193
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
JOURNAL clade: Ehrhartoideae; Oryzae; Oryza.
COMMENT 1 (bases 1 to 31)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .31
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-N15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCRA-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 518
CF300345/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L08, mRNA
sequence.
CF300345
CF300345.1 GI:33672106
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..31
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-L08"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 519
AZ333315/c
LOCUS
DEFINITION
1M0062A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0062A21 F, genomic survey sequence.
ACCESSION
AZ333315
VERSION
AZ333315.1 GI:10397811
KEYWORDS
GSS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 520
AZ375973
LOCUS
DEFINITION
1M0129D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0129D08 R, genomic survey sequence.
ACCESSION
AZ375973
VERSION
AZ375973.1 GI:10489673
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Iellam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0062 row: A column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
FEATURES
source
1..31
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0062A21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 520
AZ375973
LOCUS
DEFINITION
1M0129D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0129D08 R, genomic survey sequence.
ACCESSION
AZ375973
VERSION
AZ375973.1 GI:10489673
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: D column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
source
1. .31
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129D08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 521
AZ510092
LOCUS
DEFINITION
1M0354P14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0354P14 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ510092.1 GI:10691408
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0354 row: P column: 14
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.

FEATURES
source
1. .31
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 522
AZ623538/c
LOCUS
DEFINITION
1M0461G21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0461G21 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ623538.1 GI:11745728
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0461 row: G column: 21
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
 1..31
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0461G21"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
 source

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
 |||||
 DB 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 523
 AZ627692
 LOCUS AZ627692 31 bp DNA linear GSS 13-DEC-2000
 DEFINITION IM0469C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0469C09 R, genomic survey sequence.
 ACCESSION AZ627692
 VERSION AZ627692.1 GI:11749882
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
 AUTHORS

TITLE

JOURNAL
 COMMENT

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0469 row: C column: 09
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
 1..31
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0469C09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES
 source

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 524
 AZ778697
 LOCUS AZ778697 31 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0014002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0014002 F, genomic survey sequence.
 ACCESSION AZ778697
 VERSION AZ778697.1 GI:12908605
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

REFERENCE
AUTHORS      1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 02
Seq primer: CGTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
              Location/Qualifiers
FEATURES
source      1..31
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC2M0014002"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptored DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptored mouse DNA was annealed to
             adaptored vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||||
      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

Db

RESULT 525
AZ821215
LOCUS
DEFINITION      31 bp DNA linear GSS 20-FEB-2001
                2M0093F21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0093F21 R, genomic survey sequence.
ACCESSION      AZ821215
VERSION
KEYWORDS      GSS.
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 31)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0093 row: F column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
              Location/Qualifiers
FEATURES
source      1..31
             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC2M0093F21"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /note="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptored DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptored mouse DNA was annealed to
             adaptored vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
Query Match      1.1%; Score 31; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||||
      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

Db

RESULT 526
AZ826618
LOCUS
DEFINITION      31 bp DNA linear GSS 20-FEB-2001
                2M0102C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC2M0102C19 F, genomic survey sequence.
ACCESSION      AZ826618
VERSION
KEYWORDS      GSS.
SOURCE
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 31)
TITLE        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5605
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0102 row: C column: 19
              Seq primer: CGTTGTAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 31.
FEATURES
source      1. .31
              Location/Qualifiers
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0102C19"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      1.1%; Score 31; DB 1; Length 31;
              Best Local Similarity 100.0%; Pred. No. 2.9e+02;
              Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
              |||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 527
LOCUS    CZ917108
DEFINITION CZ917108 31 bp DNA linear GSS 08-AUG-2005
survey sequence.
ACCESSION CZ917108
VERSION    CZ917108
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS      1 (bases 1 to 31)
TITLE        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5605
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0102 row: C column: 19
              Seq primer: CGTTGTAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 31.
FEATURES
source      1. .31
              Location/Qualifiers
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0102C19"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      1.1%; Score 31; DB 1; Length 31;
              Best Local Similarity 100.0%; Pred. No. 2.9e+02;
              Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
              |||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 527
LOCUS    CZ917108
DEFINITION CZ917108 31 bp DNA linear GSS 08-AUG-2005
survey sequence.
ACCESSION CZ917108
VERSION    CZ917108
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 31)
TITLE        Walbot,V.
JOURNAL      Unpublished (2001)
COMMENT      Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Very probable ligation site of ends cut by single endonuclease.
              Reverse complemented post-ligation sequence from source sequence.
              Plate: 4021004 row: C column: 05
              Class: transposon-tagged.
FEATURES
source      1. .31
              Location/Qualifiers
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /cultivar="mixed background W23/A188/B73/K55"
              /db_xref="taxon:4577"
              /tissue_type="leaf"
              /dev_stage="adult"
              /lab_host="DH10B"
              /clone_lib="4021 - RescueMu Grid V"
              /note="Organ: leaf; Vector: RescueMu (engineered from
              pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
              RescueMu is a 4.9 kb, modified maize Mu transposon
              designed to allow plasmid rescue from total genomic DNA.
              Mu elements insert preferentially into transcription
              units. For more information on RescueMu, go to the web
              site 'http://www.mutransposon.org/project/RescueMu/'. Grid
              V was grown at University of Arizona in 2003. DNA was
              extracted from leaf strips, double digested using BamHI
              and BglII, and ligated to form circular plasmids. DH10B
              cells were transformed and then screened on LB plates with
              ampicillin."
              Query Match      1.1%; Score 31; DB 1; Length 31;
              Best Local Similarity 100.0%; Pred. No. 2.9e+02;
              Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
              |||||||
Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 528
LOCUS    DU835031/c
DEFINITION DU835031/c 31 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBR5015N15, genomic survey
sequence.
ACCESSION DU835031
VERSION    DU835031.1
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
            1 (bases 1 to 31)
            Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
            End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
            Unpublished (2005)
            Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672

```


Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
 KBrS015N15
 Seq primer: T7
 Class: BAC ends.

FEATURES

source
 1..31
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS015N15"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /notes="vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
 ssp pekinensis var. Chifu BAC library (KBrS BAC) is
 available at NIB."

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 529

DX063750
 LOCUS
 DEFINITION
 KBrB071A09F KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
 subsp. pekinensis genomic clone KBrB071A09, genomic survey
 sequence.

ACCESSION
 DX063750.1 GI:84758046

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
 Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
 Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
 Hahn,J.H. and Park,B.S.

TITLE

JOURNAL

COMMENT

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB071A09

Seq primer: T7

Class: BAC ends.

FEATURES

source
 1..31
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrB071A09"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 1.1%; Score 31; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 530

AV674152/c
 LOCUS
 DEFINITION
 AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis
 cDNA clone citb14122 5', mRNA sequence.

ACCESSION
 AV674152

VERSION
 AV674152.1 GI:10112151

KEYWORDS
 EST.

SOURCE
 Ciona intestinalis

ORGANISM
 Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Cionidae; Ciona.

Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES

source

1..34
 Location/Qualifiers
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="citb14122"
 /tissue_type="whole animal"
 /dev_stage="tailbud embryo"
 /clone_lib="Nori Satoh unpublished cDNA library"

Query Match

1.1%; Score 31; DB 1; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 33 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 531

AW334249/c
 LOCUS
 DEFINITION
 S3204 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
 AW334249
 ACCESSION
 AW334249.1 GI:6830606

VERSION
 EST.

KEYWORDS
 EST.

SOURCE
 Pneumocystis carinii

ORGANISM
 Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

Pneumocystidaceae; Pneumocystis.

1 (bases 1 to 34)

Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,

Edman,J.C., Kovacs,J. and Cushion,M.

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky

101 Morgan Building, University of Kentucky, Lexington, KY

40506-0225, USA

Tel: 606 257 2161

```

Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
1. .34
FEATURES
    source
        /organism="Pneumocystis carinii"
        /mol_type="mRNA"
        /db_xref="taxon:4754"
        /lab_host="E. coli"
        /clone_lib="AGS-1"
        /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
        P. carinii organisms (3x10e9) from a single rat (99-1-6,
        sacrificed on 3/17/99) at Cincinnati VA facilities.
        Trizol extracted RNA. Oligo dT priming, standard
        conditions described by vendor, Stratagene. Further
        details see www.uky.edu/Project/Pneumocystis/"

Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 34;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 31 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 532
CV066718 36 bp mRNA linear EST 24-AUG-2004
LOCUS WNEL7d3 Wheat EST endospERM library Triticum aestivum cDNA clone
DEFINITION WNEL7d3 5' similar to Unknown Function, mRNA sequence.
ACCESSION CV066718
VERSION CV066718
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Poodeae; Triticeae; Triticum.
1 (bases 1 to 36)
Ali.S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endospERM EST libraries for structural and
functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 36.
Location/Qualifiers
1. .36
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/clone="WNEL7d3"
/tissue_type="endospERM"
/dev_stages="developing endospERM tissue 6, 8, 10 dpa (days
post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Wheat EST endospERM library"
/note="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA
was prepared from endospERM tissues of the wheat cultivar
Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa
endospERM using Not I-oligo(dT)18 primer/adaptor
(Pharmacia Biotech), and then ligated to the Sal I-Not I
site of ZipLox vector (Life Technology) after adding a
Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan
Ali and Bill Taylor."

Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
1. .34
FEATURES
    source
        /organism="Pneumocystis carinii"
        /mol_type="mRNA"
        /db_xref="taxon:4754"
        /lab_host="E. coli"
        /clone_lib="AGS-1"
        /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
        P. carinii organisms (3x10e9) from a single rat (99-1-6,
        sacrificed on 3/17/99) at Cincinnati VA facilities.
        Trizol extracted RNA. Oligo dT priming, standard
        conditions described by vendor, Stratagene. Further
        details see www.uky.edu/Project/Pneumocystis/"

Query Match
Best Local Similarity 100.0%; Score 31; DB 1; Length 34;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
Db 1 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 533
CV0667432 34 bp mRNA linear EST 06-DEC-2002
LOCUS BQ587432
DEFINITION S013303-024-010-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ587432
VERSION BQ587432
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 34)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 34 Std Error: 0.00
Plate: 10 row: B column: 02
Seq primer: T7; GTAATACGACTCTACTATAGGCG.
Location/Qualifiers
1. .34
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185440"
/db_xref="taxon:161934"
/clone="024-010-B02"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="vector: pCMVSPOR16; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7. Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPP/GABI-Primary database:http://gabi.rzpd.de"

Query Match
Best Local Similarity 94.1%; Score 30.8; DB 1; Length 34;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 34 AAAAAAAAAAAAAAAAAAGGAAAAAAAAAAAAAAAAA 1

RESULT 534
DU832879/c

```

```

LOCUS      DU832879          34 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS011B02F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS011B02, genomic survey
            sequence.
ACCESSION  DU832879
VERSION    DU832879.1  GI:83869475
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
            Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL    Unpublished (2005)
COMMENT    Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS011B02
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..34
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS011B02"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAH."

Query Match      1.1%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      34 AAAAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 535
DX048708 34 bp      DNA      linear      GSS 10-JAN-2006
LOCUS     KBrB051B15F KBrB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrB051B15, genomic survey
            sequence.
ACCESSION  DX048708
VERSION    DX048708.1  GI:84743005
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
            Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 34)
AUTHORS    Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE      End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL    Unpublished (2005)
COMMENT    Contact: Beom-Seok Park

```

```

Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB051B15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
    1..34
    /organism="Brassica rapa subsp. pekinensis"
    /mol_type="genomic DNA"
    /cultivar="Chiifu"
    /sub_species="pekinensis"
    /db_xref="taxon:51351"
    /clone="KBrB051B15"
    /lab_host="E. coli DH10B"
    /clone_lib="KBrB, Brassica rapa BamHI BAC library"
    /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
    pekinensis var. Chiifu BAC library (KBrB BAC) is provided
    by Yong-Pyo Lim (CNU)."

Query Match      1.1%; Score 30.8; DB 1; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.2e+02;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
        ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      1 AAAAAAAAAAAAAAAAAAACAAGAAAAA 34

RESULT 536
CV848473/c 37 bp      mRNA      linear      EST 17-NOV-2004
LOCUS     ID0AEE5CH01RM1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AEE5CH01
DEFINITION 5', mRNA sequence.
ACCESSION  CV848473
VERSION    CV848473.1  GI:55814156
KEYWORDS   EST.
SOURCE     Acyrthosiphon pisum (pea aphid)
            Acyrthosiphon pisum
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
            Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE  1 (bases 1 to 37)
AUTHORS    Sabater-Munoz,B., Legeai,F., Bonhomme,J., Dang,P., Dossat,C.,
            Duclet,A., Gauthier,J.P., Hunter,W., Martinez-Torres,D., Moya,A.,
            Nakabachi,A., Prunier-Leterme,N., Rahbe,Y., Shigenobu,S.,
            Simon,J.C., Stern,D., Wincker,P. and Tagu,D.
            Annotated ESTs of the pea aphid
            Unpublished (2004)
            Contact: D. Tagu
            INRA Rennes
            UMR BiO3P, BP 35327, F-35653 Le Rheu Cedex France
            Tel: +33.2.23.48.51.65
            Fax: +33.2.23.48.51.50
            PCR Primers
            FORWARD: CAGGAACAGCTATGACC
            Plate: 5C row: H column: 1.
            Location/Qualifiers
                1..37
                /organism="Acyrthosiphon pisum"
                /mol_type="mRNA"
                /cultivar="yr2"
                /db_xref="taxon:7029"
                /clone="ID0AEE5CH01"
                /tissue_type="antennae"
                /dev_stage="L3"
                /lab_host="XL1-Blue"
                /clone_lib="ID0AEE"
                /note="Vector: pBS-SKminus; Site_1: EcoRI; Site_2: XhoI;

FEATURES
            source

```

1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL

CONTACT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.mvionajj.ac.kr.

```

organism="Oryza sativa (Japanese cultivated group)"
mol_type="mRNA"
cultivar="Nackdong"
db_xref="taxon:39947"
clone="7LEAF--08-A01"
tissue_type="leaf"
dev_stage="7 days after germination"
lab_host="E.coli DH10B"
clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

```

RESULT 539	CN546365/c	CN546365	32 bp	mRNA	linear	EST 30-APR-2001
LOCUS						
DEFINITION		EST 18318	Green Grape Berry	Lambda Triplex2	Library	Vitis vinifera
			cDNA clone B3CG1XGB016C02	3'		mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CN546365			GI:46910990	
CN546365.1				
EST.				
<i>Vitis vinifera</i>				
<i>Vitis vinifera</i>				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; <i>Vitis</i> .				

AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldchamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

JOURNAL Unpublished (2002)

COMMENT Contact: Hamdi S.

FEATURES
 source
 1. 32
 Location/Qualifiers
 Seq primer: T7.
 Email: s.hamdi@bordeaux.inra.fr
 Fax: 00-33-(0)5-57-12-25-48
 Tel: 00-33-(0)5-57-12-25-50
 France
 BP 81, 33883 Villenave D'Ornon Cedex
 71, Avenue Edouard Bourleaux
 Agronomie
 Service de Bordeaux 17, Institut National de la Recherche

```

/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB016C02"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfIIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.3e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 540
DV083947
LOCUS      327-384-10_H15_KS Nematosstella vectensis mRNA EST 01-DEC-2005
DEFINITION 327-384-10_H15_KS Nematosstella vectensis normalized cDNA library
sequence.
ACCESSION  DV083947.1 GI:82865340
VERSION     DV083947
KEYWORDS    EST.
SOURCE      Nematosstella vectensis
ORGANISM    Nematosstella vectensis
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Actiniaria;
            Edwardsiidae; Nematosstella.
            1 (bases 1 to 32)
REFERENCE   Technau,U., Rudd,S., Maxwell,P., Gordon,P.M.K., Saina,M.,
AUTHORS     Grasso,L.C., Hayward,D.C., Senses,C.W., Saint,R., Holstein,T.W.,
            Ball,E.E. and Miller,D.J.
TITLE       Maintenance of ancestral complexity and non-metazoan genes in two
            basal cnidarians
JOURNAL     Trends Genet. (2005) In press
COMMENT     Contact: Ulrich Technau
            Sars Centre for Marine Molecular Biology
            High Technology Building, Thormohlensgt. 5 5008 Bergen, Norway
            Tel: +47-55584340
            Email: ulrich.technau@sars.uib.no
            Plate: 10 row: 15 column: H
            Seq primer: KS.
FEATURES
            source
            1..32
            Location/Qualifiers
            ..
            /organism="Nematosstella vectensis"
            /mol_type="mRNA"
            /db_xref="taxon:45351"
            /clone="327-384-10_H15_KS"
            /sex="hermaphrodite"
            /tissue_type="whole embryos"
            /dev_stage="mixed stages from unfertilized eggs to primary
            polyps"
            /clone_lib="Nematosstella vectensis normalized cDNA library
            327"
            /notes="Vector: pBluescript II SK(+); Site 1: NotI; Site 2:
            EcoRI; Normalized oligo dt primed cDNA library using poly
            A+ RNA from mixed embryonic stages of Nematosstella
            vectensis. Cloned directionally into pBluescript II SK(+).
            Ligated in NotI, EcoRI"

Query Match      1.1%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.3e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAA 32

RESULT 541

```

```

AZ314322/c
LOCUS      1M0031N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0031N05 F, genomic survey sequence.
ACCESSION  AZ314322
VERSION     AZ314322.1 GI:10360096
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
            1 (bases 1 to 32)
REFERENCE   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
AUTHORS     Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausen,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0031 row: N column: 05
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 32.
FEATURES
            source
            1..32
            Location/Qualifiers
            ..
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0031N05"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: pWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      1.1%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.3e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 32 AAAAAAAAAAAAAAAAAATATAAAAAAAAAAAAAAAAA 1

RESULT 542

```

AZ579652/c
 LOCUS
 DEFINITION IM0367C12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0367C12 R, genomic survey sequence.
 ACCESSION AZ579652
 VERSION AZ579652.1 GI:11694081
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: C column: 12
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers
 1..32
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367C12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 ||||||||||||||||||||||||||||||||||||
 Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA 1
 RESULT 543

DU834670
 LOCUS
 DEFINITION KBrS014013F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS014013, genomic survey sequence.
 ACCESSION DU834670
 VERSION DU834670.1 GI:83871266
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
 TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
 JOURNAL Unpublished (2005)
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pheom@da.go.kr
 BAC end sequence of Brassica rapa spp. pekinensis Sau3AI BAC clone KBrS014013
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..32
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone="KBrS014013"
 /lab_host="E. coli DH10B"
 /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
 /note="vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa spp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
 Query Match 1.1%; Score 30.4; DB 1; Length 32;
 Best Local Similarity 96.9%; Pred. No. 3.3e+02;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
 ||||||||||||||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32
 RESULT 544
 DX033610
 LOCUS
 DEFINITION KBrB031B19R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB031B19, genomic survey sequence.
 ACCESSION DX033610
 VERSION DX033610.1 GI:84727907
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
 TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
 JOURNAL Unpublished (2005)

COMMENT

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.90.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB031B19
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..32
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB031B19"
/lab_host="E.coli DH10B"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 1.1%; Score 30.4; DB 1; Length 32;
Best Local Similarity 96.9%; Pred. No. 3.3e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 545

DRI1F7S/c

LOCUS

DEFINITION Danio rerio genomic clone DKREY-1F7, genomic survey sequence.

AL735323

VERSION AL735323.1 GI:21343938

KEYWORDS

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 32)

Humphray, S.J., Huckle, E. and Hunt, S.E.

Direct Submission

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished

This sequence was generated from the SP6 end of BAC 1F7. 1F7 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_reio/.

FEATURES

source

Location/Qualifiers

1..32
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKREY-1F7"
/tissue_type="Testis"
/note="vector pindigoBAC-536"

Query Match

Best Local Similarity 1.1%; Score 30.4; DB 1; Length 32;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 546

CF334899/c

LOCUS

DEFINITION

Accession
Version
Keywords
Source
Organism

CF334899

EST.

SOURCE

ORGANISM

Oryza sativa

(japonica cultivar-group)

Eukaryota;

Viridiplantae;

Streptophyta;

Tracheophyta;

Spermatophyta;

Magnoliophyta;

Liliopsida;

Poales;

Poaceae;

BEP

clade; Ehrhartoideae;

Oryzaceae;

Oryza.

1 (bases 1 to 33)

Kim, J. S., Jun, K. M.,

Cheong, P. J., Kim, M. J.,

Lee, T. H., Shin, Y. C.,

Song, S. I., Kim, J. K.,

Kim, Y. -K. and Nahm, B. H.

Large-scale Sequencing

Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics

Institute, GreenGene

Biotech Inc.; Division

of Bioscience and

Bioinformatics, Myongji

University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com,

bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..33

/organism="Oryza sativa

(japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--04-F19"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

CDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match

Best Local Similarity

1.1%; Score 30.4; DB 1; Length 33;

Matches 31; Conservative

0; Mismatches 1; Indels

0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 33 AAAAAAAAAACAAAAAAAAAAAAAAAAAAAAA 2

RESULT 547

AZ307192

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

```

JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunne@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0008 row: B column: 07
             Seq primer: CACACAGGAAACAGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 34.

FEATURES
    source
    1..34
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGCLM0008B07"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGCLM library"
    /note="Vector: pWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

    Query Match      1.1%; Score 30.4; DB 1; Length 34;
    Best Local Similarity 96.9%; Pred. No. 3.4e+02;
    Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    ||||||| ||||||| ||||||| ||||||| |||||||
Db  3 AAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAA 34
    ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 548
CN545906/c      36 bp mRNA linear EST 30-APR-2004
LOCUS          EST 17850 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION     clone B3CS00RL006C01 3', mRNA sequence.
ACCESSION      CN546158
VERSION        CN546158.1 GI:46910783
KEYWORDS       EST
SOURCE         Vitis vinifera
ORGANISM       Vitis vinifera
REFERENCE      1 (bases 1 to 36)
AUTHORS        Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
                Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
                Hamdi,S., Romieu,C. and Terrier,N.
                Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
                or seeds) at Various Developmental Stages
                Unpublished (2002)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
                UMR 619 - Equipe Biologie de la Vigne
                Universite de Bordeaux I, Institut National de la Recherche
                Agronomique
                71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                France
                Tel: 00-33-(0)5-57-12-25-50
                Fax: 00-33-(0)5-57-12-25-48
                Email: s.hamdi@bordeaux.inra.fr
                Seq primer: T7.

FEATURES
    source
    1..36
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL006C01"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    ||||||| ||||||| ||||||| ||||||| |||||||
Db  35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4
    ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 549
CN546158/c      36 bp mRNA linear EST 30-APR-2004
LOCUS          EST 18110 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION     clone B3CS00RL009A10 3', mRNA sequence.
ACCESSION      CN546158
VERSION        CN546158.1 GI:46910783
KEYWORDS       EST
SOURCE         Vitis vinifera
ORGANISM       Vitis vinifera
REFERENCE      1 (bases 1 to 36)
AUTHORS        Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
                Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
                Hamdi,S., Romieu,C. and Terrier,N.
                Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
                or seeds) at Various Developmental Stages
                Unpublished (2002)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
                UMR 619 - Equipe Biologie de la Vigne
                Universite de Bordeaux I, Institut National de la Recherche
                Agronomique
                71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
                France
                Tel: 00-33-(0)5-57-12-25-50
                Fax: 00-33-(0)5-57-12-25-48
                Email: s.hamdi@bordeaux.inra.fr
                Seq primer: T7.

FEATURES
    source
    1..36
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL009A10"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

```



```

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 550
CN546709/c
LOCUS
DEFINITION      36 bp mRNA linear EST 30-APR-2004
CN546709
viniifera cDNA clone B3CS37TB007H08 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
AUTHORS
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .36
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007H08"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 551
DU834429/c
LOCUS
DEFINITION      36 bp DNA linear GSS 22-DEC-2005
DU834429
KBrS014E10R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014E10, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

```

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 36)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B. S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014E10
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .36
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS014E10"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 552
CN545897/c
LOCUS
DEFINITION      37 bp mRNA linear EST 30-APR-2004
CN545897
clone B3CS00RL06B04 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 37)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .37
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL06B04"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30.4; DB 1; Length 36;
Best Local Similarity 96.9%; Pred. No. 3.5e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
    |||||||
Db 36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 553
DU834429/c
LOCUS
DEFINITION      36 bp DNA linear GSS 22-DEC-2005
DU834429
KBrS014E10R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014E10, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

```

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clones="B3CS00RL006B04"
/dev_stages="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match
Best Local Similarity 1.1%; Score 30.4; DB 1; Length 37;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 553
DN988462/c
LOCUS
DEFINITION
ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_B04.ab1 Bermuda grass line Zebra
subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_B04.ab1, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Cynodon dactylon (Bermuda grass)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Chloridoideae; Cynodonteae; Cynodon.
REFERENCE
AUTHORS
Melmaee,K., Elavarthi,S. and Guenzi,A.C.
TITLE
Identification of differentially expressed genes associated with
cold acclimation using suppression subtraction hybridization (SSH)
and cDNA microarrays
JOURNAL
COMMENT
Unpublished (2005)
Contact: Guenzi AC
Dep. of Plant and Soil Sciences
Oklahoma State University
368 Agriculture Hall, Stillwater, OK 74078-6028, USA
Tel: 405-744-6028
Fax: 405-744-6039
Email: acg@mail.pss.okstate.edu
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Seq primer: M13 Forward
Location/Qualifiers
1. 37
/organism="Cynodon dactylon"
/mol_type="mRNA"
/cultivar="Zebra"
/db_xref="taxon:28909"
/clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_B04.ab1"
/tissue_type="Crown"
/lab_host="E. coli"
/clone_lib="Bermudagrass line Zebra subtracted cold
acclimated cDNA library"
/notes="Vector: QIAGEN's pDrive; Messenger RNA was
extracted from control and cold acclimated bermudagrass
crown tissue at 2 and 28 days after acclimation and cDNA
library was constructed following Clontech PCR- select
cDNA subtraction procedure."

Query Match
Best Local Similarity 1.1%; Score 30.4; DB 1; Length 37;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 37 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

```

```

Db 37 CTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 554
CN546437/c
LOCUS
DEFINITION
EST 18581 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS57RB007A02 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS
1 (bases 1 to 38)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
COMMENT
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourdeaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7
Location/Qualifiers
1. 38
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007A02"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match
Best Local Similarity 1.1%; Score 30.4; DB 1; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 555
CN546551/c
LOCUS
DEFINITION
EST 18695 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008C04 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS
1 (bases 1 to 38)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

```

JOURNAL
COMMENT

Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

source

1. .38
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58R8008C04"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30.4; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 7

RESULT 556

CN546633/C

LOCUS

DEFINITION EST 18404 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS37TB007B04 3', mRNA sequence.

ACCESSION

CN546633

VERSION

EST.

KEYWORDS

EST.

SOURCE

Vitis vinifera

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 38)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

AUTHORS

Contact: Hamdi S.

TITLE

UMR 619 - Equipe Biologie de la Vigne

JOURNAL

Universite de Bordeaux I, Institut National de la Recherche

COMMENT

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

source

1. .38
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007B04"
/dev_stage="vexaison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/notes="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match

1.1%;

Score 30.4; DB 1; Length 38;

Best Local Similarity 96.9%; Pred. No. 3.6e+02;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 37 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 557

CN546633/C

LOCUS

DEFINITION

4013015C08.1EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic

survey sequence.

ACCESSION

CN546633

VERSION

GSS.

KEYWORDS

Zea mays

SOURCE

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 36)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013015 row: C column: 08
Class: transposon-tagged.
Location/Qualifiers
1. .36
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match

1.1%;

Score 30.2; DB 1; Length 36;

Best Local Similarity 91.4%; Pred. No. 3.6e+02;

Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743

Db 1 AAAAAAAAAACACAAAAAAAAAAAAAAAAAAAAATA 35

RESULT 558

AL038650

LOCUS

DEFINITION

30 bp

mRNA

linear

EST 06-JUL-2004

```

DEFINITION DKFZp566i1846_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKFZp566i1846_mRNA sequence.
VERSION AL038650
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..30
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566i1846"
/tissue_type="kidney"
/dev_stages="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 559
LOCUS AM044444 30 bp mRNA linear EST 20-SEP-2005
DEFINITION AM044444 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmIC13a04.q1k, mRNA sequence.
ACCESSION AM044444
VERSION AM044444.1 GI:75966537
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1..30
Location/Qualifiers
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmIC13a04.q1k"
/dev_stages="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 561
LOCUS CF280699/c 30 bp mRNA linear EST 14-AUG-2003
DEFINITION CF280699 14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H15,
mRNA sequence.
ACCESSION CF280699
VERSION CF280699.1 GI:33658085

```

```

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 560
LOCUS BG666435 30 bp mRNA linear EST 30-APR-2001
DEFINITION DRACRC02 Rat DRG Library Rattus norvegicus cDNA clone DRACRC02 5',
mRNA sequence.
ACCESSION BG666435
VERSION BG666435.1 GI:13888357
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.
TITLE Identification of gene expression profile of dorsal root ganglion
in the rat peripheral axotomy model of neuropathic pain
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
PUBMED 12060780
COMMENT Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T7
BACKWARD: T7
Seq primer: T3
POLYA=NO.
Location/Qualifiers
1..30
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRACRC02"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stages="adult"
/clone_lib="Rat DRG Library"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 561
LOCUS CF280699/c 30 bp mRNA linear EST 14-AUG-2003
DEFINITION CF280699 14ETL--07-H15.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-H15,
mRNA sequence.
ACCESSION CF280699
VERSION CF280699.1 GI:33658085

```

```

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, MyongJi University
COMMENT Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14E1L--07-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14E1L)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 562
CF292086 30 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
sequence.
ACCESSION CF292086
VERSION CF292086.1 GI:33661119
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14E1L--07-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14E1L)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 562
CF292086 30 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-M10.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M10, mRNA
sequence.
ACCESSION CF292086
VERSION CF292086.1 GI:33661119
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14E1L--07-H15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14E1L)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 564
CF312417/c 30 bp mRNA linear EST 15-AUG-2003
LOCUS CF312417

```

```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-M10"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 563
CF299555/c 30 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-K01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K01, mRNA
sequence.
ACCESSION CF299555
VERSION CF299555.1 GI:33671316
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-K01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 564
CF312417/c 30 bp mRNA linear EST 15-AUG-2003
LOCUS CF312417

```

```

DEFINITION ABF--08-C19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  ABF--08-C19, mRNA sequence.
VERSION     CF312417
KEYWORDS    CF312417.1 GI:33684178
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--08-C19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
     Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 565
CF322226/c LOCUS
DEFINITION HD--13-M02.b1 OshDAC1-overexpressing transgenic rice plasmid
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  HD--13-M02, mRNA sequence.
VERSION     CF322226
KEYWORDS    CF322226
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--08-C19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
     Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 565
CF322226/c LOCUS
DEFINITION HD--13-M02.b1 OshDAC1-overexpressing transgenic rice plasmid
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION  HD--13-M02, mRNA sequence.
VERSION     CF322226
KEYWORDS    CF322226
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="ABF--08-C19"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
     Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 566
CF327835 LOCUS
DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-H17, mRNA
            sequence.
ACCESSION  CF327835
VERSION     CF327835.1 GI:33803920
KEYWORDS    CF327835
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-H17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2M6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;

```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HB--13-M02"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2M6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;
     Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 566
CF327835 LOCUS
DEFINITION NACL--02-H17.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa (japonica cultivar-group) cDNA clone NACL--02-H17, mRNA
            sequence.
ACCESSION  CF327835
VERSION     CF327835.1 GI:33803920
KEYWORDS    CF327835
SOURCE      EST.
ORGANISM    Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
TITLE       Contact: Nahm B.H.
JOURNAL     Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT     of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES             source
     source           1..30
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="NACL--02-H17"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2M6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."
     Query Match      1.1%; Score 30; DB 1; Length 30;
     Best Local Similarity 100.0%; Pred. No. 3.3e+02;

```

```

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 567
CF336555 30 bp mRNA linear EST 18-AUG-2003
JMT--06-K13.q1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--06-K13, mRNA sequence.
CF336555
CF336555.1 GI:33821487
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..30
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--06-K13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector; PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 568
CN545913/c
LOCUS
DEFINITION
CN545913 30 bp mRNA linear EST 30-APR-2004
clone B3CS00RL006C10 3', mRNA sequence.
CN545913
CN545913.1 GI:46910538
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)

```

```

/clone="B3CS57RB007C01"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/Note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 570
CN546474/c
LOCUS
DEFINITION
EST 18618 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS57RB007D06 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Agorces,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.

FEATURES
            source
            Location/Qualifiers
            1..30
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS57RB007D06"
            /dev_stage="ripe stage"
            /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
            /note="Organ: Fruit without seeds; Vector: Lambda
            Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 571
CN546789/c
LOCUS
DEFINITION
EST 18560 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3CS38TB008G04 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
            1..30
            /organism="Oryza sativa (japonica cultivar-group)"

```

```

KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Agorces,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.

FEATURES
            source
            Location/Qualifiers
            1..30
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="B3CS38TB008G04"
            /dev_stage="veraison stage"
            /clone_lib="Turning Grape Berry Lambda Triplex2 Library"
            /note="Organ: Fruit without seeds; Vector: Lambda
            Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 572
CN546764/c
LOCUS
DEFINITION
EST 18618 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS57RB007D06 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
            1..30
            /organism="Oryza sativa (japonica cultivar-group)"

```



```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-E06"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 573
CX014987/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGES15) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
CX014987
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
SOURCE
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGES15)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 574
DR073060/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGES15) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
DR073060
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
SOURCE
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGES15)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575
AZ357603/c
LOCUS
DEFINITION
IM0099H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099H17 F, genomic survey sequence.
ACCESSION
AZ357603
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--01-E06"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 573
CX014987/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGES15) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
CX014987
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
SOURCE
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGES15)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 574
DR073060/c
LOCUS
DEFINITION
io78a02.b1 whole Heart Library (DOGES15) Canis familiaris cDNA,
mRNA sequence.
ACCESSION
DR073060
VERSION
EST.
KEYWORDS
Canis familiaris (dog)
SOURCE
Canis familiaris
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE
ESTs from Canis familiaris whole heart (dog)
JOURNAL
Unpublished (2004)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org.
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..30
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGES15)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match 1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 575
AZ357603/c
LOCUS
DEFINITION
IM0099H17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099H17 F, genomic survey sequence.
ACCESSION
AZ357603
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: H column: 17
 Seq primer: CTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

```

1..30
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0099H17"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 576
A2455741
LOCUS
DEFINITION
  A2455741
  1M0258D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0258D16 F, genomic survey sequence.
ACCESSION
  A2455741
VERSION
  A2455741.1 GI:10613866
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  1 (bases 1 to 30)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu

```

Insert Length: 10000 Std Error: 0.00
 Plate: 0258 row: D column: 16
 Seq primer: CTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

```

1..30
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0258D16"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

```

```

RESULT 577
A2481739/c
LOCUS
DEFINITION
  A2481739
  1M0306N12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0306N12 F, genomic survey sequence.
ACCESSION
  A2481739
VERSION
  A2481739.1 GI:10642804
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  1 (bases 1 to 30)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu

```

Insert Length: 10000 Std Error: 0.00
 Plate: 0306 row: N column: 12
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0306N12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 578

AZ582114/C
 LOCUS 1M0374J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0374J17 F, genomic survey sequence.

ACCESSION AZ582114
 VERSION AZ582114.1 GI:11700674
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 30)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0374 row: J column: 17
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 30.
 Location/Qualifiers

FEATURES

1..30
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0374J17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 30; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
 |||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 579

CZ917652
 LOCUS 4021006E03.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION CZ917652
 VERSION CZ917652.1 GI:71936647
 KEYWORDS GSS.

SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 30)

AUTHORS Walbot,V.

TITLE Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)

JOURNAL Contact: Walbot V

COMMENT Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.

Plate: 4021006 row: E column: 03

Class: transposon-tagged.

Location/Qualifiers

FEATURES

source

```

1. .30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

Query Match 1.1%; Score 30; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 580

CZ919796

LOCUS

DEFINITION 4021014H02.2ELy1 4021 - RescueMu Grid V Zea mays genomic, GSS 08-AUG-2005 survey sequence.

ACCESSION CZ919796

VERSION CZ919796.1

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 30)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

COMMENT

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021014 row: H column: 02

Class: transposon-tagged.

FEATURES

source

1. .30

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 30; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 581

CW020481/c

LOCUS

DEFINITION CW020481 TIGEM gene trap library Mus musculus cDNA clone A015.C10, mRNA sequence.

ACCESSION CW020481

VERSION CW020481.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Cobellis, G., Nicolaus G., Iovino, M., Romito, A., Marta, E.,

Barbarisi, M., Sardiello, M., Di Giorgio, F.P., Iovino, N., Zollo, M.,

Ballabio, A. and Cortese, R.

Tagging genes with cassette-exchange sites

Nucleic Acids Res. 33 (4), e44 (2005)

15741177

Contact: TIGEM

107

TIGEM

Via P. Castellino, 111, 80131 NAPOLI, ITALY

Tel: +390816132205

Fax: +390815790919

Email: cobellis@tigem.it

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM

Class: Gene Trap.

FEATURES

source

1. .30

/organism="Mus musculus"

/mol_type="mrna"

/strain="129 Ola"

/db_xref="taxon:10090"

/clone="A015.C10"

/sex="male"

/cell_type="Embryonic stem cell"

/cell_line="E14"

/clone_lib="TIGEM gene trap library"

/note="Vector: pFLIPI"

Query Match 1.1%; Score 30; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

DB 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 582

```

DUB35531
LOCUS      KBR5016N21F KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
DEFINITION subsp. pekinensis genomic clone KBrS016N21, genomic survey
sequence.
ACCESSION  DUB35531
VERSION    DUB35531.1 GI:83872127
KEYWORDS   GSS.
SOURCE     Brassica rapa subsp. pekinensis
ORGANISM   Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J. H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL    Unpublished (2005)
COMMENT    Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-295-1670
            Fax: +82-31-295-1672
            Email: pbeom@rda.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBR5016N21
            Seq primer: T7
            Class: BAC ends.

FEATURES             source
     source           location/Qualifiers
     1..30            /organism="Brassica rapa subsp. pekinensis"
                    /mol_type="genomic DNA"
                    /cultivar="Chiifu"
                    /sub_species="pekinensis"
                    /db_xref="taxon:51351"
                    /clone="KBR5016N21"
                    /lab_host="E. coli DH10B"
                    /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                    ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                    available at NtAB."

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 583
AG191161/C
LOCUS      AG191161
DEFINITION Pan troglodytes DNA, clone: RP43-066P20.T7, genomic survey
sequence.
ACCESSION  AG191161
VERSION    AG191161.1 GI:45223337
KEYWORDS   GSS.
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Pan.
REFERENCE  1
AUTHORS    Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
TITLE      BAC end sequences of Library RP-43
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 30)
AUTHORS    Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

```

```

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Gun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector      : pBACe3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI.
Location/Qualifiers
1..30       /organism="Pan troglodytes"
            /mol_type="genomic DNA"
            /db_xref="taxon:9598"
            /clone="RP43-066P20.T7"
            /sex="male"
            /cell_type="lymphocytes"
            /clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match      1.1%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    |||||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 584
BG292912
LOCUS      BG292912
DEFINITION 602389549F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4501164 5',
            mRNA sequence.
ACCESSION  BG292912
VERSION    BG292912.1 GI:13052227
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 31)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10368 row: b column: 13
            High quality sequence stop: 31.

FEATURES             source
     source           location/Qualifiers
     1..31            /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:4501164"
                    /tissue_type="retina"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_94"
                    /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

```

Site 2: Sali: Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life technologies.
Note: this is a NIH_MGC Library."

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 585
CN545579/c
LOCUS CN545579 31 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17523 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION clone B3CS00RL003F11 3', mRNA sequence.
CN545579
VERSION CN545579.1 GI:46910204
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 31)

TITLE Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

JOURNAL Unpublished (2002)

COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7

FEATURES
source
1..31
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003F11"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 586
CN545867/c
LOCUS CN545867 31 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17811 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION clone B3CS00RL002G09 3', mRNA sequence.
CN545867
VERSION CN545867.1 GI:46910492
KEYWORDS EST.

SOURCE
ORGANISM

Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 31)

REFERENCE
AUTHORS

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7

TITLE

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

JOURNAL
COMMENT

Unpublished (2002)

Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7

FEATURES
source
1..31
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002G09"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 587
CN545921/c

LOCUS CN545921 31 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17865 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION clone B3CS00RL006D06 3', mRNA sequence.
CN545921
VERSION CN545921.1 GI:46910546
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 31)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

TITLE

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

JOURNAL
COMMENT

Unpublished (2002)

Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

```

FEATURES
source
    Location/Qualifiers
    1..31
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL006D06"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

Query Match
    1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 588
CN546024/c
LOCUS
DEFINITION
    CN546024
    EST 17974 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
    clone B3CS00RL007F01 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Vitis vinifera
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
REFERENCE
    1 (bases 1 to 31)
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
    Unpublished (2002)
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.
    Location/Qualifiers
    1..31
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL006G05"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

Query Match
    1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 589
CN546024/c
LOCUS
DEFINITION
    CN546024
    EST 17974 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
    clone B3CS00RL007F01 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Vitis vinifera
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
REFERENCE
    1 (bases 1 to 31)
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
    Unpublished (2002)
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.
    Location/Qualifiers
    1..31
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL007F01"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

Query Match
    1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 589

```

```

CN546130/c
LOCUS
DEFINITION
    CN546130
    EST 18082 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
    clone B3CS00RL008G05 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Vitis vinifera
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
    rosids; Vitaceae; Vitis.
REFERENCE
    1 (bases 1 to 31)
    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
    Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
    Hamdi,S., Romieu,C. and Terrier,N.
    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
    or seeds) at Various Developmental Stages
    Unpublished (2002)
    Contact: Hamdi S.
    UMR 619 - Equipe Biologie de la Vigne
    Universite de Bordeaux I, Institut National de la Recherche
    Agronomique
    71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
    France
    Tel: 00-33-(0)5-57-12-25-50
    Fax: 00-33-(0)5-57-12-25-48
    Email: s.hamdi@bordeaux.inra.fr
    Seq primer: T7.
    Location/Qualifiers
    1..31
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL008G05"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiIA; Site_2: SfiIB; Oriented library"

Query Match
    1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 590
CN597046
LOCUS
DEFINITION
    CN597046
    clone UUGCLIM0410K08 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Mus musculus (house mouse)
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 31)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Federsen,T.,
    Reilly,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES

source

```
1. 31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0410K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30
```

```
RESULT 591
CZ917966
LOCUS 31 bp DNA linear GSS 08-AUG-2005
DEFINITION 4021007E11.2EL y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.
ACCESSION CZ917966
VERSION CZ917966.1 GI:71937128
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon (Unpublished (2001))
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
```

Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021007 row: E column: 11
Class: transposon-tagged.
Location/Qualifiers
1. 31

FEATURES

source

```
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
```

```
Query Match 1.1%; Score 30; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 2 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31
```

```
RESULT 592
AZ400441
LOCUS 32 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0166C14 R, genomic survey sequence.
ACCESSION AZ400441
VERSION AZ400441.1 GI:10515515
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
```

```
REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iglam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. 32
```



```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0166C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/nucleus="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      1.18; Score 30; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
      |||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

```

RESULT	593
AU013658/c	
LOCUS	33 bp mRNA linear EST 03-AUG-1998
DEFINITION	AU013658 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc08464, mRNA sequence.
ACCESSION	AU013658
VERSION	AU013658.1 GI:3368449
KEYWORDS	EST.
SOURCE	Schizosaccharomyces pombe (fission yeast)
ORGANISM	Schizosaccharomyces pombe Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes. 1 (bases 1 to 33) Morimyo.M. and Mita,K.
REFERENCE	Identification of expressed sequence tags of Schizosaccharomycetes
AUTHORS	pombe
TITLE	Unpublished (1998)
JOURNAL	Contact: Mitsuo Morimyo
COMMENT	Genome Research Group National Institute of Radiological Sciences 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan Email: morimyo@nirs.go.jp.

```

FEATURES
    source
        1..33
            Location/Qualifiers
                email="moriyosawa@r5.9.nippon-bp.co.jp"
                /organism="Schizosaccharomyces pombe"
                /mol_type="mRNA"
                /strain="972"
                /db_xref="taxon:4896"
                /clone="spc08464"
                /sex="h minus"
                /clone_l1b="Schizosaccharomyces pombe late log phase cDNA"
                /note="Vector: M13mpl9; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mpl9 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of

```

```

Schizosaccharomyces pombe are available for searching on
the world wide Web. (URL, http://www.nifs.go.jp)"

Query Match      1.1%  Score 30;  DB 1;  Length 33;
Best Local Similarity 100.0%;  Pred. No. 3.5e+02;
Matches 30;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db   30 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT	594
LOCUS	DN955605/c
DEFINITION	it91c01.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
ACCESSION	DN955605
VERSION	DN955605
KEYWORDS	DN955605.1 GI:63027743
SOURCE	EST.
ORGANISM	Gnetum gnemon Gnetum gnemon
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
AUTHORS	Brenner,E.D., Twigg,R.W., Runko,S.J., Katarai,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D. Expressed tag sequences from Gnetum female cone (NYBG) Unpublished (2003)
TITLE	Contact: W. Richard McCombie
JOURNAL	
COMMENT	

Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100 Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombie@cshl.org
 Seq primer: -21M13UnivRev.
 Location/Qualifiers
 1. .33
 /organism="Gnetum gnemon"
 /mol_type="mRNA"
 /db_xref="taxon:3382"
 /sex="female"
 /clone_lib="Gnetum female cone (NYBG)"
 /note="Organ: mature, unfertilized reproductive strobili;
 Vector: PBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
 Completed 02/11/02, submitted for sequencing 02/12/02.
 Library: Stratagene ZAP Express cDNA Synthesis Kit. The
 library was size-fractionated to enrich for large inserts.
 Sample: NYBG accession number #436/84"

Query Match	1.1%;	Score 30;	DB 1;	Length 33;	
Best Local Similarity	100.0%;	Pred. No. 3.5e+02;			
Matches 30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2738		
Db	32	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3		

RESULT 595					
CV066327					
LOCUS					
DEFINITION	CV066327	35 bp	mRNA	linear	EST 24-AUG-2004
	WNEU32e2	Wheat EST endosperm library	Triticum aestivum	cDNA clone	
	WNEU32e2	5' similar to Unknown Function,	mRNA sequence.		
ACCESSION	CV066327				
VERSION	CV066327.1	GI:51529504			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP				

```

REFERENCE
AUTHORS Ali,S, Holloway,B. and Taylor,W.C.
TITLE Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
JOURNAL Plant Mol. Biol. Rep. 18, 123-132 (2000)
COMMENT Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 35.
Location/Qualifiers
1. .33
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stages="developing endosperm tissue 6, 8, 10 dpa (days post_anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/note="Vector: _ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of _ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 30; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

CN545607 33 bp mRNA linear EST 30-APR-2004
EST 17551 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL004A03 3', mRNA sequence.
CN545607
CN545607.1 GI:46910232
EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 33)
Abbal,P., Agasse,A., Agorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48

clade: Pooideae; Triticaceae; Triticum.
1 (bases 1 to 35)
Ali,S, Holloway,B. and Taylor,W.C.
Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis
Plant Mol. Biol. Rep. 18, 123-132 (2000)
Contact: Bill Taylor
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry.
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
Tel: 61 2 6246 5223
Fax: 61 2 6246 5000
Email: Bill.Taylor@csiro.au
Seq primer: M13 reverse primer
High quality sequence stop: 35.
Location/Qualifiers
1. .33
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Hartog"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stages="developing endosperm tissue 6, 8, 10 dpa (days post_anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Wheat EST endosperm library"
/note="Vector: _ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of _ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 30; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

CN545607 33 bp mRNA linear EST 30-APR-2004
EST 17551 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL004A03 3', mRNA sequence.
CN545607
CN545607.1 GI:46910232
EST.
KEYWORDS Vitis vinifera
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 33)
Abbal,P., Agasse,A., Agorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48

```

```

Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1. .33
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004A03"
/dev_stages="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1: SfiIA; Site 2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2707 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 33 CTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 597
DX050853 33 bp DNA linear GSS 10-JAN-2006
LOCUS KRB053024R KRB, Brassica rapa BamHI BAC library, Brassica rapa
subsp. pekinensis genomic clone KRB053024, genomic survey
sequence.
ACCESSION DX050853
VERSION DX050853.1 GI:84745150
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 33)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa esp. pekinensis BamHI BAC clone
KRB053024
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .33
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KRB053024"
/lab_host="E.coli DH10B"
/clone_lib="KRB, Brassica rapa BamHI BAC library"
/note="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chifu BAC library (KRB BAC) is provided
by Yong-Pyo Lim (CNU).".

Query Match 1.1%; Score 29.8; DB 1; Length 33;
Best Local Similarity 93.9%; Pred. No. 3.6e+02;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741

```



```

Clonetech (*6854-1) "
Query Match      1.1%; Score 29.6; DB 1; Length 37;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2708 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 TGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATGAGA 1

RESULT 601
B0591372/c
LOCUS      31 bp mRNA linear EST 06-DEC-2002
DEFINITION B0591372
ACCESSION  B0591372
VERSION    B0591372.1 GI:26120955
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE  B0591372
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL    Caryophyllales; Amaranthaceae; Beta.
PUBMED    12472698
COMMENT    1 (bases 1 to 31)
           Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
           Drungewski,M., Stah,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
           Construction of a 'unigenes' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)
           Contact: Weishaar B
           ADIS DNA core facility at MP1Z
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weishaar@mpiz-koeln.mpg.de
           Insert Length: 31 Std Error: 0.00
           Plate: 17 row: 1 column: 15
           Seq primer: T7; GTAATACGACTCCTATAGGCG.
FEATURES
source
1..31
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-115"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

Clonetech (*6854-1) "
Query Match      1.1%; Score 29.6; DB 1; Length 37;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2708 TAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2743
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 36 TGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATGAGA 1

RESULT 601
B0591372/c
LOCUS      31 bp mRNA linear EST 06-DEC-2002
DEFINITION B0591372
ACCESSION  B0591372
VERSION    B0591372.1 GI:26120955
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
REFERENCE  B0591372
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL    Caryophyllales; Amaranthaceae; Beta.
PUBMED    12472698
COMMENT    1 (bases 1 to 31)
           Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
           Drungewski,M., Stah,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
           Construction of a 'unigenes' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)
           Contact: Weishaar B
           ADIS DNA core facility at MP1Z
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weishaar@mpiz-koeln.mpg.de
           Insert Length: 31 Std Error: 0.00
           Plate: 17 row: 1 column: 15
           Seq primer: T7; GTAATACGACTCCTATAGGCG.
FEATURES
source
1..31
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-115"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGC-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

Query Match      1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2706 ACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 AGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 603
CN545785/c
LOCUS      31 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17729 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION  CN545785
VERSION    CN545785.1 GI:46910410
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera
REFERENCE  CN545785
AUTHORS    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
JOURNAL    rosids; Vitaceae; Vitis.
PUBMED    1 (bases 1 to 31)
           Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
           Couture,C., Dedaldechamp,F., Delrot,S., Gliseant,D., Grimplet,J.,
           Hamdi,S., Romieu,C. and Terrier,N.
           Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
           or seeds) at Various Developmental Stages
           Unpublished (2002)
           Contact: Hamdi S.
           UMR 619 - Equipe Biologie de la Vigne
           Universite de Bordeaux I, Institut National de la Recherche
           Agronomique
           71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
           France

```

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source
 Location/Qualifiers
 1. .31
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00RL005H07"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 3.7e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 604

CN546374/c
 LOCUS
 DEFINITION
 EST 18327 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB016C11 3', mRNA sequence.

ACCESSION CN546374
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE

AUTHORS
 Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
 Couture, C., Dedalchamps, F., Delrot, S., Glissant, D., Grimpet, J.,
 Hamdi, S., Romieu, C. and Terrier, N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.

JOURNAL

COMMENT
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source
 Location/Qualifiers
 1. .31
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB016C11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 3.7e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

|||||

Db

RESULT 605

AZ486763/c
 LOCUS
 DEFINITION
 EST 18327 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB016C11 3', mRNA sequence.

ACCESSION AZ486763
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: A column: 11

Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends

High quality sequence stop: 31.
 Location/Qualifiers

FEATURES

source
 1. .31
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0315A11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 [gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.1%; Score 29.4; DB 1; Length 31;
 Best Local Similarity 96.8%; Pred. No. 3.7e+02;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

|||||

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of *Brassica rapa* BamHI (KBRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.90.kr
BAC end sequence of *Brassica rapa* ssp. *pekinensis* BamHI BAC clone
KBRB031101
Seq primer: M13 Reverse
Class: BAC ends.

TITLE JOURNAL COMMENT

225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.90.kr
BAC end sequence of *Brassica rapa* ssp. *pekinensis* BamHI BAC clone
KBRB031101
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES source

1. .31
Location/Qualifiers
/organism="Brassica rapa subsp. *pekinensis*"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRB031101"
/lab_host="E. coli DH10B"
/clone_lib="KBRB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBRB BAC) is provided
by Yong-Pyo Lim (CNU)."
Query Match 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AL038680 1.1%; Score 29.4; DB 1; Length 31;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 31

RESULT 609

AL038680 32 bp mRNA linear EST 06-JUL-2004
LOCUS
DEFINITION
DKF2p566J0246.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFp566J0246, mRNA sequence.

AL038680
AL038680.1 GI:49682182
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 32)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.

EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

FEATURES source

1. .32
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p566J0246"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 1.1%; Score 29.4; DB 1; Length 32;
Best Local Similarity 96.8%; Pred. No. 3.7e+02;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 2 TAAAAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 610

CN545857/c 34 bp mRNA linear EST 30-APR-2004
LOCUS
DEFINITION
EST 17801 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL002F10.3', mRNA sequence.

CN545857
CN545857.1 GI:46910482
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

1 (bases 1 to 34)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaidechamp, F., Delrot, S., Glissant, D., Grimpellet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 77.

Location/Qualifiers
1. .34
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002F10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 34;
Best Local Similarity 96.8%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

FEATURES source

1. .34
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL002F10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 34;
Best Local Similarity 96.8%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Query 2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 32 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 611

CN546360/c 34 bp mRNA linear EST 30-APR-2004
LOCUS
DEFINITION
EST 18313 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS1XGB016B08.3', mRNA sequence.

CN546360
CN546360.1 GI:46910985
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 34)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,

CN546734/c	CN546734	35 bp	mRNA	linear	EST 30-APR-2004
LOCUS	EST 18505	Turning Grape Berry Lambda Triplex2 Library Vitis			
DEFINITION	vinifera cDNA clone B3CS8TB00809 3', mRNA sequence.				
ACCESSION	CN546734				
VERSION	CN546734.1	GI:46911359			
KEYWORDS	EST.				

SOURCE ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 35)
AUTHORS Abbal,P., Agasse,A., Georges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES source
Location/Qualifiers
1..35
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS38TB00809"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29.4; DB 1; Length 35;
Best Local Similarity 96.8%; Pred.No.3.9e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
|||||
DB 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 615
AL036993 36 bp mRNA linear EST 06-JUL-2004
LOCUS DXFZP564F0564_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DEFINITION DXFZP564F0564, mRNA sequence.
ACCESSION DXFZP564F0564, mRNA sequence.
VERSION AL036993
KEYWORDS AL036993.1 GI:49681922
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 36)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Duesterhoeft, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES source
Location/Qualifiers
1..36
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DXFZP564F0564"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE
AUTHORS 1 (bases 1 to 36)
        Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
        Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
        Hamdi,S., Ronieu,C. and Terrier,N.
TITLE    Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL  Unpublished (2002)
COMMENT  Contact: Hamdi S.
        UMR 619 - Equipe Biologie de la Vigne
        Universite de Bordeaux I, Institut National de la Recherche
        Agronomique
        71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
        France
        Tel: 00-33-(0)5-57-12-25-50
        Fax: 00-33-(0)5-57-12-25-48
        Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES             Location/Qualifiers
     source           1..36
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultiVar="Cabernet Sauvignon"
                     /db_xref="taxon:29760"
                     /clone="B3CS37TB007F08"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 29.4; DB 1; Length 36;
Best Local Similarity 96.8%; Pred. No. 4e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||
Db  36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 618
LOCUS  CN546685               36 bp      mRNA      linear      EST 30-APR-2004
DEFINITION  EST 18456 Turning Grape Berry Lambda Triplex2 Library Vitis
            vinifera cDNA clone B3CS37TB007F08 3', mRNA sequence.
ACCESSION  CN546685
VERSION    CN546685.1   GI:45911310
KEYWORDS   EST.
SOURCE     Vitis vinifera
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; Vitaceae; Vitis.
REFERENCE  1 (bases 1 to 36)
AUTHORS   Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
           Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
           Hamdi,S., Ronieu,C. and Terrier,N.
TITLE     Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL   Unpublished (2002)
COMMENT   Contact: Hamdi S.
           UMR 619 - Equipe Biologie de la Vigne
           Universite de Bordeaux I, Institut National de la Recherche
           Agronomique
           71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
           France
           Tel: 00-33-(0)5-57-12-25-50
           Fax: 00-33-(0)5-57-12-25-48
           Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES             Location/Qualifiers
     source           1..36
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /cultiVar="Cabernet Sauvignon"
                     /db_xref="taxon:29760"
                     /clone="B3CS37TB007F08"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.1%; Score 29.4; DB 1; Length 36;
Best Local Similarity 96.8%; Pred. No. 4e+02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||
Db  36 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 618
LOCUS  CN546685/c           36 bp      mRNA      linear      EST 26-AUG-2004
DEFINITION  CN546685 cDNA non acclimated Bluecrop library Vaccinium corymbosum
            cDNA 3', mRNA sequence.
ACCESSION  CV091545
VERSION    CV091545.1   GI:51570884
KEYWORDS   EST.
SOURCE     Vaccinium corymbosum
           Vaccinium corymbosum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           asterids; Ericales; Ericaceae; Vaccinioideae; Vaccinieae;
           Vaccinium.
REFERENCE  1 (bases 1 to 36)
AUTHORS   Dhanaraj,A.L., Alkharouf,N.W., Beard,H.S., Chouikha,I.B.,
           Matthews,B.F. and Rowland,L.J.
TITLE     Monitoring gene expression changes during cold acclimation of
           blueberry (Vaccinium corymbosum L.) using a cDNA microarray
JOURNAL   Unpublished (2004)
COMMENT   Contact: Rowland, L.J.
           Fruit Lab
           US Department of Agriculture (USDA), ARS, PSI
           Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville, MD
           20705-2350, USA
           Tel: 301-504-6654
           Fax: 301-504-5653
           Email: rowlandj@ba.ars.usda.gov.

FEATURES             Location/Qualifiers
     source           1..36
                     /organism="Vaccinium corymbosum"
                     /mol_type="mRNA"
                     /cultiVar="Bluecrop"
                     /db_xref="taxon:69286"
                     /tissue_type="Flower buds including bud scales"
                     /dev_stage="Mature plants"
                     /clone_lib="cDNA non acclimated Bluecrop library"
                     /note="Vector: pBluescript SK-; cDNA clones from Vaccinium
           corymbosum cv. Bluecrop, RNA for preparation of library
           was extracted from flower buds collected in the fall from
           non acclimated plants"

Query Match      1.1%; Score 29.4; DB 1; Length 36;
Best Local Similarity 90.9%; Pred. No. 4e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2708 TAAAAA
      |||
Db  33 TCAAA
      |||

RESULT 620
LOCUS  AL038356               34 bp      mRNA      linear      EST 06-JUL-2004

```

```

DEFINITION DKFZ566L152_r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKFZ566L152, mRNA sequence.
VERSION AL038356
KEYWORDS AL038356.1 GI:49682097
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 34)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
1..34
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ566L152"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
Query Match 1.1%; Score 29.2; DB 1; Length 34;
Best Local Similarity 91.2%; Pred. No. 4e+02;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 1 AAGAGAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAA 34
T50295 35 bp mRNA linear EST 06-FEB-1995
Yb16g12.s1 Stratagene fetal spleen (#937205) Homo sapiens cDNA
clone IMAGE:71398 3' similar to similar to gb:LI9437 TRANSALDOLASE
(HUMAN), mRNA sequence.
ACCESSION T50295
VERSION T50295.1 GI:652155
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 35)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
and Marra, M.
1 (bases 1 to 35)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
PUBMED 8889549
COMMENT Other ESTs: yb16g12.r1
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1

```

```

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
FEATURES
source
1..35
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:493063"
/db_xref="taxon:9606"
/clone="IMAGE:71398"
/tissue_type="fetal spleen"
/dev_stage="fetal"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene fetal spleen (#937205)"
/notes="Organ: spleen; Vector: paluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGCAGG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
Query Match 1.1%; Score 29.2; DB 1; Length 35;
Best Local Similarity 88.6%; Pred. No. 4e+02;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
Db 35 TCATAAAAAAAAAAAAAAAAAAAAAAAAAATATATAAAAAA 1
RESULT 622
ACCESSION AZ351309
LOCUS 1M0089K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION Clone UUGC1M0089K13 F, genomic survey sequence.
ACCESSION AZ351309
VERSION AZ351309.1 GI:10430546
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 35)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, W., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84102, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: K column: 13
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 35.
FEATURES
source
1..35
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089K13"

```

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: pWD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29.2; DB 1; Length 35;
 Best Local Similarity 91.2%; Pred. No. 4e+02;
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
 |||||
 Db 2 AAAAAAAAAAAAAAAAAATTTAAAAAAAAAAAAAAAAAAAA 35

RESULT 623

LOCUS C2914519
 DEFINITION 4013007D07.2EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
 ACCESSION C2914519
 VERSION C2914519.1 GI:71931175
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 35)
 Walbot.V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4013007 row: D column: 07
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES

source
 1..35
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /issue_type="leaf"
 /tissue_type="adult"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="4013 - RescueMu Grid O"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 29.2; DB 1; Length 35;
 Best Local Similarity 91.2%; Pred. No. 4e+02;
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2742
 |||||
 Db 2 AAAAAAAAAAAAAAAAAAGTAAAAAAAAAAAAAAAAAAA 35

RESULT 624

LOCUS AM044739
 DEFINITION AM044739 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmIC32g07.q1k, mRNA sequence.
 ACCESSION AM044739
 VERSION AM044739.1 GI:75967229
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 29)
 Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.
 Location/Qualifiers

FEATURES

source
 1..29
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmIC32g07.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="Country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 625

LOCUS AM048584
 DEFINITION AM048584 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmIC12e02.q1k, mRNA sequence.

ACCESSION AM048584
 VERSION AM048584.1 GI:75968755
 KEYWORDS EST.
 SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S., Nikolaïdou-Katariadou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of *Schistosoma mansoni*
 JOURNAL Unpublished (2005)
 COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1. .29
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC12e02.gik"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /notes="country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 626
 CF279536/c 29 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--05-N22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-N22, mRNA sequence.

ACCESSION CF279536.1 GI:33656922
 VERSION
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source 1. .29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--05-N22"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 628
 CF312601 29 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-G22, mRNA sequence.

ACCESSION CF312601
 VERSION
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 627
 CF299920 29 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--04-C02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-C02, mRNA sequence.

ACCESSION CF299920
 VERSION CF299920.1 GI:33671681
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 CONTACT: Nahm B.H.
 GENOMICS and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES
 source 1. .29
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--04-C02"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.1%; Score 29; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 628
 CF312601 29 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--08-G22.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--08-G22, mRNA sequence.

ACCESSION CF312601
 VERSION CF312601.1 GI:33684362
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 29)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 310 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
1..29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-G22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF" (ABF)
cDNA library (ABF)
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 629

CN545237/c 29 bp mRNA linear EST 30-APR-2004
LOCUS EST 17181 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00GL004G11 3', mRNA sequence.

ACCESSION CN545237.1 GI:46909862

VERSION EST:

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM

REFERENCE 1 (bases 1 to 29)
Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..29

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00GL004G11"

FEATURES

source

/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 630

CN546188/c

LOCUS

DEFINITION

EST 18140 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

clone B3CS00RL009D04 3', mRNA sequence.

ACCESSION CN546188.1 GI:46910813

VERSION EST:

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM

REFERENCE 1 (bases 1 to 29)

AUTHORS

Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..29

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL009D04"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 631

CN546382/c

LOCUS

DEFINITION

EST 18335 Green Grape Berry Lambda Triplex2 Library Vitis vinifera

cDNA clone B3CS1XGB016D07 3', mRNA sequence.

ACCESSION CN546382

VERSION CN546382.1 GI:46911007

KEYWORDS EST.

SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB016D07"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 632
CN546438/c
LOCUS EST 18582 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS57RB007A03 3', mRNA sequence.
ACCESSION CN546438
VERSION
KEYWORDS
SOURCE
ORGANISM Vitis vinifera

REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007A03"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 633
CN546557/c
LOCUS EST 18701 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
DEFINITION CDNA clone B3CS58RB008C10 3', mRNA sequence.
ACCESSION CN546557
VERSION
KEYWORDS
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 29)
AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source Location/Qualifiers
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008C10"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 634

```

CV999708/c
LOCUS          CV999708                29 bp    mRNA    linear    EST 03-DEC-2004
DEFINITION    ivs2f08.b1 Right Cardiac Ventricle (DOGESt6) Canis familiaris CDNA,
               mRNA sequence.
ACCESSION     CV999708
VERSION       CV999708.1   GI:56271125
KEYWORDS      EST.
SOURCE        Canis familiaris (dog)
ORGANISM      Canis familiaris
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE        ESTs from Canis familiaris right cardiac ventricle (dog)
JOURNAL      Unpublished (2004)
COMMENT      Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mcombie@cshl.org.

FEATURES             source
   1..29
   /organism="Canis familiaris"
   /mol_type="mRNA"
   /db_xref="taxon:9615"
   /sex="Unknown"
   /tissue_type="Cardiac muscle"
   /dev_stage="3 month old normal canine"
   /lab_host="XL10 Gold"
   /clone_lib="Right Cardiac Ventricle (DOGESt6)"
   /note="Organ: Heart; Vector: pBluescript II SK; Site: 1:
   EcoRI; Site 2: XhoI; Library constructed using pBluescript
   XR kit from Stratagene. Cloned cDNA was size selected
   between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
   Pathology and Medical Genetics, School of Veterinary
   Medicine, University of Pennsylvania, 3800 Spruce Street,
   Philadelphia, PA 19104-6051"

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 635
AZ389566      29 bp    DNA    linear    GSS 02-OCT-2000
LOCUS          IM0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    Clone UUGC1M0150D21 F, genomic survey sequence.
ACCESSION     AZ389566
VERSION       AZ389566.1   GI:10503274
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0150 row: D column: 21
               Seq primer: CGTTGTAACACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 29.

FEATURES             source
   1..29
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUGC1M0150D21"
   /sex="Male"
   /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
   /clone_lib="Mouse 10kb plasmid UUGC1M library"
   /note="Vector: pMD42nv. Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a

```

```

FEATURES             source
   1..29
   /organism="Ginkgo biloba"
   /mol_type="mRNA"
   /db_xref="taxon:3311"
   /sex="female"
   /clone_lib="Ginkgo female leaf (NYBG)"
   /note="Organ: leaf; Vector: pBK-CMV; Site: 1: XhoI;
   Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
   The library was size-fractionated to enrich for large
   inserts."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
      |||||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 636
AZ389566      29 bp    DNA    linear    GSS 02-OCT-2000
LOCUS          IM0150D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    Clone UUGC1M0150D21 F, genomic survey sequence.
ACCESSION     AZ389566
VERSION       AZ389566.1   GI:10503274
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 29)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0150 row: D column: 21
               Seq primer: CGTTGTAACACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 29.

FEATURES             source
   1..29
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUGC1M0150D21"
   /sex="Male"
   /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
   /clone_lib="Mouse 10kb plasmid UUGC1M library"
   /note="Vector: pMD42nv. Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a

```


0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 637
AZ414283/c
LOCUS
DEFINITION
1M0188G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0188G12 R, genomic survey sequence.

ACCESSION
AZ414283
VERSION
GSS.
KEYWORDS
GSS.
SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0188 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
Location/Qualifiers
1. ..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0188G12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114]gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 638
AZ451930/c
LOCUS
DEFINITION
1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0251E05 R, genomic survey sequence.

ACCESSION
AZ451930
VERSION
GSS.
KEYWORDS
GSS.
SOURCE
Mus musculus
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES
Location/Qualifiers
1. ..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0251E05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 639
AZ468402/c

LOCUS AZ468402 29 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0281G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0281G24 F, genomic survey sequence.

ACCESSION AZ468402
VERSION AZ468402.1 GI:10626527
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0281G24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
source

1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0281G24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 640
AZ46793/c

LOCUS AZ46793 29 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315N21 F, genomic survey sequence.

ACCESSION AZ46793
VERSION AZ46793.1 GI:10653915
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
source

1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD2 (gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 |||||
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT	642				
AZ784208					
LOCUS	AZ784208	29 bp	DNA	linear	GSS 16-FEB-2001
DEFINITION	2M0026113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0026113 R. genomic survey sequence.				

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AZ784208	AZ784208.1	GI:12919703	GSS.	
			Mus musculus (house mouse)	
			Mus musculus	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus	

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 29)	Sciurognathi: Muroidea; Muridae; Murinae; Mus.		
	Dunn,B., Aoyagi,A., Barber,M., Becsorn,T., Duval,B., Hamil,C., Tsun,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,I., Pridmore,M., Rose,K., Stokoe,R., Tingey,A., von Ritzmann,K., and White,D.		
	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
	Unpublished (2000)		

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: 1 column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.

```

FEATURES
    source
        high quality sequence scop: 29.
        Location/Qualifiers
            1..29
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0026113"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PW042nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydridynamically sheared by repeated passage through a

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 643

AZ806470 29 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0068102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0068102 R, genomic survey sequence.

ACCESSION AZ806470
VERSION AZ806470.1 GI:12969849

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0068 row: I column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

source

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0068102"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 644

AZ812242 29 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0078J13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0078J15 R, genomic survey sequence.

ACCESSION AZ812242
VERSION AZ812242.1 GI:12981296

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0078 row: J column: 15

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

source

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0078J15"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 645

AZ868731
LOCUS
DEFINITION
29 bp DNA linear GSS 21-FEB-2001
clone UUGC2M0180L02 R, genomic survey sequence.

ACCESSION
AZ868731
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Mus musculus
(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

AUTHORS

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0180 row: L column: 02

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

FEATURES

source

1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180L02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 646

CZ919318
LOCUS
DEFINITION
29 bp DNA linear GSS 08-AUG-2005
4021012F10.2EL.Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.

ACCESSION
CZ919318
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Zea mays
(maize)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 29)

REFERENCE

Maize genomic sequences found using engineered RescueMu transposon
Walbot.V.

AUTHORS

Unpublished (2001)

TITLE

Contact: Walbot V

JOURNAL

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021012 row: F column: 10

Class: transposon-tagged.

Location/Qualifiers

1..29

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with

```

ampicillin."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 647
DU833998/c
LOCUS      29 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS013D17f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS013D17, genomic survey
            sequence.
ACCESSION  DU833998
VERSION     DU833998.1 GI:83870594
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM    Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 29)
AUTHORS     Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
            Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
            Hahn, J. H. and Park, B.S.
            End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
            Unpublished (2005)
            Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel.: +82-31-299-1670
            Fax: +82-31-299-1672
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
            KBrS013D17
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
                1..29
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS013D17"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAB."

FEATURES             source
    source
        1..29
        /organism="Brassica rapa subsp. pekinensis"
        /mol_type="genomic DNA"
        /cultivar="Chiifu"
        /sub_species="pekinensis"
        /db_xref="taxon:51351"
        /clone="KBrS016B12"
        /lab_host="E. coli DH10B"
        /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
        /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
        ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
        available at NIAB."

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
    |||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 649
AG193759
LOCUS      29 bp      DNA      linear      GSS 06-MAR-2004
DEFINITION Pan troglodytes DNA, clone: RP43-071B06.T7, genomic survey
            sequence.
ACCESSION  AG193759
VERSION     AG193759.1 GI:45225935
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Pan.
REFERENCE   1
AUTHORS     Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
            Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
            BAC end sequences of Library RP-43
            Unpublished
            2 (bases 1 to 29)
            Direct Submission
            Hoon, S. T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
            Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
            Tel: 82-42-866-7181, Fax: 82-42-860-4409)

Query Match      1.1%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
    |||||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 648
DU835145
LOCUS      29 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBrS016B12f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBrS016B12, genomic survey
            sequence.
ACCESSION  DU835145
VERSION     DU835145.1 GI:83871741

```

COMMENT

Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI

FEATURES

source

Location/Qualifiers

1..29
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-071B06.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match

Best Local Similarity 1.1%; Score 29; DB 1; Length 29;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 650

TA334G090/c

LOCUS

DEFINITION

Genomic survey sequence.

Accession

AL491938

Keywords

Source

Organism

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 29)

Authors

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Meiville,S.E., Rajadream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000)

Trypanosoma brucei genome sequencing

project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at <http://www.sanger.ac.uk/Projects/T-brucei/>.

FEATURES

source

1..29

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="334G09"

Query Match

Best Local Similarity 1.1%; Score 29; DB 1; Length 29;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 651

BG865511

LOCUS

DEFINITION

602783643F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909811 5',

mRNA sequence.

Accession

BG865511

Version

BG865511.1

Keywords

Source

Organism

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Reference

NIH-MGC <http://mgc.ncl.nih.gov/>.

Authors

National Institutes of Health, Mammalian Gene Collection (MGC)

Journal

Unpublished (1999)

Comment

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM10809 row: e column: 12

High quality sequence stop: 30.

Location/Qualifiers

1..30

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4909811"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_SG2"

/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1;

NotI; Site: 2; Sali; Cloned unidirectionally. Primer: Oligo

dt. Average insert size 1.3 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

Query Match

Best Local Similarity 1.1%; Score 29; DB 1; Length 30;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 652

CN545845/c

LOCUS

DEFINITION

EST 17789 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

clone B3CS00RL002E09 3', mRNA sequence.

Accession

CN545845

Version

CN545845.1

Keywords

Source

Organism

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 30)

Reference

Abbal, P., Agase, A., Ageorges, A., Atanasova, R., Barrieu, F.,

Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimpellet, J.,

Hamdi, S., Romieu, C. and Terrier, N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7

FEATURES source

Location/Qualifiers
 1..30
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00RL002E09"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
 Query Match 1.1%; Score 29; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 653

CZ914262/c
 LOCUS CZ914262 31 bp DNA linear GSS 08-AUG-2005
 DEFINITION 4013006B10.2EL_y1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
 ACCESSION CZ914262
 VERSION CZ914262.1 GI:71930750
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 31)
 Walbot V.
 Maize genomic sequences found using engineered RescueMu transposon survey sequence.
 Unpublished (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4013006 row: B column: 10
 Class: transposon-tagged.

FEATURES

Location/Qualifiers
 1..31
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="4013 - RescueMu Grid O"
 /note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.1%; Score 29; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
 Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 654

CN546517/c
 LOCUS CN546517 32 bp mRNA linear EST 30-APR-2004
 DEFINITION EST 18661 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS57R5007H05 3', mRNA sequence.
 ACCESSION CN546517
 VERSION CN546517.1 GI:46911142
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Abbal P., Agasse A., Ageorges A., Atanassova R., Barrieu F., Couture C., Dedaldecamp F., Delrot S., Glissant D., Grimplet J., Hamdi S., Romieu C. and Terrier N.
 Title Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7

Location/Qualifiers
 1..32
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS57R5007H05"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

FEATURES source

Location/Qualifiers
 1..32
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS57R5007H05"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.1%; Score 29; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 Db 29 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 655


```

DN955775/c
LOCUS       DN955775       32 bp      mRNA      linear      EST 04-MAY-2005
DEFINITION  It93f12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION   DN955775
VERSION     DN955775.1  GI:63027913
KEYWORDS    EST.
SOURCE      Gnetum gnemon
            Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
            1 (bases 1 to 32)
REFERENCE   1  (bases 1 to 32)
AUTHORS    Brenner,E.D., Twigg,R.W., Runko,S.J., Katar,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
            Expressed tag sequences from Gnetum female cone (NYBG)
            Unpublished (2003)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.
            Location/Qualifiers
                1..32
                /organism="Gnetum gnemon"
                /mol_type="mRNA"
                /db_xref="taxon:3382"
                /sex="female"
                /clone_lib="Gnetum female cone (NYBG)"
                /note="Organ: mature, unfertilized reproductive strobili;
                Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                Completed 02/11/02, submitted for sequencing 02/12/02.
                Library: Stratagene ZAP Express cDNA Synthesis kit. The
                library was size-fractionated to enrich for large inserts.
                Sample: NYBG accession number #436/84"

Query Match      1.1%; Score 29; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db   32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 656
BU431802/c
LOCUS       BU431802       34 bp      mRNA      linear      EST 09-SEP-2002
DEFINITION  601654630r1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839742 3',
mRNA sequence.
ACCESSION   BU431802
VERSION     BU431802.1  GI:22770284
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 34)
REFERENCE   1  (bases 1 to 34)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Prepared by: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

Query Match      1.1%; Score 29; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db   32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 656
BU431802/c
LOCUS       BU431802       34 bp      mRNA      linear      EST 09-SEP-2002
DEFINITION  601654630r1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839742 3',
mRNA sequence.
ACCESSION   BU431802
VERSION     BU431802.1  GI:22770284
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
            1 (bases 1 to 34)
REFERENCE   1  (bases 1 to 34)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Prepared by: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM528 row: k column: 07
High quality sequence stop: 34.
Location/Qualifiers
    1..34
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:3839742"
    /tissue_type="glioblastoma"
    /lab_host="DH10B (T1 phage-resistant)"
    /clone_lib="NIH_MGC_57"
    /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
    SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc);
    Double-stranded cDNA was prepared from cell line RNA.
    and 3' adaptors were used in cloning as follows: 5'
    adaptor sequence: 5'-CACGCGCATATGCC-3' and 3' adaptor
    sequence: 5'-ATTTAGAGCGGCGGCGGCGACATG-dT(30)BN-3'
    (where B = A, C, or G and N = A, C, G, or T). Average
    insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
    contained inserts by PCR. This library was enriched for
    full-length clones and was constructed by Clontech
    Laboratories (Palo Alto, CA)."

Query Match      1.1%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db   29 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 657
CV064432
LOCUS       CV064432       35 bp      mRNA      linear      EST 24-AUG-2004
DEFINITION  WNEL10H12 Wheat EST endosperm library Triticum aestivum cDNA clone
similar to Unknown Function, mRNA sequence.
ACCESSION   CV064432
VERSION     CV064432.1  GI:51527609
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
            Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
            clade; Pooidae; Triticeae; Triticum.
            1 (bases 1 to 35)
REFERENCE   1  (bases 1 to 35)
AUTHORS    Ali,S, Holloway,B. and Taylor,W.C.
            Normalisation of cereal endosperm EST libraries for structural and
            functional genomic analysis
            Plant Mol. Biol. Rep. 18, 123-132 (2000)
            Contact: Bill Taylor
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry.
            CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
            Tel: 61 2 6246 5223
            Fax: 61 2 6246 5000
            Email: Bill.Taylor@csiro.au
            Seq primer: M13 reverse primer
            High quality sequence stop: 35.
            Location/Qualifiers
                1..35
                /organism="Triticum aestivum"
                /mol_type="mRNA"
                /cultivar="Hartog"
                /db_xref="taxon:4565"
                /clone="WNEL10H12"
                /tissue_type="endosperm"
                /dev_stage="developing endosperm tissue 6, 8, 10 dpa (days
                post_anthesis)"
                /lab_host="DH10B (Life Technology)"
                /clone_lib="Wheat EST endosperm library"
                /note="Vector: _ZipLox; Site_1: Sal I; Site_2: Not I; mRNA

```

was prepared from endosperm tissues of the wheat cultivar Hartog. cDNA was synthesised from pooled 6, 8, and 10 dpa endosperm using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan Ali and Bill Taylor."

Query Match 1.1%; Score 29; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 658
AM044046 36 bp mRNA linear EST 11-AUG-2005
LOCUS AM044046 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC21b12.q1k, mRNA sequence.
ACCESSION AM044046
VERSION AM044046.1 GI:72292514
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 36)
AUTHORS Dillon,G.P., Felkwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers

FEATURES
source
1..36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC21b12.q1k"
/dev_stages="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"

Query Match 1.1%; Score 29; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||
Db 8 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 659
CF318239 32 bp mRNA linear EST 15-AUG-2003
LOCUS HD--08-E17.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-E17, mRNA sequence.
ACCESSION CF318239
VERSION CF318239.1 GI:33690000
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)

AUTHORS
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

source

1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-E17"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 1.0%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 660
AZ627842/c
LOCUS 1M0474G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGC1M0474G03 F, genomic survey sequence.
ACCESSION AZ627842
VERSION AZ627842.1 GI:11750128
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 32)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: G column: 03
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES

```
source
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 1.0%; Score 28.8; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 32 AAAAAAAAAAAAAAAAAAGTAAAAAAAAAAAA 1

RESULT 661
AJ800678/c
LOCUS
DEFINITION
AJ800678 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_4_11_b17, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Antirrhinum majus (snapdragon)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamials; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
1 (bases 1 to 34)
Bey M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Saedler, H. and Zachgo, S.
Characterization of Antirrhinum Petal Development and Identification of Target Genes of the Class B MADS Box Gene DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
15539471
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
source
1. .34
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_4_11_b17"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

Query Match 1.0%; Score 28.8; DB 1; Length 34;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740
|||||
Db 34 AACAAATATAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 662
AM043639
LOCUS
DEFINITION
AM043639 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC23b07.qik, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 36)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaidou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1. .36
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC23b07.qik"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.0%; Score 28.8; DB 1; Length 36;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2701 TTGTGACTAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 5 TTTTATTATAAAAAAAAAAAAAAAAAAAAAA 36

RESULT 663
CN546288/c
LOCUS
DEFINITION
CN546288 Green Grape Berry Lambda Triplex2 Library Vitis vinifera cDNA clone B3CS1XGB015D07.3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal, P., Agasse, A., Agasse, A., Atanassova, R., Barrieu, F., Couture, C., Dedaidech, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche

Agronomie
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

FEATURES

source

Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015D07"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2, Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 664

AZ443322
LOCUS IM0237L20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0237L20 R, genomic survey sequence.

ACCESSION AZ443322
VERSION AZ443322.1 GI:10591190

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0237 row: L column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

FEATURES

source

1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0237L20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 665

AZ458127/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0261 row: I column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1..30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0261I24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match          1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 666
LOCUS C2917310
DEFINITION C2917310 30 bp DNA linear GSS 08-AUG-2005
survey sequence.
ACCESSION C2917310
VERSION C2917310
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 30)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
JOURNAL clade: Panicoideae; Andropogoneae; Zea.
COMMENT Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2221
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021005 row: B column: 07
Class: transposon-tagged.
FEATURES
    source
        Location/Qualifiers
            1..30
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="mixed background W23/A188/B73/K55"
                /db_xref="taxon:4577"
                /tissue_type="leaf"
                /dev_stage="adult"
                /lab_host="DH10B"
                /clone_lib="4021 - RescueMu Grid V"
                /note="Organ: leaf; Vector: RescueMu (engineered from
                pluescript backbone); Site 1: BamHI; Site 2: BglII;
                RescueMu is a 4.9 kb, modified maize Mu transposon
                designed to allow plasmid rescue from total genomic DNA.
                Mu elements insert preferentially into transcription
                units. For more information on RescueMu, go to the web
                site 'http://www.mutransposon.org/project/RescueMu/'. Grid

```

V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

Query Match          1.0%; Score 28.4; DB 1; Length 30;
Best Local Similarity 96.7%; Pred. No. 4.2e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 667
LOCUS DU833997/c
DEFINITION DU833997 30 bp DNA linear GSS 22-DEC-2005
subsp. pekinensis genomic clone KBrS013D15, genomic survey
sequence.
ACCESSION DU833997
VERSION DU833997.1 GI:83870593
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
REFERENCE 1 (bases 1 to 30)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS013D15
Seq primer: T7
Class: BAC ends.
FEATURES
    source
        Location/Qualifiers
            1..30
                /organism="Brassica rapa subsp. pekinensis"
                /mol_type="genomic DNA"
                /cultivar="Chiifu"
                /sub_species="pekinensis"
                /db_xref="taxon:51351"
                /clone="KBrS013D15"
                /lab_host="E. coli DH10B"
                /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                available at NIAB."

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 668
LOCUS CN546007/c
DEFINITION CN546007 32 bp mRNA linear EST 30-APR-2004
EST 17956 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA

```

```

clone B3CS00RL007D07 3', mRNA sequence.
ACCESSION   CN546007
VERSION     CN546007.1  GI:46910632
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
            Vitis vinifera
REFERENCE   1 (bases 1 to 32)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: F7.
            Location/Qualifiers
                1..32
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CS00RL007D07"
                /dev_stage="ripening stage"
                /clone_lib="Ripe Grape Skin Triplex2 Library"
                /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                SfiIA; Site_2: SfiIB; Oriented library"

FEATURES             source
LOCUS               32
DEFINITION         CN546531
ACCESSION          CN546531
VERSION            CN546531.1  GI:46911156
KEYWORDS           EST.
SOURCE             Vitis vinifera
ORGANISM           Vitis vinifera
REFERENCE          1 (bases 1 to 33)
AUTHORS            Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE              Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL            Unpublished (2002)
COMMENT            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France

clone B3CS00RL007D07 3', mRNA sequence.
ACCESSION   CN546007
VERSION     CN546007.1  GI:46910632
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
            Vitis vinifera
REFERENCE   1 (bases 1 to 32)
AUTHORS     Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Universite de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France

```

```

Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: F7.
            Location/Qualifiers
                1..33
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiVar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clones="B3CS59RB008A08"
                /dev_stage="ripe stage"
                /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
                /note="Organ: Fruit without seeds; Vector: Lambda
                Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 670
LOCUS       CV725332/C
DEFINITION  CV725332 33 bp mRNA linear EST 04-NOV-2004
            14Salt--02-F20-g1 Salt treated rice leaf lambda phage cDNA library
            (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
            14Salt--02-F20, mRNA sequence.
ACCESSION   CV725332
VERSION     CV725332.1  GI:55412956
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            Clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 33)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
            Location/Qualifiers
                1..33
                /organism="Oryza sativa (japonica cultivar-group)"
                /mol_type="mRNA"
                /cultiVar="Nackdong"
                /db_xref="taxon:39947"
                /clones="14Salt--02-F20"
                /issue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_hosts="E.coli SOLR"
                /clone_lib="Salt treated rice leaf lambda phage cDNA
                library (14Salt)"
                /note="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                XhoI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs.
                cDNA was inserted into lamda Uni-ZAP XR vector at 5' end
                with EcoRI and 3' end with XhoI site."

Query Match      1.0%; Score 28.4; DB 1; Length 33;
Best Local Similarity 96.7%; Pred. No. 4.4e+02;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2707 CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

```


71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS00RL009B01"

/dev_stage="ripening stage"

/clone_lib="Ripe Grape Skin Triplex2 Library"

/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 674

CN546416/c

LOCUS

DEFINITION EST 18369 Green Grape Berry Lambda Triplex2 Library Vitis vinifera

CDNA clone B3CS1XGB016G05 3', mRNA sequence.

ACCESSION CN546416

VERSION CN546416.1

KEYWORDS GI:46911041

SOURCE EST.

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Couture,C., Agasse,A., Agorces,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS1XGB016G05"

/dev_stage="green stage"

/clone_lib="Green Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 675

CN546519/c

LOCUS

DEFINITION EST 18663 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera

CDNA clone B3CS57RB007H07 3', mRNA sequence.

ACCESSION CN546519

VERSION CN546519.1

KEYWORDS GI:46911144

SOURCE EST.

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..35

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS57RB007H07"

/dev_stage="ripe stage"

/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28.4; DB 1; Length 35;

Best Local Similarity 96.7%; Pred. No. 4.5e+02;

Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738

Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 676

CN546666/c

LOCUS

DEFINITION CN546666 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA clone B3CS37TB007E01 3', mRNA sequence.

ACCESSION CN546666

VERSION CN546666.1

KEYWORDS GI:46911291

SOURCE EST.

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 35)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Ronieu,C. and Terrier,N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

```

seq primer: 17
Location/Qualifiers
1..35
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS37TB007E01"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library;"

Query Match
Best Local Similarity 1.0%; Score 28.4; DB 1; Length 35;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACA 6

```

RESULT 677	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
LOCUS	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
DEFINITION	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
ACCESSION	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
VERSION	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
KEYWORDS	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
SOURCE	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
ORGANISM	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
REFERENCE	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
AUTHORS	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
TITLE	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
JOURNAL	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
PUBMED	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004
COMMENT	AJ791259	Antirrhinum majus whole plant	33 bp	linear	EST 08-DEC-2004

```

FEATURES
  source
    1. .33
      /organism="Antirrhinum majus"
      /mol_type="mRNA"
      /db_xref="taxon:4151"
      /clone="018.2.08.d21"
      /tissue_type="whole plant"
      /clone_lib="Antirrhinum majus whole plant"

Query Match      1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy	2707	CTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2739
Dd	33	CCAAACCAAAAAAAAAAAAAAAAAAAAAAAAAA	1
RESULT	678		
LOCUS	CF335736/c		
DEFINITION	JMT--05-I12.b1 ATJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa [japonica cultivar-group] cDNA clone JMT--05-I12, mRNA sequence.	33 bp	mRNA linear EST 18-AUG-2003
ACCESSION	CF335736		
VERSION	CF335736.1	GI:33819839	
KEYWORDS	EST.		
SOURCE	Oryza sativa [japonica cultivar-group]		
ORGANISM	Oryza sativa [japonica cultivar-group] Eukaryota; Viridiplantae; Streptophyta; SpERMatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP		
REFERENCE	1 (bases 1 to 33) Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)		
AUTHORS	Contact: Nahm B.H.		
TITLE	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myungji University		
JOURNAL	Xongan, Kyeongsig, Korea		
COMMENT	Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@qbio.com, bhnahm@bio.mv.ac.kr.		

```

FEATURES             Location/Qualifiers
     source            1..33
                        /organism="Oryza sativa (japonica cultivar-group)"
                        /mol_type="mRNA"
                        /cultivar="Nackdong"
                        /db_xref="taxon:39947"
                        /clone="JMT--05-112"
                        /tissue_type="leaf"
                        /dev_stage="14 days after germination"
                        /lab_host="E.coli DH108"
                        /clone_lib="AtJMT-overexpressing transgenic rice plasmid
                        cDNA library (JMT)"
                        /note="Vector: pCRA-TOPO; Site_1: EcoRI; Oligo-capped mRNA
                        was reverse transcribed and then used for PCR. mRNA was
                        prepared from Arabidopsis Jasmonate Carboxyl
                        methyltransferase overexpression line."

Query Match          1.0%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 4.5e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2741
         |||||
Db       33 AAAAAAAAAAACAAACCAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT	679
CZ919845	
LOCUS	CZ919845
DEFINITION	4021015A06.2EL_y1_4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.
ACCESSION	CZ919845
VERSION	CZ919845.1
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 33)
REFERENCE	Walbot,V.
AUTHORS	Maize genomic sequences found using engineered RescueMu transposon
TITLE	

and Dixon, L.
Development of a porcine cDNA microarray
Unpublished (2004)
Contact: Hopwood PA
Dept. of Preclinical Veterinary Sciences
Royal School for Veterinary Studies
Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM
Sequencing was performed by ARK genomics. This clone is available
from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS,
UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES
source
1. .35
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001822c_A11"
/tissue_type="muscle"
/cell_type="macrophage"
/clone_lib="muscle - muscle minus alveolar macrophage"

Query Match 1.0%; Score 28.2; DB 1; Length 35;
Best Local Similarity 90.9%; Pred. No. 4.6e+02;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2701 TTGTACTAAAAA 28 bp mRNA linear EST 28-JUN-2004
||||| 2733
Db 33 TTTTTTTAAAAA 28 bp mRNA linear EST 28-JUN-2004
||||| 2733

RESULT 683
AJ666435/c
LOCUS
DEFINITION
AJ666435 CSEQRAN09 Sus scrofa cDNA clone C0000033_L21, mRNA
sequence.
ACCESSION
AJ666435
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
1 (bases 1 to 28)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector: pBluescriptII(KS+) R. Site.1:
EcoRI R. Site.2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1. .28
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_L21"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736
Db 28 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736

RESULT 684
AM043789/c
LOCUS
DEFINITION
AM043789 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC19g02.q1k, mRNA sequence.
ACCESSION
AM043789
VERSION
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 28)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1. .28
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC19g02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736
Db 28 AAAAAAAAAA 28 bp mRNA linear EST 11-AUG-2005
||||| 2736

RESULT 685
AM043903/c
LOCUS
DEFINITION
AM043903 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC19b04.q1k, mRNA sequence.
ACCESSION
AM043903
VERSION
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 28)
Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S.,
Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1. .28
/organism="Schistosoma mansoni"
/mol_type="mRNA"

```

/db_xref="taxon:6183"
/clone="SmlC19b04.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 686
AM043968      28 bp mRNA linear EST 11-AUG-2005
LOCUS
DEFINITION
  AM043968 Schistosoma mansoni lung schistosomulum Schistosoma
  mansoni cDNA clone SmlC20h11.q1k, mRNA sequence.
ACCESSION
  AM043968
VERSION
  AM043968.1 GI:72292357
KEYWORDS
  EST.
SOURCE
  Schistosoma mansoni
  Schistosoma mansoni
  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
  Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
  1 (bases 1 to 28)
AUTHORS
  Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
  Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
  Microarray analysis identifies genes preferentially expressed in
  the lung schistosomulum of Schistosoma mansoni
JOURNAL
  Unpublished (2005)
COMMENT
  Contact: Ivens AC
  Pathogen Microarrays Group
  Wellcome Trust Sanger Institute
  Hinxton, CB10 1SA, UNITED KINGDOM.
  Location/Qualifiers
    1..28
    /organism="Schistosoma mansoni"
    /mol_type="mRNA"
    /db_xref="taxon:6183"
    /clone="SmlC20h11.q1k"
    /dev_stage="lung schistosomulum"
    /clone_lib="Schistosoma mansoni lung schistosomulum"
    /note="country: Puerto Rico"

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 687
AM044512/c
LOCUS
DEFINITION
  AM044512 Schistosoma mansoni lung schistosomulum Schistosoma
  mansoni cDNA clone SmlC28d06.q1k, mRNA sequence.
ACCESSION
  AM044512
VERSION
  AM044512.1 GI:75966804
KEYWORDS
  EST.
SOURCE
  Schistosoma mansoni
  Schistosoma mansoni
  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
  Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
  1 (bases 1 to 28)
AUTHORS
  Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
  Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE
  Microarray analysis identifies genes preferentially expressed in
  the lung schistosomulum of Schistosoma mansoni

```

```

JOURNAL
COMMENT
  Unpublished (2005)
  Contact: Ivens AC
  Pathogen Microarrays Group
  Wellcome Trust Sanger Institute
  Hinxton, CB10 1SA, UNITED KINGDOM.
  Location/Qualifiers
    1..28
    /organism="Schistosoma mansoni"
    /mol_type="mRNA"
    /db_xref="taxon:6183"
    /clone="SmlC28d06.q1k"
    /dev_stage="lung schistosomulum"
    /clone_lib="Schistosoma mansoni lung schistosomulum"
    /note="country: Puerto Rico"

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 688
CF282351/c
LOCUS
DEFINITION
  CF282351 14ETL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
  Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-N05,
  mRNA sequence.
ACCESSION
  CF282351
VERSION
  CF282351.1 GI:33659738
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 28)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..28
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="14ETL--09-N05"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_hosts="E.coli DH10B"
    /clone_lib="Rice etiolated leaf plasmid cDNA library
    (14ETL)"
    /note="vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 689
CF321885/c
LOCUS
DEFINITION
HD--13-E16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-J14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Desacetylase overexpression line."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 690
CF330748/c
LOCUS
DEFINITION
NACL--06-J14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-J14, mRNA sequence.

ACCESSION
VERSION
SOURCE
KEYWORDS
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--13-E16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Desacetylase overexpression line."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 691
CF330938
LOCUS
DEFINITION
NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-N19, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-N19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-J14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
DB 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 691
CF330938
LOCUS
DEFINITION
NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--06-N19, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-N19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 ||||||||||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 697
 AZ471744/c

LOCUS AZ471744 28 bp DNA linear GSS 04-OCT-2000
 DEFINITION IM0286K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286K08 R, genomic survey sequence.

ACCESSION AZ471744
 VERSION AZ471744.1 GI:10629965
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0286 row: K column: 08
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0286K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

FEATURES

source

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 ||||||||||||||||||||||||||||||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 698
 AZ493138

LOCUS AZ493138 28 bp DNA linear GSS 05-OCT-2000
 DEFINITION IM0327F02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0327F02 R, genomic survey sequence.

ACCESSION AZ493138
 VERSION AZ493138.1 GI:10666359
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)
 JOURNAL Contact: Robert B. Weiss
 COMMENT University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0327 row: F column: 02
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0327F02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 699
AZ653365/c
LOCUS
DEFINITION
28 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0527E02 F, genomic survey sequence.

ACCESSION
AZ653365
VERSION
GI:11790511

KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Journal
COMMENT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0527 row: E column: 02

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0527E02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 700

AZ785035/c

LOCUS

DEFINITION
28 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0028J01 R, genomic survey sequence.

ACCESSION
AZ785035

VERSION
GI:12921373

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Journal
COMMENT
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: J column: 01

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1..28

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0028J01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 701
A2824519/C
LOCUS
DEFINITION 28 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0099109 F, genomic survey sequence.

ACCESSION A2824519
VERSION A2824519.1 GI:12994427

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

REFERENCE AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0039 row: I column: 09

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099109"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 702

A2833425

LOCUS

DEFINITION 28 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0115D04 R, genomic survey sequence.

ACCESSION A2833425

VERSION A2833425.1 GI:13003333

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

REFERENCE AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0115 row: D column: 04

Seq primer: CACACAGGAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES

source

1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0115D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 703
AZ866569/c
LOCUS
DEFINITION
28 bp DNA linear GSS 21-FEB-2001
clone UUGC2M0177B08 F, genomic survey sequence.

ACCESSION
AZ866569
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0177 row: B column: 08

Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

FEATURES
source

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0177B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 704
CZ912316/c

LOCUS
DEFINITION
28 bp DNA linear GSS 08-AUG-2005
4012010A02.1EL_Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.

ACCESSION
CZ912316
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 28)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012010 row: A column: 02
Class: transposon-tagged.

Location/Qualifiers

FEATURES
source

1..28
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
BB was grown at UC Berkeley in 2001. DNA was extracted
from leaf strips, double digested using BamHI and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 705

CZ913960
LOCUS 4013005A02.1EL_x1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
DEFINITION CZ913960 28 bp DNA linear GSS 08-AUG-2005
ACCESSION CZ913960
VERSION CZ913960.1 GI:71930279
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 28)
AUTHORS Walbot V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: A column: 02
Class: transposon-tagged.
Location/Qualifiers
1. .28
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28
RESULT 706
DU828712/c 28 bp DNA linear GSS 22-DEC-2005
LOCUS DU828712 28 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS003K05R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS003K05, genomic survey sequence.
ACCESSION DU828712
VERSION DU828712.1 GI:83865308
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Embryophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS003K05
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBrS003K05"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 707
DU835260 28 bp DNA linear GSS 22-DEC-2005
LOCUS DU835260 28 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016F07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016F07, genomic survey sequence.
ACCESSION DU835260
VERSION DU835260.1 GI:83871856
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016F07
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .28

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS003K05
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBrS003K05"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."
Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
RESULT 707
DU835260 28 bp DNA linear GSS 22-DEC-2005
LOCUS DU835260 28 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016F07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016F07, genomic survey sequence.
ACCESSION DU835260
VERSION DU835260.1 GI:83871856
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016F07
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .28

```

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016P07"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 708
DU835584 28 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS016P17F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016P17, genomic survey sequence.
DEFINITION
ACCESSION DU835584
VERSION DU835584.1 GI:83872180
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016P17
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS016P17"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 710
TA291A01Q 28 bp DNA linear GSS 13-DEC-2000
LOCUS TA291A01Q T. brucei sheared genomic DNA clone 291a01, reverse sequence, genomic survey sequence.
DEFINITION
ACCESSION AL486613
VERSION AL486613.1 GI:11853602
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission

```

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@igr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="291a01"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 711
TA379D11P/c
LOCUS TA379D11P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 379d11, forward sequence, genomic survey sequence.
ACCESSION AL497637
VERSION AL497637.1 GI:11873359
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 28)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@igr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="379d11"

Query Match 1.0%; Score 28; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 712
CN545883/c
LOCUS CN545883 29 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17827 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA Clone B3CS00RL006A02 3', mRNA sequence.
ACCESSION CN545883
VERSION CN545883.1 GI:46910508
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
1 (bases 1 to 29)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Gliseant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.

FEATURES
source
1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A02"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 713
CZ912823/c
LOCUS CZ912823 29 bp DNA linear GSS 08-AUG-2005
DEFINITION 4012012A03.2EL_y1 4012 - RescueMu Grid BB Zea mays genomic, genomic survey sequence.
ACCESSION CZ912823
VERSION CZ912823.1 GI:71928421
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

```

REFERENCE
AUTHORS      clade; Panicoidae; Andropogoneae; Zea.
TITLE        Walbot, V.
JOURNAL      Maize genomic sequences found using engineered RescueMu transposon
COMMENT      Unpublished (2001)
              Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Possible ligation site of ends cut by 2 different endonucleases.
              Reverse complemented post-ligation sequence from source sequence.
              Plate: 4012012 row: A column: 03
              Class: transposon-tagged.
              Location/Qualifiers
                1..29
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /cultivar="mixed background W23/A188/B73/K55"
                  /db_xref="taxon:4577"
                  /tissue_type="leaf"
                  /dev_stage="adult"
                  /lab_host="DH10B"
                  /clone_lib="4012 - RescueMu Grid BB"
                  /note="Organ: leaf; Vector: RescueMu (engineered from
                  pluescript backbone); Site 1: BamHI; Site 2: BglII;
                  RescueMu is a 4.9 kb, modified maize Mu transposon
                  designed to allow plasmid rescue from total genomic DNA.
                  Mu elements insert preferentially into transcription
                  units. For more information on RescueMu, go to the web
                  site 'http://www.mutransposon.org/project/RescueMu/'. Grid
                  BB was grown at UC Berkeley in 2001. DNA was extracted
                  from leaf strips, double digested using BamHI and BglII,
                  and ligated to form circular plasmids. DH10B cells were
                  transformed and then screened on LB plates with
                  ampicillin."

FEATURES
source
1..29
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from
pluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
BB was grown at UC Berkeley in 2001. DNA was extracted
from leaf strips, double digested using BamHI and BglII,
and ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match      1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA.....AAAAAAAAAAAAAAAA 2734
Db 28 CTAAGAAAAA.....AAAAAAAAAAAAAAAA 1

RESULT 714
CZ914240
LOCUS      29 bp DNA linear GSS 08-AUG-2005
DEFINITION survey sequence.
ACCESSION CZ914240
VERSION    CZ914240.1 GI:71930716
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 29)
            Walbot, V.
            Maize genomic sequences found using engineered RescueMu transposon
            Unpublished (2001)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Possible ligation site of ends cut by 2 different endonucleases.

```

```

Reverse complemented post-ligation sequence from source sequence.
Plate: 4013006 row: B column: 03
Class: transposon-tagged.
Location/Qualifiers
  1..29
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /cultivar="mixed background W23/A188/B73/K55"
    /db_xref="taxon:4577"
    /tissue_type="leaf"
    /dev_stage="adult"
    /lab_host="DH10B"
    /clone_lib="4013 - RescueMu Grid O"
    /note="Organ: leaf; Vector: RescueMu (engineered from
    pluescript backbone); Site 1: BamHI; Site 2: BglII;
    RescueMu is a 4.9 kb, modified maize Mu transposon
    designed to allow plasmid rescue from total genomic DNA.
    Mu elements insert preferentially into transcription
    units. For more information on RescueMu, go to the web
    site 'http://www.mutransposon.org/project/RescueMu/'. Grid
    O was grown at Stanford in 2001. DNA was extracted from
    leaf strips, double digested using BamHI and BglII, and
    ligated to form circular plasmids. DH10B cells were
    transformed and then screened on LB plates with
    ampicillin."

Query Match      1.0%; Score 28; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA.....AAAAAAAAAAAAAAAA 2736
Db 1 AAAAAA.....AAAAAAAAAAAAAAAA 28

RESULT 715
CN545968/c
LOCUS      30 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17916 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
ACCESSION CN545968
VERSION    CN545968.1 GI:46910593
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
            1 (bases 1 to 30)
            Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
            Couture, C., Dedaidecham, F., Delrot, S., Glissant, D., Grimplet, J.,
            Hamdi, S., Romieu, C. and Terrier, N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Université de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: 17
            Location/Qualifiers
              1..30
                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultivar="Cabernet Sauvignon"
                /db_xref="taxon:29760"
                /clone="B3CS00RL007A02"
                /dev_stage="ripening stage"

```

/clone.lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
 SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 ||||||||||||||||||||||||||||||||||
 Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 716
 CN546523/c 30 bp mRNA linear EST 30-APR-2004
 LOCUS
 DEFINITION EST 18667 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS57RB007H12 3', mRNA sequence.

ACCESSION CN546523
 VERSION CN546523.1 GI:46911148

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.

REFERENCE 1. (bases 1 to 30)

AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Romieu,C. and Terrier,N.

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

JOURNAL Unpublished (2002)

COMMENT Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

FEATURES

source

1..30 Location/Qualifiers

/organism="vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS57RB007H12"

/dev_stages="ripe stage"

/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 28; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

||||||||||||||||||||||||||||||||

Db 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 717
 C2919540 30 bp DNA linear GSS 08-AUG-2005
 LOCUS
 DEFINITION 4021013F10.2EL_y1 4021 - RescueMu Grid V Zea mays genomic, genomic
 survey sequence.

ACCESSION C2919540

VERSION C2919540.1 GI:71940164

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 30)

Walbot,V.

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

CONTACT: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021013 row: F column: 10

Class: transposon-tagged.

FEATURES

source

1..30 Location/Qualifiers

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="mixed background W23/A188/B73/K55"

/db_xref="taxon:4577"

/tissue_type="leaf"

/dev_stage="adult"

/lab_hosts="DH10B"

/clone_lib="4021 - RescueMu Grid V"

/note="Organ: leaf; Vector: RescueMu (engineered from

pBluescript backbone); Site 1: BamHI; Site 2: BglII;

RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA.

Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web

site 'http://www.mutransposon.org/project/RescueMu/'. Grid

V was grown at University of Arizona in 2003. DNA was

extracted from leaf strips, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B

cells were transformed and then screened on LB plates with

ampicillin."

Query Match 1.0%; Score 28; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

||||||||||||||||||||||||||||||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 718

AW245279/c

LOCUS

DEFINITION 2820044.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820044 3',

mRNA sequence.

ACCESSION AW245279

VERSION AW245279.1 GI:6588272

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 31)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2820044.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapsb-remail.nih.gov

Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project
 Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 31 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM3 row: C column: 21.

FEATURES

source

```

1. .31
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820044"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match
 Best Local Similarity 90.3%; Pred. No. 4.5e+02; Length 31;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739

Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 719

CV057897

LOCUS

DEFINITION CV057897 31 bp mRNA linear EST 24-AUG-2004
 BNEL32a8 Barley EST endospERM library Hordeum vulgare subsp. vulgare cDNA clone BNEL32a8 5' similar to Unknown Function, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Poideae; Triticeae; Hordeum.

REFERENCE

AUTHORS

TITLE

Ali S. Holloway, B. and Taylor, W.C.
 Normalisation of cereal endospERM EST libraries for structural and functional genomic analysis

JOURNAL

COMMENT

Plant Mol. Biol. Rep. 18, 123-132 (2000)
 Contact: Bill Taylor
 Commonwealth Scientific and Industrial Research Organisation
 Division of Plant Industry
 CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
 Tel: 61 2 6246 5223
 Fax: 61 2 6246 5000
 Email: Bill.Taylor@csiro.au
 Seq primer: M13 reverse primer
 High quality sequence stop: 31.

FEATURES

source

1. .31
 Location/Qualifiers

```

/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Himalaya"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="BNEL32a8"
/tissue_type="endospERM"
/dev_stage="developing endospERM tissue 10, 12, 15 dpa (days post anthesis)"
/lab_host="DH10B (Life Technology)"
/clone_lib="Barley EST endospERM library"
/notes="Vector: ZipLox; Site 1: Sal I; Site 2: Not I; mRNA was prepared from endospERM tissues of the Barley cultivar Himalaya. cDNA was synthesised from pooled 10, 12, and 15 dpa endospERM using Not I-oligo(dT)18 primer/adaptor (Pharmacia Biotech), and then ligated to the Sal I-Not I site of ZipLox vector (Life Technology) after adding a Sal I-XhoI I adaptor (Stratagene). Constructed by Shanjahan Ali and Bill Taylor."
```

Query Match
 Best Local Similarity 100.0%; Pred. No. 4.5e+02; Length 31;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 720

AM046790

LOCUS

DEFINITION AM046790 32 bp mRNA linear EST 11-AUG-2005
 mansoni cDNA clone SmlC27e08.q1k, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Schistosoma mansoni
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomidae; Schistosoma.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Dillon, G.P., Feltwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
 Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

source

```

1. .32
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC27e08.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/notes="Country: Puerto Rico"
```

Query Match
 Best Local Similarity 96.6%; Pred. No. 4.5e+02; Length 32;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29

RESULT 721

CD577661

LOCUS

CD577661 32 bp mRNA linear EST 15-JUN-2004

DEFINITION Iqor1.A02.Q3.007 ESTs from wild-caught Anopheles funestus populations Anopheles funestus cDNA 5', mRNA sequence.
 ACCESSION CD577661
 VERSION CD577661.1 GI:48718676
 KEYWORDS EST.
 SOURCE Anopheles funestus

ORGANISM Anopheles funestus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.

REFERENCE 1 (bases 1 to 32)

AUTHORS Besansky,N.J., Serazin,A.C. and Dana,A.

TITLE Towards the transcriptome of Anopheles funestus: a molecular snapshot

JOURNAL Unpublished (2003)

COMMENT Contact: Andrew Serazin

Collins/Besansky Lab

Center for Tropical Disease Research and Training, University of

Notre Dame

317 Galvin Life Science, Notre Dame, IN 46556, USA

Tel: 5746319321

Email: nbesansk@nd.edu

These sequences may be of either nuclear or mitochondrial origin.

FEATURES Location/Qualifiers

source

1..32

/organism="Anopheles funestus"

/mol_type="mRNA"

/strains="West African"

/db_xref="taxon:62324"

/sex="male and female"

/dev_stages="embryo, larvae, pupae, and adult"

/clone_lib="ESTs from wild-caught Anopheles funestus populations"

/note="Vector: LambdaTriplex2"

Query Match 1.0%; Score 28; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 722
 AZ397471
 LOCUS iM0162P23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0162P23 F, genomic survey sequence.

ACCESSION AZ397471

VERSION AZ397471.1 GI:10512543

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

1 (bases 1 to 32)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weise,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical

Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0162 row: P column: 23
 Seq primer: CGTTGTAAACGACGGCCACT
 Class: plasmid ends
 High quality sequence stop: 32.
 Location/Qualifiers

FEATURES

source

1..32

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0162P23"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (GI4732114[gb|AF129072.1]), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.0%; Score 28; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 723

AV743346

LOCUS AV743346

DEFINITION AV743346 CB Homo sapiens cDNA clone CBMABD12 5', mRNA sequence.

ACCESSION AV743346

VERSION AV743346.1 GI:10860927

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 33)

Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,

Chen,S., Mao,M. and Chen,Z.

Homo sapiens CB library cDNA clones

Unpublished (2000)

Contact: Zhu Chen

Shanghai Institute of Hematology, Rui-Jin Hospital

197 Rui-Jin II Road, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: mbshe@ms.stn.sh.cn

This clone is available at Shanghai Hematology Institute in

Shanghai.

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES

source

1..33

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBMABD12"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/notes="vector: pBluescript; Site_1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"

Query Match      1.0%; Score 28; DB 1; Length 33;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA 31 bp mRNA linear EST 07-JAN-2000
LOCUS 2821429.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821429 3',
DEFINITION mRNA sequence.
ACCESSION AW249485
VERSION AW249485.1 GI:6592478
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: 2821429.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbr/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 20
contiguous PHRED high quality bases followed vector sequence. Very
Low Quality Sequence: Trace file contained 31 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L1CM6 row: M column: 14
High quality sequence stop: 20.
Location/Qualifiers
1. .31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821429"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      1.0%; Score 27.8; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 4.6e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 31 bp mRNA linear EST 06-DEC-2004
LOCUS 1077d03.g1 Whole Heart Library (DOEST5) Canis familiaris cDNA,
DEFINITION mRNA sequence.
ACCESSION CX014884
VERSION CX014884.1 GI:56397295
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 31)
AUTHORS Balija, V.S., Nascimento, L.U. and McCombie, W.R.
TITLE ESTs from Canis familiaris whole heart (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
Location/Qualifiers
1. .31
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/clone_lib="Whole Heart Library (DOEST5)"
/notes="Organ: Heart; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      1.0%; Score 27.8; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 4.6e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 31 bp mRNA linear EST 04-NOV-2004
LOCUS 14Salt--05-Mi3.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CV727574
VERSION CV727574.1 GI:55415198
KEYWORDS EST.

Query Match      1.0%; Score 27.8; DB 1; Length 31;
Best Local Similarity 93.5%; Pred. No. 4.6e+02;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 31 bp mRNA linear EST 04-NOV-2004
LOCUS 14Salt--05-Mi3.g1 Salt treated rice leaf lambda phage cDNA library
DEFINITION (14Salt) Oryza sativa (japonica cultivar-group) cDNA clone
ACCESSION CV727574
VERSION CV727574.1 GI:55415198
KEYWORDS EST.
```


RESULT 730

Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers

1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004B01"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 4.7e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAACAAAAA 2735

Db 29 CCNAAAAAAAAA 1

RESULT 732

CN546518/c
LOCUS 29 bp mRNA linear EST 30-APR-2004
DEFINITION EST 18662 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
CDNA clone B3CS57RB007H06 3', mRNA sequence.

ACCESSION CN546518
VERSION CN546518.1 GI:46911143

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 29)

AUTHORS Abbal P., Agase A., Ageorges A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Komieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

JOURNAL Contact: Hamdi S.

COMMENT UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33- (0)5-57-12-25-50

Fax: 00-33- (0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007H06"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27.4; DB 1; Length 29;
Best Local Similarity 96.6%; Pred. No. 4.7e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAA 2737

Db 29 AAAAAAAAAA 1

RESULT 733

LOCUS 29 bp DNA linear GSS 20-FEB-2001

DEFINITION clone UUGC2M0100N08 F, genomic survey sequence.
ACCESSION AZ825156
VERSION AZ825156.1 GI:12995064

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 29)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0100 row: N column: 08

Seq primer: CGTTGTTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0100N08"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 1.0%; Score 27.4; DB 1; Length 29;

Best Local Similarity 96.6%; Pred. No. 4.7e+02;

Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 735	LOCUS	DEFINITION	ACCESSION
------------	-------	------------	-----------

```

/clone="DKFZp566J1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAAAGAGAAAAAATNAAAAA 2736
Db 2 TAAAAAAGAGAAAAAATNAAAAA 30

RESULT 737
LOCUS AU267300 30 bp mRNA linear EST 26-APR-2004
DEFINITION AU267300 VS Dictyostelium discoideum cDNA clone VSH345 5', mRNA
sequence.
ACCESSION AU267300
VERSION AU267300.1 GI:20526098
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
REFERENCE 1 (bases 1 to 30)
AUTHORS Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium
discoideum
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED 15010511
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
Location/Qualifiers
1..30
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strains="AX4"
/db_xref="taxon:44689"
/clone="VSH345"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match      1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAGAAAAAATNAAAAA 2738
Db 1 AAAAAAAGAAAAAATNAAAAA 30

RESULT 738
LOCUS CN546316 30 bp mRNA linear EST 30-APR-2004
DEFINITION CN546316 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS1XGB015F11 3', mRNA sequence.
ACCESSION CN546316
VERSION CN546316.1 GI:46910941
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

```

```

rosids; Vitaceae; Vitis.
1 (bases 1 to 30)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Ronieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
Location/Qualifiers
1..30
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS1XGB015F11"
/dev_stage="green stage"
/clone_lib="Green Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 96.6%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAGAAAAAATNAAAAA 2737
Db 30 AAAAAAAGAAAAAATNAAAAA 2

RESULT 739
LOCUS DR31A15T 30 bp DNA linear GSS 22-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-31A15, genomic survey sequence.
ACCESSION AL987581
VERSION AL987581.1 GI:25176586
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquerry@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 31A15. 31A15 is
part of the Daniokey BAC library created by R. Plasterk and N.V.
Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES
source
Location/Qualifiers
1..30
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-31A15"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"

Query Match      1.0%; Score 27.4; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```


DEFINITION 2821274.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821274 3', mRNA sequence.

ACCESSION AW250841

VERSION AW250841.1 GI:6593834

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 32)

TITLE NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Other_ESTs: 2821274.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-x@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing project

Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bbrp/image/image.html

Base Calling / Quality Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu/LowQuality/

Sequence: 32 contiguous PHRED high quality bases followed by vector sequence. Very Low Quality Sequence: Trace file contained 32 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM6 row: G column: 3

High quality sequence stop: 32.

Location/Qualifiers

1..32

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2821274"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 7"

/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 1.0%; Score 27.2; DB 1; Length 32;

Best Local Similarity 90.6%; Pred. No. 5.1e+02;

Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 32 AAAAAAAAAAAAAAAAAATCCAAAAAAAAA 1

RESULT 746

LOCUS CZ467504

DEFINITION c01856-3prime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 3' end of piggyBac, genomic survey sequence.

ACCESSION CZ467504

VERSION CZ467504.1 GI:62961517

KEYWORDS GSS.

SOURCE Schistosoma mansoni

DEFINITION Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

AUTHORS 1 (bases 1 to 32)

TITLE Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Densky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, P., Swimmer, C., Kopczyński, C., Duyk, G., Winberg, W.L. and Margolis, J.

COMMENT A complementary transposon tool kit for Drosophila melanogaster using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: RHoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of piggyBac element.

This piggyBac insertion position is unspecified in the 32 bases. The insertion position refers to the first base of the 4 base TTAA target recognition sequence.

Class: transposon insertion site.

Location/Qualifiers

1..32

/organism="Drosophila melanogaster"

/mol_type="genomic DNA"

/strain="isogenic w- strain"

/db_xref="taxon:7227"

/clone_lib="Exelixis piggyBac PB insertions"

/note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70-piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37°C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

Query Match 1.0%; Score 27.2; DB 1; Length 32;

Best Local Similarity 90.6%; Pred. No. 5.1e+02;

Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2740

Db 1 AAAAAAAAAAAAAAAAAATCCAAAAAAAAA 32

RESULT 747

LOCUS AM048211/c

DEFINITION AM048211 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC29a09.gik, mRNA sequence.

ACCESSION AM048211

VERSION AM048211.1 GI:75968183

KEYWORDS EST.

SOURCE Schistosoma mansoni

```

ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 27)
TITLE Dillon.G.P., Feltwell.T., Skelton.J.P., Ashton.P.D., Coulson.P.S.,
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC29a09 q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 748
CF291968/c
LOCUS 27 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA
sequence.
ACCESSION CF291968
VERSION CF291968.1 GI:33661001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-J21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 27)
TITLE Dillon.G.P., Feltwell.T., Skelton.J.P., Ashton.P.D., Coulson.P.S.,
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
FEATURES
source
1..27
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC29a09 q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 748
CF291968/c
LOCUS 27 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa (japonica cultivar-group) cDNA clone 14ROOT--02-J21, mRNA
sequence.
ACCESSION CF291968
VERSION CF291968.1 GI:33661001
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-J21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 749
CF329725/c
LOCUS 27 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--05-C12, mRNA
sequence.
ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 750
CF330557/c
LOCUS 27 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-F04, mRNA
sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

```

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .27
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL-06-F04"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 751
 CF335229/c
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group)
 SOURCE Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 ORGANISM Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 27)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1. .27
 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--04-N08"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtUMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 752
 AW327923
 LOCUS
 DEFINITION dr02g08.x1 NIH MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA
 sequence.
 ACCESSION AW327923
 VERSION AW327923.1 GI:6798418
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.

REFERENCE 1 (bases 1 to 27)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Edge Biosystems
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Plate: LLC0029 row: M column: 16
 Seq primer: -21m13 forward primer (ABI).

FEATURES
 source
 1. .27
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
 /tissue_type="Burkitt lymphoma"
 /cell_line="MGC4"
 /clone_lib="NIH_MGC_3"
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 753
 CN545326/c
 LOCUS
 DEFINITION EST 17270 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00GL006G12 3', mRNA sequence.
 ACCESSION CN545326
 VERSION CN545326.1 GI:46909951
 KEYWORDS EST.
 SOURCE Vitis vinifera


```

/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 762
CN546559/c
LOCUS
DEFINITION
EST 18703 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008C12 3', mRNA sequence.
ACCESSION
CN546559
VERSION
CN546559.1 GI:46911184
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008C12"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 764
CN546574/c
LOCUS
DEFINITION
EST 18718 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008E04 3', mRNA sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:46911199
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008C12"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 763
CN546574/c
LOCUS
DEFINITION
EST 18718 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008E04 3', mRNA sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:46911199
KEYWORDS
EST.
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
REFERENCE
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL
Unpublished (2002)
COMMENT
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008E04"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 764
CN546574/c
LOCUS
DEFINITION
EST 18718 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
cDNA clone B3CS58RB008E04 3', mRNA sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:67050778
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Ginkgo biloba
REFERENCE
AUTHORS
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE
Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL
Unpublished (2005)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..27
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS58RB008E04"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match      1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 764
CN546574/c
LOCUS
DEFINITION
EST 18718 Ripe Grape female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
CN546574
VERSION
CN546574.1 GI:67050778
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Ginkgo biloba
REFERENCE
AUTHORS
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE
Expressed tag sequences from Ginkgo female leaf (NYBG)
JOURNAL
Unpublished (2005)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source
1..27
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"

```

/clone lib="Ginkgo female leaf (NVBG)"
 /note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 765
 AZ344642/c
 LOCUS
 DEFINITION 27 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0078H15 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,N., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: H column: 15
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES

source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0078H15"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 766
 AZ401672/c

LOCUS
 DEFINITION 27 bp DNA linear GSS 03-OCT-2000
 clone UUGC1M0168K04 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 row: K column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES

Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0168K04"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
D'b 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 767	AZ486791	27 bp	DNA	linear	GSS 05-OCT-2000
AZ486791/c	1M0315K21F	Mouse 10kb	plasmid	U9C1M library	Mus musculus genomic
LOCUS	clone U9C1M0315K21 F,	genomic survey	sequence.		
DEFINITION					

ACCESSION	AZ486791
VERSION	AZ486791.1
KEYWORDS	GI:10653911
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 27)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: K column: 21
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match          1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 768	AZ511894/c	AZ511894	27 bp	DNA	linear	GSS 05-OCT-2000
LOCUS		IN0357E11F	Mouse 10kb	plasmid	UUGC1M	library Mus musculus genomic
DEFINITION						clone UUGC1M0357E11 F, genomic survey sequence.

ACCESSION AZ511894
VERSION AZ511894.1 GI:10693210
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Mail, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error:
 Plate: 0357 row: E column: 11
 Seq primer: CGTTGTAACAGCCGACGT
 Class: plasmid ends
 High quality sequence stop: 27.

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 769
AZ580921/c
LOCUS
DEFINITION
1M0369824F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0369E24 F, genomic survey sequence.

ACCESSION
AZ580921
VERSION
KEYWORDS
SOURCE
GSS.
GI:11695417

Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: E column: 24
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1..27
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0369E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
DB 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 770
AZ616094/c
LOCUS
DEFINITION
1M0445E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0445E17 R, genomic survey sequence.

ACCESSION
AZ616094
VERSION
KEYWORDS
SOURCE
GSS.
GI:11738284

Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0445 row: E column: 17
Seq primer: CACACGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1..27
Location/Qualifiers

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0445E17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 771
AZ623186/c
LOCUS
DEFINITION
1M0460D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460D12 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ623186
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: D column: 12
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1. .27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460D12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); Obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 772
AZ627847/c
LOCUS
DEFINITION
1M0474O11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474O11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AZ627847
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: O column: 11
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1. .27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474O11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); Obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 773
 AZ809295
 LOCUS 27 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0073B15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0073B15 F, genomic survey sequence.
 ACCESSION AZ809295
 VERSION AZ809295.1 GI:12975450
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduun@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0073 row: B column: 15
 Seq primer: CGTTGTAAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0073B15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 774
 CZ917070
 LOCUS 27 bp DNA linear GSS 08-AUG-2005
 DEFINITION 4021004B03.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.
 ACCESSION CZ917070
 VERSION CZ917070.1 GI:71935597
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 27)
 Walbot,V.
 Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4021004 row: B column: 03
 Class: transposon-tagged.

FEATURES
 source
 1..27
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="4021 - RescueMu Grid V"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 1.0%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

```

RESULT 775
DX046035
LOCUS
DEFINITION
27 bp DNA linear GSS 10-JAN-2006
KBrB047117R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB047117, genomic survey
sequence.
ACCESSION
DX046035
VERSION
DX046035.1 GI:84740332
SOURCE
Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 27)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL
Unpublished (2005)
COMMENT
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB047117
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1..27
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB047117"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chilifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

FEATURES
source
1..27
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB047117"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chilifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 776
DX056021
LOCUS
DEFINITION
27 bp DNA linear GSS 10-JAN-2006
KBrB060M12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB060M12, genomic survey
sequence.
ACCESSION
DX056021
VERSION
DX056021.1 GI:84750318
SOURCE
Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 27)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

```

```

TITLE
JOURNAL
COMMENT
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB060M12
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..27
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB060M12"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chilifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 777
AG829428/c
LOCUS
DEFINITION
27 bp DNA linear GSS 01-DEC-2004
AG829428, BAC clone L243P12, shotgun sequence of subclone
L243P12S001F01, read with M13Reverse primer, genomic survey
sequence.
ACCESSION
AG829428
VERSION
AG829428.1 GI:56375926
KEYWORDS
GSS.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE
1
Tanaka, M., Suzuki, K., Morozumi, T., Kobayashi, E., Matsumoto, T.,
Domukai, M., Eguchi-Ogawa, T., Shinkai, H., Awata, I. and Uenishi, H.
Genomic structure of the distal extended-class II region in swine
Unpublished
2 (bases 1 to 27)
Uenishi, H., Tanaka, M. and Awata, T.
Direct Submission
Submitted (25-OCT-2004) Hirohide Uenishi, National Institute of
Agrobiological Sciences, Animal Genome Laboratory, Genome Research
Department; 2 Ikenodai, Tsukuba, Ibaraki, 305-8602, Japan
(E-mail: huenishi@affrc.go.jp, Tel: 81-29-838-8627,
Fax: 81-29-838-8627)
Correspondence to:
Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department, National
Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, JAPAN
Tel: +81-29-838-8627
Fax: +81-29-838-8627
e-mail: huenishi@affrc.go.jp
Sequencing was carried out in Animal Genome Research Program

```

(Japan)
by National Institute of Agrobiological Sciences
and STAFF-Institute.
Subclones of BAC clones were constructed with pUC18 vector.
Basecalling was performed by Phred 0.020425.c.
Vector sequences were eliminated by crossmatch version 0.990319.
Low quality bases were trimmed based on the quality values with the
aid of the trim_alt option of Phred.

FEATURES

source
1. .27
Location/Qualifiers

/organism="Sus scrofa"
/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="L243P12"
/sub_clones="L243P12S001F01"
/clone_lib="Sus scrofa shotgun BAC sequence"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||

Db 27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 778

TA355B06P 27 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 355B06, forward sequence,
genomic survey sequence.

ACCESSION
AL493923
VERSION
AL493923.1 GI:11870552
KEYWORDS
GSS.

SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

1 (bases 1 to 27)

REFERENCE
AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh1@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .27
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="355B06"

Query Match 1.0%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||

Db

1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 779

AL048439

LOCUS

DEFINITION

DKFZp586I1924_r1 586 (synonym: hutei) Homo sapiens cDNA clone

DKFZp586I1924 mRNA sequence.

ACCESSION

AL048439

VERSION

AL048439.1 GI:4727579

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 28)

Wiemann, S.

EST (Duesterhoeft, et al.)

JOURNAL

Unpublished (1999)

COMMENT

Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1. .28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp586I1924"

/tissue_type="uterus"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="586 (synonym: hutei)"

/note="vector: pSPot1; Site_1: NotI; Site_2: SalI/MluI"

Query Match 1.0%; Score 27; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.9e+02;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

|||||

CF322082

HD--13-123.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--13-123, mRNA sequence.

ACCESSION

CF322082

VERSION

CF322082.1 GI:33693843

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 28)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnahm@gsb.co.kr, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .28

Location/Qualifiers

or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source

Location/Qualifiers
 1..28
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB015D11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 784

CN546304/c

LOCUS

DEFINITION EST 18256 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 CDNA clone B3CS1XGB015E11 3', mRNA sequence.

ACCESSION CN546304

VERSION CN546304.1

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source

Location/Qualifiers
 1..28
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XGB015E11"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
 Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 785

CN988459/c

LOCUS

DEFINITION DN988459 28 bp mRNA linear EST 17-MAY-2005
 ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl Bermudagrass line Zebra
 subtracted cold acclimated cDNA library Cynodon dactylon cDNA clone
 ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl, mRNA sequence.

ACCESSION DN988459

VERSION DN988459.1

KEYWORDS EST.

SOURCE Cynodon dactylon

ORGANISM Cynodon dactylon

REFERENCE 1 (bases 1 to 28)
 AUTHORS Melmaiee,K., Elavarathi,S. and Guenzi,A.C.
 TITLE Identification of differentially expressed genes associated with
 cold acclimation using suppression subtraction hybridization (SSH)
 and cDNA microarrays
 JOURNAL Unpublished (2005)
 COMMENT Contact: Guenzi AC
 Dep. of Plant and Soil Sciences
 Oklahoma State University
 368 Agriculture Hall, Stillwater, OK 74078-6028, USA
 Tel: 405-744-6028
 Fax: 405-744-6039
 Email: acg@mail.pss.okstate.edu
 PCR Primers
 FORWARD: M13 forward
 BACKWARD: M13 Reverse
 Seq primer: M13 Forward

FEATURES

source

Location/Qualifiers
 1..28
 /organism="Cynodon dactylon"
 /mol_type="mRNA"
 /cultivar="Zebra"
 /db_xref="taxon:28909"
 /clone="ZEBRA_2F_2-II_03_ZEBRA_2F_2-II_03_C05.abl"
 /tissue_type="Crown"
 /lab_host="E. coli"
 /clone_lib="Bermudagrass line Zebra subtracted cold
 acclimated cDNA library"
 /note="vector: Qiagen's pDrive; Messenger RNA was
 extracted from control and cold acclimated bermudagrass
 crown tissue at 2 and 28 days after acclimation and cDNA
 library was constructed following Clontech PCR- select
 cDNA subtraction procedure."

Query Match 1.0%; Score 27; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 786

CZ918534/c

LOCUS

DEFINITION CZ918534 28 bp DNA linear GSS 08-AUG-2005
 4021009H02.1EL.x1 4021 - RescueMu Grid V Zea mays genomic,
 survey sequence.

```

ACCESSION      CZ918534
VERSION        CZ918534.1  GI:71938162
KEYWORDS       GSS.
SOURCE         Zea mays
ORGANISM       Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Zea.
               1 (bases 1 to 28)

REFERENCE
AUTHORS        Walbot,V.
TITLE          Maize genomic sequences found using engineered RescueMu transposon
JOURNAL        Unpublished (2001)
COMMENT        Contact: Walbot V
               Department of Biological Sciences
               Stanford University
               855 California Ave, Palo Alto, CA 94304, USA
               Tel: 650 723 2227
               Fax: 650 725 8221
               Email: walbot@stanford.edu
               Very probable ligation site of ends cut by single endonuclease.
               Reverse complemented post-ligation sequence from source sequence.
               Plate: 4021009 row: H column: 02
               Class: transposon-tagged.
               Location/Qualifiers
               1..28
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /cultivar="mixed background W23/A188/B73/K55"
               /db_xref="taxon:4577"
               /tissue_type="leaf"
               /dev_stage="adult"
               /lab_host="DH10B"
               /clone_lib="4021 - RescueMu Grid V"
               /notes="Organ: leaf; Vector: RescueMu (engineered from
               pBluescript backbone); Site 1: BamHI; Site 2: BglII;
               RescueMu is a 4.9 kb, modified maize Mu transposon
               designed to allow plasmid rescue from total genomic DNA.
               Mu elements insert preferentially into transcription
               units. For more information on RescueMu, go to the web
               site 'http://www.mutransposon.org/project/RescueMu/'. Grid
               V was grown at University of Arizona in 2003. DNA was
               extracted from leaf strips, double digested using BamHI
               and BglII, and ligated to form circular plasmids. DH10B
               cells were transformed and then screened on LB plates with
               ampicillin."

FEATURES
source
Query Match      1.0%; Score 27; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 787
CA853459/c
LOCUS          32 bp mRNA linear EST 01-AUG-2003
DEFINITION     B08E06 seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
               B08E06 5', mRNA sequence.
ACCESSION      CA853459
VERSION        CA853459.1  GI:33390252
KEYWORDS       EST.
SOURCE         Glycine max (soybean)
ORGANISM       Glycine max
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Glycine.
               1 (bases 1 to 32)

REFERENCE
AUTHORS        Alkharouf,N., Khan,R. and Matthews,B.
TITLE          Analysis of expressed sequence tags from roots of resistant soybean
               infected by the soybean cyst nematode

JOURNAL        Genome 47 (2), 380-388 (2004)
PUBMED         15060591
COMMENT        Contact: Alkharouf, N.W.
               Soybean Genomics and Improvement Laboratory (SGIL)
               US Department of Agriculture (USDA), ARS, PSI
               Bldg-006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
               USA
               Tel: 301 504 5750
               Fax: 301 504 5728
               Email: alkharouf@ars.usda.gov.
               Location/Qualifiers
               1..32
               /organism="Glycine max"
               /mol_type="mRNA"
               /cultivar="Peking"
               /db_xref="taxon:3847"
               /clone="B08E06"
               /tissue_type="Roots"
               /dev_stage="Seedlings"
               /clone_lib="cDNA Peking library 12hr SCN3"
               /note="Vector: pBluescript SK-; cDNA clones from mRNA
               extracted from roots of soybean cv. Peking 12 hrs after
               infection by SCN race 3. These are cloned in pBluescript
               SK- phagemid."

Query Match      1.0%; Score 27; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
      |||||||
Db 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 788
R16114/c
LOCUS          32 bp mRNA linear EST 13-APR-1995
DEFINITION     ya51f03.s2 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
               IMAGE:66461 3', similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE
               ZETA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION      R16114
VERSION        R16114.1  GI:767923
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
               1 (bases 1 to 32)

REFERENCE
AUTHORS        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
               Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
               Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
               Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
               Wilson,R.
               The WashU-Merck EST Project
               Unpublished (1995)
               Contact: Wilson RK
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@watson.wustl.edu
               High quality sequence starts: 1
               High quality sequence stops: 1
               Source: IMAGE Consortium, LLNL
               This clone is available royalty-free through LLNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Trace considered overall poor quality
               Seq primer: -21ml3
               High quality sequence stop: 1.
               Location/Qualifiers
               1..32
               /organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:66461"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
(5' AACTGGAAGATTAAAGATCTTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 1.0%; Score 27; DB 1; Length 32;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2708 TAAAAA..... 30 bp DNA linear GSS 08-AUG-2005
| | | | | | | | | | | | | | | | | | | | | |
Db 30 TNAANA..... 30 TNAANA..... 1

RESULT 789
CZ913832
LOCUS 4013004D04.2EL x1 4013 - RescueMu Grid O Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION CZ913832
VERSION CZ913832
KEYWORDS GSS.
SOURCE CZ913832.1 GI:719330085
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013004 row: D column: 04
Class: transposon-tagged.
FEATURES
source
1..30
Location/Qualifiers
1..30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
O was grown at Stanford in 2001. DNA was extracted from
leaf strips, double digested using BamHI and BglII, and
ligated to form circular plasmids. DH10B cells were
transformed and then screened on LB plates with
ampicillin."

Query Match 1.0%; Score 26.8; DB 1; Length 30;
Best Local Similarity 93.3%; Pred. No. 5.2e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAA..... 32 bp mRNA linear EST 18-AUG-2003
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAA..... 30
| | | | | | | | | | | | | | | | | | | | | |

RESULT 790
CF332296/c
LOCUS CF332296.1 GI:33812816
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone NACL--08-M01, mRNA
sequence.
ACCESSION CF332296
VERSION CF332296.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--08-M01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TORO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2708 TAAAAA..... 32 bp mRNA linear EST 05-NOV-2004
| | | | | | | | | | | | | | | | | | | | | |
Db 30 TCACAAAA..... 1
| | | | | | | | | | | | | | | | | | | | | |

RESULT 791
CV733741/c
LOCUS CV733741.1 GI:55440856
DEFINITION FLO--08-M16-g1 Rice flower lambda phage cDNA library (FLO) Oryza
sativa (japonica cultivar-group) cDNA clone FLO--08-M16, mRNA
sequence.
ACCESSION CV733741
VERSION CV733741.1
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 32)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..32
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="FLO--08-M16"
/tissue_type="flower"
/lab_host="E.coli SOLR"
/clone_lib="Rice flower lambda phage cDNA library (FLO)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site."

Query Match 1.0%; Score 26.8; DB 1; Length 32;
Best Local Similarity 93.3%; Pred. No. 5.3e+02;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAGAAAAAAGAAAAAAGAAAAA 2734
DB 30 TCCCAAAAAAAGAAAAAAGAAAAAAGAAAAA 1

RESULT 792
CF300359/c
LOCUS
DEFINITION
CF300359
33 bp mRNA linear EST 15-AUG-2003
7LEAF--04-L15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L15, mRNA
sequence.
ACCESSION
CF300359
VERSION
CF300359.1 GI:33672120
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..33
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-L15"
/tissue_type="leaf"

```

```

/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 1.0%; Score 26.6; DB 1; Length 33;
Best Local Similarity 87.9%; Pred. No. 5.6e+02;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2709 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2741
DB 33 AAAGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1

RESULT 793
CF307749/c
LOCUS
DEFINITION
CF307749
28 bp mRNA linear EST 15-AUG-2003
ABF--01-E17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--01-E17, mRNA sequence.
ACCESSION
CF307749
VERSION
CF307749.1 GI:33679510
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 28)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..28
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--01-E17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2736
DB 28 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1

RESULT 794
AW332443/c
LOCUS
DEFINITION
AW332443
28 bp mRNA linear EST 31-JAN-2000
SBE7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

```

```

ACCESSION      AW332443
VERSION        AW332443.1  GI:6828800
KEYWORDS       EST.
SOURCE         Pneumocystis carinii
ORGANISM       Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
               Pneumocystidaceae; Pneumocystis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
               Edman,J.C., Kovacs,J. and Cushion,M.
TITLE          Expressed sequence tags from Pneumocystis carinii
JOURNAL        Unpublished (2000)
COMMENT        Contact: Staben C
               School of Biological Sciences
               University of Kentucky
               101 Morgan Building, University of Kentucky, Lexington, KY
               40506-0225, USA
               Tel: 606 257 2161
               Fax: 606 257 1717
               Email: staben@pop.uky.edu.
FEATURES       Location/Qualifiers
               1..28
               /organism="Pneumocystis carinii"
               /mol_type="mRNA"
               /db_xref="taxon:4754"
               /lab_host="E. coli"
               /clone_lib="AGS-1"
               /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
               P. carinii organisms (3x10e9) from a single rat (99-1-6,
               sacrificed on 3/17/99) at Cincinnati VA facilities.
               Trizol extracted RNA. Oligo dT priming, standard
               conditions described by vendor, Stratagene. Further
               details see www.uky.edu/Project/Pneumocystis/"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 795
CN545659/c
LOCUS          CN545659 28 bp mRNA linear EST 30-APR-2004
DEFINITION    EST 17603 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
               clone B3CS00RL004E11 3', mRNA sequence.
ACCESSION     CN545659
VERSION       CN545659.1  GI:46910284
KEYWORDS      EST.
SOURCE        Vitis vinifera
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
               rosids; Vitaceae; Vitis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
               Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimpellet,J.,
               Hamdi,S., Romieu,C. and Terrier,N.
TITLE          Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
               or seeds) at Various Developmental Stages
JOURNAL        Unpublished (2002)
COMMENT        Contact: Hamdi S.
               UMR 619 - Equipe Biologie de la Vigne
               Universite de Bordeaux I, Institut National de la Recherche
               Agronomique
               71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
               France
               Tel: 00-33- (0)5-57-12-25-50
               Fax: 00-33- (0)5-57-12-25-48
               Email: s.hamdi@bordeaux.inra.fr
               Seq primer: T7.

```

```

FEATURES       Location/Qualifiers
               1..28
               /organism="Vitis vinifera"
               /mol_type="mRNA"
               /cultiivar="Cabernet Sauvignon"
               /db_xref="taxon:29760"
               /clone="B3CS00RL004E11"
               /dev_stage="ripening stage"
               /clone_lib="Ripe Grape Skin Triplex2 Library"
               /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
               SfiIA; Site_2: SfiIB; Oriented library"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    |||||||
Db 28 CCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 796
CX001046/c
LOCUS          CX001046 28 bp mRNA linear EST 03-DEC-2004
DEFINITION    t124G08.b7 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
               mRNA sequence.
ACCESSION     CX001046
VERSION       CX001046.1  GI:56272462
KEYWORDS      EST.
SOURCE        Canis familiaris (dog)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
               Canis.
REFERENCE      1 (bases 1 to 28)
AUTHORS        Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE          ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL        Unpublished (2004)
COMMENT        Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mccombie@cshl.org.
FEATURES       Location/Qualifiers
               1..28
               /organism="Canis familiaris"
               /mol_type="mRNA"
               /db_xref="taxon:9615"
               /sex="Unknown"
               /tissue_type="Cardiac muscle"
               /dev_stage="3 month old normal canine"
               /lab_host="XL10 Gold"
               /clone_lib="Left Cardiac Ventricle (DOGEST7)"
               /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
               EcoRI; Site 2: XhoI; Library constructed using pBluescript
               XR kit from Stratagene. Cloned cDNA was size selected
               between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,
               Pathology and Medical Genetics, School of Veterinary
               Medicine, University of Pennsylvania, 3800 Spruce Street,
               Philadelphia, PA 19104-6051"
Query Match    1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
    |||||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 797

```

DR062845
 LOCUS 28 bp mRNA linear EST 06-JUN-2005
 DEFINITION iq22809.g1 Cytas ovule (NYBG) Cytas rumphii cDNA 3', mRNA sequence.
 ACCESSION DR062845
 VERSION DR062845.1 GI:66986411
 KEYWORDS EST.
 SOURCE Cytas rumphii
 ORGANISM Cytas rumphii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cytas.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N., O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W., Benfey, P., Coruzzi, G. and Stevenson, D.
 TITLE Expressed tag sequences from Cytas ovules (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES
 source
 1..28
 Location/Qualifiers

/organism="Cytas rumphii"
 /mol_type="mRNA"
 /db_xref="taxon:58031"
 /sex="Female"
 /clone_lib="Cytas ovule (NYBG)"
 /notes="Organ: Ovules; Vector: pBK-CMV; Site 1: XhoI;
 Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 1.0%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 5.3e+02;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAA 2733
 Db 1 AATAAAAAA 28

RESULT 798
 AZ514352/c
 LOCUS 28 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0360F06R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0360F06 R, genomic survey sequence.

ACCESSION AZ514352
 VERSION AZ514352.1 GI:10695668
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah
 Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: F column: 06
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES
 source
 1..28
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0360F06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCGM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF125072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 1.0%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 5.3e+02;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 2736
 Db 28 AAAAAA 1

RESULT 799

AZ824574/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 1000 Std Error: 0.00
 Plate: 0039 row: D column: 17
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers

FEATURES

```

1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099D17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGClm library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 1.0%; Score 26.4; DB 1; Length 28;
 Best Local Similarity 96.4%; Pred. No. 5.3e+02;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2736

Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 800

CZ916890
 LOCUS 4021003D05.2EL.y1 4021 - RescueMu Grid V Zea mays genomic, GSS 08-AUG-2005
 DEFINITION survey sequence.

ACCESSION CZ916890

VERSION CZ916890.1 GI:71935275

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 28)

AUTHORS Walbot.V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4021003 row: D column: 05

Class: transposon-tagged.

FEATURES

source

```

Location/Qualifiers
1..28
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

```

Query Match 1.0%; Score 26.4; DB 1; Length 28;

Best Local Similarity 96.4%; Pred. No. 5.3e+02;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2736

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

RESULT 801

TA29A09P/c

LOCUS TA29A09P

DEFINITION T. brucei sheared genomic DNA clone 29a09, forward sequence,

genomic survey sequence.

ACCESSION AL453073

VERSION AL453073.1 GI:11854584

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 28)

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajadream,M.A. and Barrell,B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..28

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="29a09"


```

Query Match          1.0%; Score 26.4; DB 1; Length 28;
Best Local Similarity 96.4%; Pred. No. 5.3e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||
Db  28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 802
LOCUS CF328476
DEFINITION NACL--03-G12.b1 Rice callus plasmid cDNA library (NACL) Oryza
          sativa (japonica cultivar-group) cDNA clone NACL--03-G12, mRNA
          sequence.
ACCESSION CF328476
VERSION CF328476.1 GI:33805199
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
        Oryza sativa (japonica cultivar-group)
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
        clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
        source
        1..29
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="NACL-03-G12"
        /tissue_type="callus"
        /dev_stage="proliferated callus on 2N6 media for 30 days"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice callus plasmid cDNA library (NACL)"
        /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."

Query Match          1.0%; Score 26.4; DB 1; Length 29;
Best Local Similarity 96.4%; Pred. No. 5.4e+02;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
      |||||
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAAACAA 28

RESULT 803
LOCUS AU268044
DEFINITION AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
          sequence.
ACCESSION AU268044
VERSION AU268044.1 GI:20526842
KEYWORDS EST.
SOURCE Dictyostelium discoideum
          Dictyostelium discoideum
          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
          1 (bases 1 to 31)
REFERENCE 1
AUTHORS Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
          Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.

```

```

TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium
        discoideum
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED 15010511
COMMENT Contact: Hideko Urushihara
          Institute of Biological Sciences
          University of Tsukuba
          1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
          Tel: 81-298-53-4664
          Fax: 81-298-53-6614
          Email: hideko@biol.tsukuba.ac.jp.

FEATURES
        source
        1..31
        /organism="Dictyostelium discoideum"
        /mol_type="mRNA"
        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="VSH836"
        /sex="mat A"
        /dev_stage="vegetative"
        /clone_lib="VS"

Query Match          1.0%; Score 26.2; DB 1; Length 31;
Best Local Similarity 90.3%; Pred. No. 5.7e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
      |||||
Db  1 AAAAAACAAAAAAAAAAAAAAAAATTAAAAA 31

RESULT 804
LOCUS CF297930
DEFINITION CF297930
          CF297930
          CF297930.1 GI:33669691
          EST.
          Oryza sativa (japonica cultivar-group)
          Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzeae; Oryza.
          1 (bases 1 to 31)
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
        source
        1..31
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="7LEAF--01-B17"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."

Query Match          1.0%; Score 26.2; DB 1; Length 31;

```

```

' Best Local Similarity 90.3%; Pred. No. 5.8e+02;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2739
    ||||| ||||| ||||| ||||| |||||
Db 32 AAAAAACAAAAAACAAAAACAAAAACAAAAACAAAA 2
    ||||| ||||| ||||| ||||| |||||

```

RESULT 806	
AJ659204	
LOCUS	26 bp mRNA linear EST 28-JUN-2004
DEFINITION	AJ659204 KN277 Sus scrofa cDNA clone C0005215_E14, mRNA sequence.
ACCESSION	AJ659204
VERSION	AJ659204.1 GI:49343335
KEYWORDS	EST.
SOURCE	Sus scrofa (pig)
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS	1 (bases 1 to 26)
TITLE	Anderson,S.I., Finlayson,H.A. and Archibald,A.L. Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL	Unpublished (2004)
COMMENT	Contact: Anderson SI Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -mismatch 12 options. Vector:pBluescriptII(SK+) R. Site1: ECORI R. Site2: NOTI 5', Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

```

/clone="C0005215_E14"
/tissue_type="embryo"
/clone_lib="VN277"
/notes/vector: pBluescriptII(SK+); Site.1: EcoRI; Site.2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."

Query Match          0.9%;   Score 26;   DB 1;   Length 26;
Best Local Similarity 100.0%;   Pred. No. 5.4e+02;
Matches 26;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
      |||||||
DB   1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 807
AM043187
LOCUS   AM043187 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION  mansoni cDNA clone SmLC20c10.q1k, mRNA sequence.
ACCESSION  AM043187
VERSION    AM043187.1 GI:75970051
KEYWORDS   EST.
SOURCE     Schistosoma mansoni
           Schistosoma mansoni
REFERENCE  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
           Strigeliida; Schistosomatidae; Schistosomatidae; Schistosoma.
AUTHORS    1 (bases 1 to 26)
           Dillon,G.P.,Faltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

```

Query Match 1.0%; Score 26.2; DB 1; Length 32;

Nikoiaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

TITLE
JOURNAL
COMMENT

FEATURES
 source
 1. .26
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC20c10.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /notes="country: Puerto Rico"

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 808
 AM045820
 LOCUS
 DEFINITION
 AM045820 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC18f01.q1k, mRNA sequence.
 AM045820
 VERSION
 AM045820.1 GI:75969112
 EST.
 SOURCE
 Schistosoma mansoni
 ORGANISM
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Dillion,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikoiaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

TITLE
JOURNAL
COMMENT

FEATURES
 source
 1. .26
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC18f01.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /notes="country: Puerto Rico"

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 809
 AM046959
 LOCUS
 DEFINITION
 AM046959 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC23c06.q1k, mRNA sequence.

AM046959
 VERSION
 AM046959.1 GI:72292765
 EST.
 SOURCE
 Schistosoma mansoni
 ORGANISM
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Dillion,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikoiaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

TITLE
JOURNAL
COMMENT

FEATURES
 source
 1. .26
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC23c06.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 1 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 810
 AM047208/c
 LOCUS
 DEFINITION
 AM047208 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC12e04.q1k, mRNA sequence.
 AM047208
 VERSION
 AM047208.1 GI:72293264
 EST.
 SOURCE
 Schistosoma mansoni
 ORGANISM
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 Dillion,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikoiaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni
 Unpublished (2005)
 CONTACT: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

TITLE
JOURNAL
COMMENT

FEATURES
 source
 1. .26
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC12e04.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734


```

/clone lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    ||||||||||||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 817
AW327613/c
LOCUS      26 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--07-J02.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa (japonica cultivar-group) cDNA clone NACL--07-J02, mRNA
           sequence.
ACCESSION  CF331439.1 GI:33811097
VERSION     CF331439
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 26)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
    1..26
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="NACL--07-J02"
    /tissue_type="callus"
    /dev_stages="proliferated callus on 2N6 media for 30 days"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice callus plasmid cDNA library (NACL)"
    /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."

Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    ||||||||||||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 818
AW327613/c
LOCUS      26 bp mRNA linear EST 28-JAN-2000
DEFINITION dq01b09.y1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA
           sequence.
ACCESSION  AW327613

```

```

VERSION  AW327613.1 GI:6798108
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 26)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Edge BioSystems
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Plate: LLCM0028 row: C Column: 17
            Seq primer: M13Rpl reverse primer (ABI).
            Location/Qualifiers
                1..26
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:2846536"
                /tissue_type="T cell leukemia"
                /cell_line="MGC2"
                /clone_lib="NIH_MGC_2"
                /note="Organ: Blood; Vector: pOTB7a; Library prepared by
                Edge BioSystems."

Query Match      0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
    ||||||||||||||||||||||||||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 819
CN545213/c
LOCUS      26 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17157 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
           clone B3CS00GL004E11 3', mRNA sequence.
ACCESSION  CN545213
VERSION     CN545213.1 GI:46909668
KEYWORDS    EST.
SOURCE      Vitis vinifera
ORGANISM    Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE   1 (bases 1 to 26)
AUTHORS    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Ronieu,C. and Terrier,N.
            Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
            Unpublished (2002)
            Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne
            Université de Bordeaux I, Institut National de la Recherche
            Agronomique
            71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
            France
            Tel: 00-33-(0)5-57-12-25-50
            Fax: 00-33-(0)5-57-12-25-48
            Email: s.hamdi@bordeaux.inra.fr
            Seq primer: T7.

```


Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers
1..26

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006A07"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 823

CN546608/c

LOCUS

DEFINITION EST 18752 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera

CDNA clone B3CS58RB008H03 3', mRNA sequence.

ACCESSION CN546608

VERSION EST.

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 26)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Romieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..26

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS58RB008H03"

/dev_stage="ripe stage"

/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 824

CN546649/c

LOCUS

DEFINITION EST 18420 Turning Grape Berry Lambda Triplex2 Library Vitis

vinifera cDNA clone B3CS37TB007C08 3', mRNA sequence.

ACCESSION CN546649

VERSION EST.

KEYWORDS Vitis vinifera

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; Vitaceae; Vitis.

1 (bases 1 to 26)

Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,

Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,

Hamdi,S., Romieu,C. and Terrier,N.

Generation of Expressed Sequence Tag from Grape Berry (skin, pulp

or seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne

Universite de Bordeaux I, Institut National de la Recherche

Agronomique

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,

France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: s.hamdi@bordeaux.inra.fr

Seq primer: T7.

Location/Qualifiers

1..26

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS37TB007C08"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda

Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 825

CN546649/c

LOCUS

DEFINITION it64e03.g1 Gnetum female cone (NYBG) Gnetum gnetum cDNA 3', mRNA

sequence.

ACCESSION DN953783

VERSION DN953783.1

KEYWORDS EST.

SOURCE Gnetum gnetum

ORGANISM Gnetum gnetum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetum.

1 (bases 1 to 26)

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0102 row: H column: 23
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source

```

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0102H23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 829
AZ376664
LOCUS
DEFINITION
 1M0130508R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0130808 R, genomic survey sequence.
ACCESSION
VERSION
 AZ376664.1 GI:10490364
KEYWORDS
 GSS.
SOURCE
 Mus musculus (house mouse)
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL COMMENT
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0130 row: E column: 08
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
 source

```

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0130E08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 830
AZ389765
LOCUS
DEFINITION
 1M0150D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150D13 R, genomic survey sequence.
ACCESSION
VERSION
 AZ389765.1 GI:10503473
KEYWORDS
 GSS.
SOURCE
 Mus musculus (house mouse)
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
 1 (bases 1 to 26)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: D column: 13
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150D13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 831
AZ414673
LOCUS
AZ414673 26 bp DNA linear GSS 03-OCT-2000
DEFINITION
IM0189M07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0189M07 F, genomic survey sequence.
ACCESSION
AZ414673
VERSION
AZ414673.1 GI:10538686
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: M column: 07
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES
source

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 832
AZ593300
LOCUS
AZ593300 26 bp DNA linear GSS 13-DEC-2000
DEFINITION
IM0404E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0404E16 R, genomic survey sequence.
ACCESSION
AZ593300
VERSION
AZ593300.1 GI:11715490
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0404 row: E column: 16
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0404E16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

1. .26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0404E16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 833
AZ612722/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ612722 26 bp DNA linear GSS 13-DEC-2000
 1M0439E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0439E17 R, genomic survey sequence.
 AZ612722.1 GI:11734912
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
JOURNAL
COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0439 row: E column: 17
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.
 Location/Qualifiers
 1. .26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0439E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

1. .26
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0439E17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
 |||||
 Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 834
AZ624441/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ624441 26 bp DNA linear GSS 13-DEC-2000
 1M0463G07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0463G07 F, genomic survey sequence.
 AZ624441
 AZ624441.1 GI:11746631
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 26)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0463 row: G column: 07
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES
source
1. 26

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0463G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 835
AZ627846/C
LOCUS
DEFINITION
1M0474H08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474H08 F, genomic survey sequence.

ACCESSION
AZ627846
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 08
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES
source
1. 26

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 836
AZ652515
LOCUS
DEFINITION
1M0525H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0525H15 R, genomic survey sequence.

ACCESSION
AZ652515
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0525 row: H column: 15
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0525H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 837
AZ800453/c
LOCUS
DEFINITION
2M0058023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0058023 F, genomic survey sequence.

ACCESSION
AZ800453
VERSION
AZ800453.1 GI:12952583
GSS.

SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0058 row: O column: 23
Seq primer: GGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0058O23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
DB 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 838
AZ963974/c
LOCUS
DEFINITION
2M0233N01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0233N01 F, genomic survey sequence.

ACCESSION
AZ963974
VERSION
AZ963974.1 GI:13835201
GSS.

SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

TITLE
Niederhauser, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: N column: 01
Seq primer: CGTTGTAACAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233N01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 839
CZ490199/c
LOCUS 26 bp DNA linear GSS 29-APR-2005
DEFINITION f07397-3prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic sequence recovered from 3' end of piggyBac,
genomic survey sequence.

ACCESSION CZ490199
VERSION CZ490199.1 GI:62987637
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 26)

REFERENCE
AUTHORS Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,

TITLE
JOURNAL
PUBMED
COMMENT

Ryner, L., Cheung, L.M., Chong, A., Brickson, C., Fisher, W.W.,
Greer, K., Hartouni, S.R., Howie, S., Jakkula, L., Joo, D., Killpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, P.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is unspecified in the 26 bases.
This insertion position refers to the first base of the 4 base TTTAA
target recognition sequence.
Class: transposon insertion site.

FEATURES

source
1..26
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac WH insertions"
/note="Vector: piggyBac WH (GenBank accession number
AY515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin-piggyBac transposase source.
We remobilized the WH element from a single amnion
element on the Binsney balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homologous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

Query Match 0.9%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 840
CZ910095
LOCUS 26 bp DNA linear GSS 08-AUG-2005

DEFINITION 4012001C02.2EL.y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.

ACCESSION CZ910095
VERSION CZ910095.1 GI:71923489
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 26)
Walbot, V.

REFERENCE
AUTHORS Maize genomic (2001)
TITLE Unpublished (2001)
JOURNAL
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University

855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012001 row: C column: 02
Class: transposon-tagged.

FEATURES

Location/Qualifiers
1..26

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="4012 - RescueMu Grid BB"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription site. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 841

DU832827/c

LOCUS

DEFINITION
DU832827 26 bp DNA linear GSS 22-DEC-2005
KBrS010P08F KBrS, Brassica rapa Sau3AI BAC library
subsp. pekinensis genomic clone KBrS010P08, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 26)

AUTHORS
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL

COMMENT

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS010P08

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..26

FEATURES

source

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBrS010P08"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 842

DU835360/c

LOCUS

DEFINITION
DU835360 26 bp DNA linear GSS 22-DEC-2005
KBrS016I05R KBrS, Brassica rapa Sau3AI BAC library
subsp. pekinensis genomic clone KBrS016I05, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 26)

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL

COMMENT

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBrS016I05

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1..26

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clones="KBrS016I05"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 26; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


```

RESULT 843
DX034224
LOCUS
DEFINITION
  KBrB031P17R KBrB, Brassica rapa BamHI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrB031P17, genomic survey
  sequence.
ACCESSION
DX034224
VERSION
DX034224.1 GI:84728521
KEYWORDS
GSS.
SOURCE
  Brassica rapa subsp. pekinensis
ORGANISM
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 26)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa BamHI (KBrB) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  KBrB031P17
  Seq primer: M13 Reverse
  Class: BAC ends.
FEATURES
  Location/Qualifiers
    1..26
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBrB031P17"
      /lab_host="E.coli DH10B"
      /clone_lib="KBrB, Brassica rapa BamHI BAC library"
      /notes="Vector: pCUGIBAC1; Site1: BamHI; Brassica rapa spp
      pekinensis var. Chifu BAC library (KBrB BAC) is provided
      by Yong-Pyo Lim (CNU)."
```

```

JOURNAL
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
  nh1@sanger.ac.uk
COMMENT
  Constructed at the Institute for Genomic Research (TIGR),
  Rockville, MD. Genomic DNA isolated from a cloned population of
  Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
  to give a tight size distribution (
  4 kb). The v + i method used for the library construction is
  described in detail in Smith, H. and Venter, J.C. (Making small
  insert libraries for whole genome shotgun sequencing projects. In
  Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
  Barrell, Oxford University Press, 1999).
  Email: nelsayed@tigr.org
  Details of T. brucei sequencing at the Sanger Centre are available
  at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
  Location/Qualifiers
    1..26
      /organism="Trypanosoma brucei"
      /mol_type="genomic DNA"
      /strain="TREU927"
      /db_xref="taxon:5691"
      /clone="324d07"
Query Match
  0.9%; Score 26; DB 1; Length 26;
Best Local Similarity
  100.0%; Pred. No. 5.4e+02;
Matches
  26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
  2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
  |||||
Db
  1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26
RESULT 845
CN545777/c
LOCUS
DEFINITION
  EST 17721 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
  clone B3CS00RL005G11 3', mRNA sequence.
ACCESSION
CN545777
VERSION
CN545777.1 GI:46910402
KEYWORDS
EST.
SOURCE
  Vitis vinifera
  ORGANISM
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; Vitaceae; Vitis.
  1 (bases 1 to 27)
REFERENCE
  1
  Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
  Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
  Hamdi,S., Romieu,C. and Terrier,N.
  Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
  or seeds) at Various Developmental Stages
  Unpublished (2002)
  Contact: Hamdi S.
  UMR 619 - Equipe Biologie de la Vigne
  Universite de Bordeaux I, Institut National de la Recherche
  Agronomique
  71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
  France
  Tel: 00-33-(0)5-57-12-25-50
  Fax: 00-33-(0)5-57-12-25-48
  Email: s.hamdi@bordeaux.inra.fr
  Seq primer: T7.
FEATURES
  Location/Qualifiers
    1..27
      /organism="Vitis vinifera"
      /mol_type="mRNA"
      /cultivar="Cabernet Sauvignon"
      /db_xref="taxon:29760"
      /clone="B3CS00RL005G11"
      /dev_stages="ripening stage"
      /clone_lib="Ripe Grape Skin Triplex2 Library"
      /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:"

```

```

SfiIIA; Site_2: SfiIB; Oriented library"

Query Match          0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 846
CN545880/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CN545880 27 bp mRNA linear EST 30-APR-2004
EST 17824 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3C500RL002H10 3', mRNA sequence.
CN545880
CN545880.1 GI:46910505
EST.
Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 27)
Abbal,P., Agase,A., Ageorges,A., Atanasova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpiet,J.,
Hamdi,S., Romeu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33083 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..27
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C500RL002H10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIIA; Site_2: SfiIB; Oriented library"

Query Match          0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 847
CN545880/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CN545880 27 bp DNA linear GSS 08-AUG-2005
4021014C04.2EL y1 4021 - RescueMu Grid v Zea mays genomic, genomic
survey sequence.
CN545880
CN545880.1 GI:71940417
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

SfiIIA; Site_2: SfiIB; Oriented library"

Query Match          0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 848
CN545880/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CN545880 27 bp DNA linear GSS 13-DEC-2000
TA257807P
T. brucei sheared genomic DNA clone 257b07, forward sequence,
genomic survey sequence.
AL483278
AL483278.1 GI:11849602
GSS.
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,S., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 27)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021014 row: C column: 04
Class: transposon-tagged.
Location/Qualifiers
1..27

source
1..27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

Query Match 0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 848
CN545880/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 27)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,S., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared

to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="257b07"
Query Match 0.9%; Score 26; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.5e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27

RESULT 849

AJ658314 29 bp mRNA linear EST 28-JUN-2004
LOCUS AJ658314 KN277 Sus scrofa cDNA clone C0005212_K01, mRNA sequence.
DEFINITION AJ658314
ACCESSION AJ658314
VERSION AJ658314.1 GI:49342383
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 29)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred V0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector: pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source
1. .29
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005212_K01"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."
Query Match 0.9%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 850

AZ819924 29 bp DNA linear GSS 20-FEB-2001
LOCUS AZ819924
DEFINITION 2M0091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0091A19 R, genomic survey sequence.

ACCESSION AZ819924
VERSION AZ819924.1 GI:12989832
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: A column: 19

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 29.

FEATURES

source
1. .29
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 26; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

```

Db      1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 851
CN545889/c
LOCUS   EST 17833 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE
AUTHORS Abbal,P., Agasse,A., Agorces,A., Atanasova,R., Barrieu,F.,
        Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
        Hamdi,S., Komieu,C. and Terrier,N.
        Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
        or seeds) at Various Developmental Stages
        Unpublished (2002)
        Contact: Hamdi S.
        UMR 619 - Equipe Biologie de la Vigne
        Universite de Bordeaux I, Institut National de la Recherche
        Agronomique
        71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
        France
        Tel: 00-33-(0)5-57-12-25-50
        Fax: 00-33-(0)5-57-12-25-48
        Email: s.hamdi@bordeaux.inra.fr
        Seq primer: 77.
FEATURES             Location/Qualifiers
     source           1..30
                     /organism="Vitis vinifera"
                     /mol_type="cDNA"
                     /db_xref="taxon:29760"
                     /clone="B3CS00RL006A08"
                     /dev_stage="ripening stage"
                     /clone_lib="Ripe Grape Skin Triplex2 Library"
                     /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
                     SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.9%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db      26  TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 852
AZ962183
LOCUS   2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
        Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
        Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dduun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0230 row: I column: 24
Seq primer: CACACAGAGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 30.
FEATURES             Location/Qualifiers
     source           1..30
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0230124"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptor DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of PWD42 (gil4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid RL. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptor mouse DNA was annealed to
                     adaptor vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

Query Match      0.9%; Score 26; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db      1  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 853
AM044314
LOCUS   AM044314 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE
AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
        Nikolaidou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
        Microarray analysis identifies genes preferentially expressed in
        the lung schistosomulum of Schistosoma mansoni
        Unpublished (2005)
JOURNAL

```


AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romeu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES Location/Qualifiers
source 1..29
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006G11"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25.8; DB 1; Length 29;
Best Local Similarity 93.1%; Pred. No. 5.8e+02;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
|||||||
Db 29 AAAAAAAAAAGGAAAAAAAAAAAAAAAAAAAA 1

RESULT 857
R59306/c
LOCUS R59306 32 bp mRNA linear EST 24-MAY-1995
DEFINITION YH6C10.81 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:37903 3', similar to gb:M29064 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEINS A2/B1 (HUMAN);, mRNA sequence.

ACCESSION R59306
VERSION R59306.1 GI:830001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchothelres; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 32)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marta, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: SP6
High quality sequence stop: 1.

FEATURES Location/Qualifiers
source 1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0048A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES Location/Qualifiers
source 1..32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
ACTGGAGAAATTCGCGCGCAGGAATTTTITTTTITTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.9%; Score 25.6; DB 1; Length 32;
Best Local Similarity 87.5%; Pred. No. 6.3e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
|||||
Db 32 TTCTAAGGAGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 858
AZ326012
LOCUS AZ326012 32 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0048A19R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0048A19 R, genomic survey sequence.

ACCESSION AZ326012
VERSION AZ326012.1 GI:10383271
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchothelres; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: A column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES Location/Qualifiers
source 1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0048A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"


```

Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAGAAA 32
|||||
RESULT 861
AZ434285
LOCUS   1M0220808R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0220808 R, genomic survey sequence.
ACCESSION
AZ434285
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 08
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0220808"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAGGAGAGAAA 32
|||||
RESULT 861
AZ434285
LOCUS   1M0220808R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0220808 R, genomic survey sequence.
ACCESSION
AZ434285
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 08
Seq primer: CACACAGGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0220808"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

```

Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27
|||||
RESULT 862
AZ458228
LOCUS   1M0262C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0262C12 F, genomic survey sequence.
ACCESSION
AZ458228
VERSION
KEYWORDS
SOURCE
GSS.
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0262 row: C column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0262C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.9%; Score 25.4; DB 1; Length 27;
Best Local Similarity 96.3%; Pred. No. 5.9e+02;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```



```

Db      1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 27
|||||
RESULT 863
AZ941721/c
LOCUS   AZ941721
DEFINITION 27021004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0201004 R, genomic survey sequence.
ACCESSION  AZ941721
VERSION     GSS.
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 27)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: 0 column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     1..27
         /organism="Mus musculus"
         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0201004"
         /sex="Female"
         /lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC2M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|9B|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
     Query Match      0.9%; Score 25.4; DB 1; Length 27;
     Best Local Similarity 96.3%; Pred. No. 5.9e+02;
     Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
|||||
RESULT 864
AZ970621/c
LOCUS   AZ970621
DEFINITION 2M0243N14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243N14 R, genomic survey sequence.
ACCESSION  AZ970621
VERSION     GSS.
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 27)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: N column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     1..27
         /organism="Mus musculus"
         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0243N14"
         /sex="Female"
         /lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC2M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|9B|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
     Query Match      0.9%; Score 25.4; DB 1; Length 27;
     Best Local Similarity 96.3%; Pred. No. 5.9e+02;
     Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

```

```

Db      27 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 127
|||||
RESULT 864
AZ970621/c
LOCUS   AZ970621
DEFINITION 2M0243N14R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0243N14 R, genomic survey sequence.
ACCESSION  AZ970621
VERSION     GSS.
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 27)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0243 row: N column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES             Location/Qualifiers
     1..27
         /organism="Mus musculus"
         /mol_type="genomic DNA"
         /strain="C57BL/6J"
         /db_xref="taxon:10090"
         /clone="UUGC2M0243N14"
         /sex="Female"
         /lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
         /clone_lib="Mouse 10kb plasmid UUGC2M library"
         /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G1|4732114|9B|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
     Query Match      0.9%; Score 25.4; DB 1; Length 27;
     Best Local Similarity 96.3%; Pred. No. 5.9e+02;
     Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735

```


and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 889549
 COMMENT
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21ml3
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:494737"
 /db_xref="taxon:9606"
 /clone="IMAGE:73072"
 /tissue_type="fetal spleen"
 /dev_stage="fetal"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Stratagene fetal spleen (#937205)"
 /notes="Organ: spleen; Vector: Bluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally.
 Oligo dr. Pooled spleens. Average insert size: 1.0 Kb;
 Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGG
 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

FEATURES source

1. .28
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0130K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 25.4; DB 1; Length 28;
 Best Local Similarity 92.9%; Pred. No. 6e+02;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2736
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAATNAAA 1

RESULT 868 AZ836072/c

LOCUS 28 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0130K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0130K08 R, genomic survey sequence.

ACCESSION AZ836072
 VERSION AZ836072.1 GI:13005980
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 28)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00
 Plate: 0130 row: K column: 08
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1. .28

FEATURES source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0130K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 25.4; DB 1; Length 28;
 Best Local Similarity 96.3%; Pred. No. 6e+02;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2735
 |||||
 Db 28 AAAAAAAAAAAAAAAAAAGAAAAA 2

RESULT 869 CF299716/c

LOCUS 30 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--03-N11, mRNA
 sequence.

ACCESSION CF299716
 VERSION CF299716.1 GI:33671477

KEYWORDS

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL COMMENT

Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 Location/Qualifiers
 1. .30
 /organism="Oryza sativa (japonica cultivar-group)"

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-N11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.9%; Score 25.2; DB 1; Length 30;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 30 AAAAGAGACAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 870
CZ919253
LOCUS
DEFINITION
4021012D11.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION
CZ919253
VERSION
CZ919253.1 GI:71939587
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 30)
Walbot.V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021012 row: D column: 11
Class: transposon-tagged.
FEATURES
Location/Qualifiers
1..30
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
unite. For more information on RescueMu, go to the web
site 'http://www.mutransposon.org/project/RescueMu/'. Grid
V was grown at University of Arizona in 2003. DNA was
extracted from leaf strips, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

Query Match
0.9%; Score 25.2; DB 1; Length 30;

```

```

Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 871
DX082113
LOCUS
DEFINITION
KBrB095E11R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB095E11, genomic survey
sequence.
ACCESSION
DX082113
VERSION
DX082113.1 GI:84776409
KEYWORDS
GSS.
SOURCE
Brassica rapa subsp. pekinensis
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 30)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
KBrB095E11
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Location/Qualifiers
1..30
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095E11"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match
0.9%; Score 25.2; DB 1; Length 30;
Best Local Similarity 90.0%; Pred. No. 6.4e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2701 TTTGTACTAAAAAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 TTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 30

RESULT 872
CZ918715/c
LOCUS
DEFINITION
4021010E09.2EL x1 4021 - RescueMu Grid V Zea mays genomic, genomic
survey sequence.
ACCESSION
CZ918715
VERSION
CZ918715.1 GI:71938523
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 31)

REFERENCE AUTHORS TITLE JOURNAL COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021010 row: E column: 09
Class: transposon-tagged.

FEATURES source

1..31
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 25.2; DB 1; Length 31;
Best Local Similarity 90.0%; Pred. No. 6.5e+02;
Matches 27; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2738
|||||
Db 31 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 873 CF291048/c LOCUS

DEFINITION
14ROOT--01-F05.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-F05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE AUTHORS

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE JOURNAL COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

FEATURES source

Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-F05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 874 CF291646/c

LOCUS
DEFINITION
14ROOT--02-C14.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--02-C14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE AUTHORS

1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

TITLE JOURNAL COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source

Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-C14"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
|||||

```

Db      25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 875
CF299288
LOCUS   25 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-E01, mRNA
sequence.
ACCESSION
CF299288
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db      1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 876
CF300333/c
LOCUS   25 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L02, mRNA
sequence.
ACCESSION
CF300333
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-E01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db      1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 876
CF300333/c
LOCUS   25 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-L02, mRNA
sequence.
ACCESSION
CF300333
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db      25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 877
CF316323/c
LOCUS   25 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION
HD--05-J05.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-J05, mRNA sequence.
ACCESSION
CF316323
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-J05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-L02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db      25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 877
CF316323/c
LOCUS   25 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION
HD--05-J05.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-J05, mRNA sequence.
ACCESSION
CF316323
VERSION 1
KEYWORDS
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-J05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 878
CF317714/c
LOCUS
DEFINITION
HD--07-103_g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
CF317714
HD--07-103, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-103"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-103"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 879
CF319073/c
LOCUS
DEFINITION
HD--09-H05_g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
CF319073
HD--09-H05, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-103"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```

ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--09-H05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
DB 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 880
CF330786/c
LOCUS
DEFINITION
NAC1--06-K11.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--06-K11, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

```

/cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="NACL--06-K11"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 881
 CN545505/c
 LOCUS
 DEFINITION EST 17449 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00GL005H06 3', mRNA sequence.
 CN545505
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 882
 CN546041/c
 LOCUS
 DEFINITION EST 17993 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00RL007G10 3', mRNA sequence.
 CN546041
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 883
 CN546397/c
 LOCUS
 DEFINITION EST 18350 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB016E10 3', mRNA sequence.
 CN546397
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

LOCUS
 DEFINITION EST 17993 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00RL007G10 3', mRNA sequence.
 CN546041
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 881
 CN545505/c
 LOCUS
 DEFINITION EST 17449 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00GL005H06 3', mRNA sequence.
 CN545505
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 882
 CN546041/c
 LOCUS
 DEFINITION EST 17993 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
 clone B3CS00RL007G10 3', mRNA sequence.
 CN546041
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 883
 CN546397/c
 LOCUS
 DEFINITION EST 18350 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS1XGB016E10 3', mRNA sequence.
 CN546397
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES

source Location/Qualifiers
 1. 25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS1XG8016E10"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 884

CN546477/c
 LOCUS
 DEFINITION
 EST 18621 Ripe Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS57RB007D09 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source Location/Qualifiers
 1. 25
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS57RB007D09"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS8TB008B03"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS8TB008B03"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS8TB008B03"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS8TB008B03"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 25

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="B3CS8TB008B03"

/dev_stage="veraison stage"

/clone_lib="Turning Grape Berry Lambda Triplex2 Library"

/note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db

RESULT 886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

QY

Db

RESULT 885

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

####

COMMENT

Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

FEATURES

source

1. .25
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /sex="Unknown"
 /tissue_type="Cardiac muscle"
 /dev_stages="3 month old normal canine"
 /lab_host="XL10 Gold"
 /clone_lib="Right Cardiac Ventricle (DOGEST6)"
 /note="Organ: Heart; Vector: pBluescript II SK; Site 1:
 EcoRI; Site 2: XhoI; Library constructed using pBluescript
 XR kit from Stratagene. Cloned cDNA was size selected
 between 1-3 Kb. Tissue supplied by Mark Haskins VMD, PhD,
 Pathology and Medical Genetics, School of Veterinary
 Medicine, University of Pennsylvania, 3800 Spruce Street,
 Philadelphia, PA 19104-6051"

Query Match

Best Local Similarity 0.9%; Score 25; DB 1; Length 25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 887

DR073093

LOCUS ik85h08.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.

ACCESSION

DR073093

VERSION DR073093.1 GI:67050943

KEYWORDS

EST.

SOURCE

Ginkgo biloba

Ginkgo biloba (maidenhair tree)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .25

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;

Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.

The library was size-fractionated to enrich for large

inserts."

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Query Match

0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 888

DR073104/c

LOCUS

ik86c01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION sequence.

ACCESSION

DR073104

VERSION

DR073104.1 GI:67050954

KEYWORDS

EST.

SOURCE

Ginkgo biloba

Ginkgo biloba (maidenhair tree)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .25

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;

Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.

The library was size-fractionated to enrich for large

inserts."

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Query Match

0.9%; Score 25; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733

Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 889

DR073105/c

LOCUS

ik86c07.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

DEFINITION sequence.

ACCESSION

DR073105

VERSION

DR073105.1 GI:67050956

KEYWORDS

EST.

SOURCE

Ginkgo biloba

Ginkgo biloba (maidenhair tree)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

Query Match

0.9%; Score 25; DB 1; Length 25;

COMMENT

Contact: W. Richard McCombie
Lita Anunberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES

```
Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

94

25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

```
Query Match          0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred.No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0078 row: I column: 24
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0078124"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 893
 AZ350777/c
 LOCUS
 DEFINITION
 1M0088A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0088A04 R, genomic survey sequence.
 ACCESSION
 AZ350777.1 GI:10430014
 VERSION
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0088 row: A column: 04
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0088A04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 894
 AZ389458
 LOCUS
 DEFINITION
 1M0150B06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0150B06 F, genomic survey sequence.
 ACCESSION
 AZ389458
 VERSION
 AZ389458.1 GI:10503166
 GSS.
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0150 row: B column: 06
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0150B06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 895
 AZ609234/c
 LOCUS 25 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0433H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0433H19 R, genomic survey sequence.
 ACCESSION AZ609234
 VERSION AZ609234.1 GI:11731424
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0433 row: H column: 19
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0433H19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 |||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 896
 AZ623157/c
 LOCUS 25 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0460L02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0460L02 R, genomic survey sequence.
 ACCESSION AZ623157
 VERSION AZ623157.1 GI:11745347
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0460 row: L column: 02
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

1. 25
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0460L02"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 897
 AZ788646/c
 LOCUS
 DEFINITION
 2M0035L19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035L19 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Ielam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
 University of Utah Genome Center

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0035 row: L column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.

FEATURES

1. 25
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0035L19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
 Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 898
 AZ949287
 LOCUS
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 25)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Ielam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
 University of Utah Genome Center

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0212 row: 0 column: 08
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source
 1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0212008"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.98; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 ||||||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 899
 AZ980407/c
 LOCUS AZ980407 25 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0257M19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0257M19 F, genomic survey sequence.

ACCESSION AZ980407
 VERSION AZ980407.1 GI:13851634
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0257 row: M column: 19
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source
 1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0257M19"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 25; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
 ||||||||||||||||||||||||||||
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 900
 CZ914066
 LOCUS CZ914066 25 bp DNA linear GSS 08-AUG-2005
 DEFINITION 4013005D04.2EL_Y1_4013 - RescueMu Grid 0 Zea mays genomic survey sequence.

ACCESSION CZ914066
 VERSION CZ914066.1 GI:71930467
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE 1 (bases 1 to 25)
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
 JOURNAL Contact: Walbot V
 COMMENT Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221

EMAIL: walbot@stanford.edu
 POSSIBLE ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.
 Plate: 4013005 row: D column: 04
 Class: transposon-tagged.

FEATURES
source

Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 25
|||||

RESULT 901
LOCUS

DEFINITION CZ918479 25 bp DNA linear GSS 08-AUG-2005
4021009F02.2EL x1 4021 - RescueMu Grid v Zea mays genomic, genomic survey sequence.

ACCESSION CZ918479
VERSION CZ918479.1 GI:71938052
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)

AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021009 row: F column: 02
Class: transposon-tagged.

FEATURES
source

Location/Qualifiers
1..25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid v"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon

designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid v was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||

Db 25 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 902
LOCUS

DEFINITION DUB29648 25 bp DNA linear GSS 22-DEC-2005
KBR5005E24F KBR5, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBR5005E24, genomic survey sequence.

ACCESSION DUB29648
VERSION DUB29648.1 GI:83866244
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis

ORGANISM

Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 25)

REFERENCE
AUTHORS

Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J. H. and Park,B.S.

TITLE
JOURNAL

COMMENT End sequence of Brassica rapa Sau3AI (KBR5) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team

National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBR5005E24
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBR5005E24"
/lab_host="E. coli DH10B"
/clone_lib="KBR5, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBR5 BAC) is available at NIAB."

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||

Db 25 AAAAAAAAAAAAAAAAAAAAAA 1
|||||


```

RESULT 903
DUB32111/c
LOCUS
DEFINITION
  KBR-S009K01R KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
  subsp. pekinensis genomic clone KBrS009K01, genomic survey
  sequence.
ACCESSION
  DUB32111
VERSION
  DUB32111.1 GI:83868707
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBR-S009K01
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
    1..25
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBR-S009K01"
      /lab_host="E. coli DH10B"
      /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
      ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
      available at NIAB."
  Query Match 0.9%; Score 25; DB 1; Length 25;
  Best Local Similarity 100.0%; Pred. No. 6e+02;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
  source
    QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
    Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 905
DUB34424/c
LOCUS
DEFINITION
  DUB34424 25 bp DNA linear GSS 22-DEC-2005
  KBR-S014E03R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrS014E03, genomic survey
  sequence.
ACCESSION
  DUB34424
VERSION
  DUB34424.1 GI:83871020
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBR-S014E03
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
    1..25
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"

FEATURES
  source
    QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2733
    Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 904
DUB34405/c
LOCUS
DEFINITION
  DUB34405 25 bp DNA linear GSS 22-DEC-2005
  KBR-S014D09F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
  subsp. pekinensis genomic clone KBrS014D09, genomic survey
  sequence.
ACCESSION
  DUB34405
VERSION
  DUB34405.1 GI:83871001
KEYWORDS
  GSS.
SOURCE
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 25)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J. H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBR-S014D09
  Seq primer: M13 Reverse
  Class: BAC ends.
  Location/Qualifiers
    1..25
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
  
```

```

/clone="KBrS014E03"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NTAB."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 906
DU834577
LOCUS
DEFINITION
KBrS014K15F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS014K15, genomic survey
sequence.
ACCESSION
DU834577
VERSION
DU834577.1 GI:83871173
KEYWORDS
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 25)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014K15
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS014K15"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NTAB."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 907
DX075967/c
LOCUS
DEFINITION
KBrS087B17F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB087B17, genomic survey
sequence.
ACCESSION
DX075967
VERSION
DX075967.1 GI:84770263
KEYWORDS
GSS.
SOURCE
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 25)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB087B17
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB087B17"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match      0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 908
TA324E10P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 324e10, forward sequence,
genomic survey sequence.
ACCESSION
AL493396
VERSION
AL493396.1 GI:11867761
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 25)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),

```

Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 Gurat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: melsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="324e10"

Query Match 0.9%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 909
AL038686 26 bp mRNA linear EST 06-JUL-2004
LOCUS DKF2P566J0546_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION DKF2P566J0546, mRNA sequence.
ACCESSION AL038686
VERSION AL038686.1 GI:49682186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 26)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2P566J0546"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pMPF1; Site_1: NotI; Site_2: SalI"

Query Match 0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 2 TAAAAAAAAAAAAAAAAAAAAA 26

RESULT 910
AL587774/c 26 bp mRNA linear EST 02-MAR-2001
LOCUS AL587774

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL587774 BP Chicken Brain Library Gallus gallus cDNA clone
ROS63A11, mRNA sequence.
AL587774
AL587774.1 GI:13192808

EST.
Gallus gallus (chicken)
Gallus gallus
Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianidae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 26)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTT TTT TTT TTT TTT TTT TTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13P.

FEATURES
source
Location/Qualifiers

1..26
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS63A11"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTT TTT TTT TTT TTT TTT TTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||
Db 26 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 911
AM048107

LOCUS AM048107 26 bp mRNA linear EST 20-SEP-2005
DEFINITION AM048107 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC22b02.glk, mRNA sequence.

ACCESSION AM048107
VERSION AM048107.1 GI:75967881
KEYWORDS EST.
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Dillon, G.P., Fellwell, T., Skelton, J.P., Ashton, P.D., Coulson, P.S., Nikolaïdou-Katsaridou, N., Quail, M.A., Wilson, R.A. and Ivens, A.C.
TITLE Microarray analysis identifies genes preferentially expressed in the lung schistosomulum of *Schistosoma mansoni*

JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
1..26

FEATURES
source
1..26

```

/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmiC22B02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 912
CN545723/c
LOCUS
DEFINITION
30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--07-G13, mRNA
sequence.
ACCESSION
CF296851
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaemggbio.com, bhnaem@bio.myongji.ac.kr.

FEATURES
source
1..26
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--07-G13"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 26 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 913
CN545723/c
LOCUS
DEFINITION
CN545723
EST 17667 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL005C03 3', mRNA sequence.
ACCESSION
CN545723

```

```

CN545723.1 GI:46910348
EST
SOURCE
Vitis vinifera
ORGANISM
Vitis vinifera
REFERENCE
1 (bases 1 to 26)
AUTHORS
Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
JOURNAL
Contact: Hamdi S.
COMMENT
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES
source
1..26
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL005C03"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1:
SfiI; Site 2: SfiI; Oriented library"

Query Match      0.9%; Score 25; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 914
AJ789548
LOCUS
DEFINITION
AJ789548 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
018.2.03.c14, mRNA sequence.
ACCESSION
AJ789548
KEYWORDS
VERSION
AJ789548.1 GI:51058064
SOURCE
EST.
ORGANISM
Antirrhinum majus (snapdragon)
Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.,
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of target Genes of the Class B MADS Box Gene
DEFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.

FEATURES
source
1..27
Location/Qualifiers

```

```

/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_2_03_c14"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

Query Match      0.9%; Score 25; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 915
TA244G08P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 244g08, forward sequence,
genomic survey sequence.
ACCESSION
AL483539
VERSION
AL483539.1 GI:11849040
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 31)
AUTHORS
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Melville S.B., Rajandream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project. Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..31
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="244g08"

Query Match      0.9%; Score 25; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 916
CZ469056/c
LOCUS
DEFINITION
C04188-5prime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
genomic survey sequence.
ACCESSION
CZ469056

/organism="Drosophila melanogaster (fruit fly)"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (GenBank accession number
AF151146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 37°C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped
to a chromosome by standard genetic methods, examined for
homologous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

Query Match      0.9%; Score 24.8; DB 1; Length 28;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2736
Db 28 AAAAAAAAAAAAAAAAAAATTTAAAAAAAAA 1

RESULT 917
AM042970
LOCUS
DEFINITION
AM042970 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC25dl1.q1k, mRNA sequence.
ACCESSION
AM042970
VERSION
AM042970.1 GI:75969635

CZ469056.1 GI:62963069
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 28)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,
Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,
Greer, K., Hartouni, S.R., Howie, B., Jakkula, L., Joo, D., Kilpack, K.,
Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,
Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,
Swimmer, C., Kopczyński, C., Duyk, G., Winberg, M.L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is unspecified in the 28 bases.
This insertion position refers to the first base of the 4 base TTAAG
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1..28
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (GenBank accession number
AF151146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 37°C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped
to a chromosome by standard genetic methods, examined for
homologous viability, and used for recovery of flanking
genomic sequence by inverse PCR."

```

```

KEYWORDS
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 26)
Dillon,G.P., Fellwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
TITLE Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
LOCATION/Qualifiers
1..26
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmiC25d11.q1k"
/dev_stages="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 918
CR546444
LOCUS DKFZp459P0513_r1 459 (synonym: pcorl) Pongo pygmaeus CDNA clone
DEFINITION DKFZp459P0513 5', mRNA sequence.
ACCESSION CR546444
VERSION CR546444.1 GI:49898669
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pongo.
REFERENCE 1 (bases 1 to 26)
AUTHORS Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
TITLE Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European
Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZp459P0513) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.
LOCATION/Qualifiers
1..26
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp459P0513"
/tissue_type="cortex"

FEATURES
source
1..26
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="459 (synonym: pcorl)"
/note="Vector: pSPori_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 919
AZ355083
LOCUS 1M0094D14R Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0094D14 R, genomic survey sequence.
ACCESSION AZ355083
VERSION AZ355083.1 GI:10467134
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 14
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 26.
LOCATION/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0094D14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and 14
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

```

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 920
AZ623156/c
LOCUS
DEFINITION
A2623156 26 bp DNA linear GSS 13-DEC-2000
1M0460L01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460L01 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 01
Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 26.

Location/Qualifiers

FEATURES
source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460L01"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||
Db 26 AAAAAAAAAAAAAAAAAATAAAAAAAAA 1

RESULT 921
AZ635695/c
LOCUS
DEFINITION
A2635695 26 bp DNA linear GSS 13-DEC-2000
1M0493G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0493G18 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: G column: 18
Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends
High quality sequence stop: 26.

Location/Qualifiers

FEATURES
source

1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0493G18"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||

Db 26 AAAAAAAAAAGAAAAAAAAAAAAAAAAA 1
|||||

RESULT 922
CZ917641/c
LOCUS
DEFINITION 26 bp DNA linear GSS 08-AUG-2005
survey sequence.
ACCESSION
VERSION CZ917641
KEYWORDS
SOURCE GSS.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 26)

REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021006 row: D column: 12
Class: transposon-tagged.

FEATURES
source
1..26
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||

Db 26 AAAAAAAAAAGAAAAAAAAAAAAAAAAA 1
|||||

RESULT 923
CZ919575/c

DEFINITION 26 bp DNA linear GSS 08-AUG-2005
survey sequence.
ACCESSION
VERSION CZ919575
KEYWORDS
SOURCE GSS.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 26)

REFERENCE
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4021013 row: G column: 11
Class: transposon-tagged.

FEATURES
source
1..26
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 6.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2734
|||||

Db 26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 924
AG201580/c
LOCUS
DEFINITION 26 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-084C22.T7, genomic survey
sequence.
ACCESSION
VERSION AG201580
KEYWORDS
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
AUTHORS

Hominidae; Pan.
1 Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of Library RP-43

REFERENCE
JOURNAL

2 (bases 1 to 26)

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission

TITLE
JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://pbs.grc.kribb.re.kr/
Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.

COMMENT

Sequencing: T7

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

FEATURES
source

Location/Qualifiers
1..26
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-084C22.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match

Best Local Similarity 0.9%; Score 24.4; DB 1; Length 26;

Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2734

Db

26 AAAAAAAAAAAGAAAAAAAAAAAAAAAAA 1

RESULT 925

DT471186

LOCUS

WS01212.BR.N05 PT-GT-FL-A-3 Populus trichocarpa cDNA clone

DEFINITION

DT471186 27 bp mRNA linear EST 29-AUG-2005

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

AUTHORS

1 (bases 1 to 27)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Bohlmann,J.

The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries

TITLE
JOURNAL

COMMENT

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114

FEATURES
source

Location/Qualifiers
1..27
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01212_N05"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-GT-FL-A-3"
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Young and
mature leaves, along with green stems, from 8 year old
trees harvested within the Boise Cascade region of
Washington state on May 15th, 2001. mRNA was isolated from
each tissue source independently and equal quantities of
mRNA from each tissue were then pooled. cDNA was prepared
from 20 micrograms of mRNA according to the full-length
cDNA library construction method described by Carninci P.
et al. (2000), Genome Research 10(10):1617-1630 and
directionally ligated into the pBluescript II SK (+) XR
vector digested with SstI (5' end) and XhoI (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (Invitrogen) for propagation."

Query Match

Best Local Similarity 0.9%; Score 24.4; DB 1; Length 27;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

2702 TTGTACTAAAAAAAAAAAAAAAAAAAAA 2728

Db

1 TTTTACNAAAAAAAAAAAAAAAAAAAAA 27

RESULT 926

N52529/c

LOCUS

DEFINITION

N52529 27 bp mRNA linear EST 15-FEB-1996
YV35a12.s1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone
IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

N52529.1 GI:1193695
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 27)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE
JOURNAL

COMMENT

The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward

High quality sequence stop: 1.
Location/Qualifiers
1..27


```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2734
Db 1 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 929
T52836/c
LOCUS
DEFINITION
T52836 28 bp mRNA linear EST 06-FEB-1995
IMAGE:68057 3' similar to gb:X53463 GLUTATHIONE
PROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
ACCESSION
T52836
VERSION
T52836.1 GI:654696
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 28)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevasakis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 51
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 51 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 1.
FEATURES
source
1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:504314"
/db_xref="taxon:9606"
/clone="IMAGE:68057"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGCG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

Query Match 0.9%; Score 24.4; DB 1; Length 28;
Best Local Similarity 96.2%; Pred. No. 6.9e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2734
Db 26 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 930
AZ481286/c
LOCUS
DEFINITION
AZ481286 28 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0303L24 F, genomic survey sequence.
ACCESSION
AZ481286
VERSION
AZ481286.1 GI:10642351
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 28)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0303 row: L column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
FEATURES
source
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0303L24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

RESULT 931
CF299155/c

```

LOCUS       CF299155                29 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--03-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
             sativa (japonica cultivar-group) cDNA clone 7LEAF--03-B02, mRNA
             sequence.
ACCESSION    CF299155
VERSION      CF299155
KEYWORDS     EST.
SOURCE       Oryza sativa (japonica cultivar-group)
             Oryza sativa (japonica cultivar-group)
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
             clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 29)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, Myongji University
             Yongin, Gyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..29
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /culturivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="7LEAF--03-B02"
                     /tissue_type="leaf"
                     /dev_stage="7 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAA 29 bp    DNA    linear    GSS 10-JUL-2004
      |||
      1 TTTTAAAAA 2731
      |||

RESULT 932
LOCUS       DR073498                29 bp    mRNA    linear    EST 08-JUN-2005
DEFINITION   ik80c04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
             sequence.
ACCESSION    DR073498
VERSION      DR073498
KEYWORDS     EST.
SOURCE       Ginkgo biloba (maidenhair tree)
             Ginkgo biloba
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
             1 (bases 1 to 29)
REFERENCE    Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
             O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W.,
             Benfey,P., Coruzzi,G. and Stevenson,D.
             Expressed tag sequences from Ginkgo female leaf (NYBG)
             Unpublished (2005)
AUTHORS      Contact: W. Richard McCombie
             Lita Annenberg Hazen Genome Sequencing Center
             Cold Spring Harbor Laboratory
             PO Box 100, Cold Spring Harbor, NY 11724, USA
             Tel: 516 367 8884
             Fax: 516 367 8874
             Email: mcombie@cshl.org

Query Match      0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAA 29 bp    DNA    linear    GSS 10-JUL-2004
      |||
      1 TTTTAAAAA 2731
      |||

RESULT 932
LOCUS       DR073498                29 bp    DNA    linear    GSS 10-JUL-2004
DEFINITION   PRI0160a.G06.2 - PRI0160a.BR (29) Mixed stage fosmid library of P.
             pacificus var. California Pristionchus pacificus genomic, genomic
             survey sequence.
ACCESSION    CL693162
VERSION      CL693162.1 GI:50215070
KEYWORDS     GSS.
SOURCE       Pristionchus pacificus
             Pristionchus pacificus
             Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
             Neodiplogasteridae; Pristionchus.
             1 (bases 1 to 29)
REFERENCE    Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
             AppaDB: an AcedB database for the nematode satellite organism
             Pristionchus pacificus
             Nucleic Acids Res. 32 (1), D421-D422 (2004)
             14681447
AUTHORS      Contact: Sommer RJ
             Evolutionary Biology
             Max-Planck-Institute for Developmental Biology
             Spemannstr. 37-39, Tuebingen D-72076, Germany
             Tel: 00497071601371
             Fax: 00497071601498
             Email: ralf.sommer@tuebingen.mpg.de
             This library was generated at Caltech, Pasadena, USA and end
             sequenced at Vancouver, Canada.
             Seq primer: 17
             Class: fosmid ends.
             Location/Qualifiers
     source           1..29
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pBpifos-5 Fosmid vector"

Query Match      0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAA 2737
      |||
      1 AAAAAA 29
      |||

```

```

Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
             Location/Qualifiers
     source           1..29
                     /organism="Ginkgo biloba"
                     /mol_type="mRNA"
                     /db_xref="taxon:3311"
                     /sex="female"
                     /clone_lib="Ginkgo female leaf (NYBG)"
                     /note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
                     Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
                     The library was size-fractionated to enrich for large
                     inserts."

Query Match      0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2700 GTTTGTACTAAAAA 2728
      |||
      1 GTTTGTAAGAAAAA 29
      |||

```

```

RESULT 933
LOCUS       CL693162                29 bp    DNA    linear    GSS 10-JUL-2004
DEFINITION   PRI0160a.G06.2 - PRI0160a.BR (29) Mixed stage fosmid library of P.
             pacificus var. California Pristionchus pacificus genomic, genomic
             survey sequence.
ACCESSION    CL693162
VERSION      CL693162.1 GI:50215070
KEYWORDS     GSS.
SOURCE       Pristionchus pacificus
             Pristionchus pacificus
             Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
             Neodiplogasteridae; Pristionchus.
             1 (bases 1 to 29)
REFERENCE    Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
             AppaDB: an AcedB database for the nematode satellite organism
             Pristionchus pacificus
             Nucleic Acids Res. 32 (1), D421-D422 (2004)
             14681447
AUTHORS      Contact: Sommer RJ
             Evolutionary Biology
             Max-Planck-Institute for Developmental Biology
             Spemannstr. 37-39, Tuebingen D-72076, Germany
             Tel: 00497071601371
             Fax: 00497071601498
             Email: ralf.sommer@tuebingen.mpg.de
             This library was generated at Caltech, Pasadena, USA and end
             sequenced at Vancouver, Canada.
             Seq primer: 17
             Class: fosmid ends.
             Location/Qualifiers
     source           1..29
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pBpifos-5 Fosmid vector"

Query Match      0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2709 AAAAAA 2737
      |||
      1 AAAAAA 29
      |||

```

```

RESULT 934
TA378G07P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 378g07, forward sequence,
genomic survey sequence.
ACCESSION
AL497621
VERSION
AL497621.1 GI:11873343
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 29)
AUTHORS
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Melville S.B., Rajandream M.A. and Barrell B.G.
DIRECT SUBMISSION
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="378g07"

Query Match 0.9%; Score 24.2; DB 1; Length 29;
Best Local Similarity 89.7%; Pred. No. 7.2e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2702 TTGCTACTAAAAA 2730
|||
29 TTTTAAAAA 1

RESULT 935
AJ921827
LOCUS
DEFINITION
AJ921827 Theileria annulata piroplasm Theileria annulata CDNA clone
TAC20g08_pika, mRNA sequence.
ACCESSION
AJ921827
VERSION
AJ921827.1 GI:67492152
KEYWORDS
EST.
SOURCE
Theileria annulata
ORGANISM
Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
Theileria.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
Kerhornou A., Aslett M., Bishop R., Bouchier C., Cochet M.,
Coulson R.M.R., Cronin A., de Villiers E., Fraser A., Fosker N.,
Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Katzer F.,
Larke N., Lord A., Maser P., McKellar S., Mooney P., Morton F.,
Nene V., O'Neill S., Price C., Quail M.A., Rabinowitsch E.,
Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T.,
Squares R., Squares S., Tivey A., Walker A.R., Woodward J.,
Dobbelare D.A.E., Langsley G., Rajandream M.-A., McKeever D.,
Shiels B., Tait A., Barrell B. and Hall N.

```

```

TITLE
The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
JOURNAL
Unpublished (2005)
COMMENT
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
FEATURES
Location/Qualifiers
source
1..24
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="TAC20g08_pika"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/clone="country: Turkey:Ankara"
/note="country: Turkey:Ankara"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA 2732
|||
1 AAAAAA 24

RESULT 936
AM043978
LOCUS
DEFINITION
AM043978 Schistosoma mansoni lung schistosomulum Schistosoma
mansoni cDNA clone SmlC20c02.q1k, mRNA sequence.
ACCESSION
AM043978
VERSION
AM043978.1 GI:72292377
KEYWORDS
EST.
SOURCE
Schistosoma mansoni
ORGANISM
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Dillon G.P., Feltwell T., Skelton J.P., Ashton P.D., Coulson P.S.,
Nikolaïdou-Katsaridou N., Quail M.A., Wilson R.A. and Ivens A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)
JOURNAL
Contact: Ivens AC
COMMENT
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.
Location/Qualifiers
source
1..24
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC20c02.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/clone="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA 2732
|||
1 AAAAAA 24

RESULT 937
AM045511

```

LOCUS AM045511 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM045511 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC18g01.q1k, mRNA sequence.

ACCESSION AM045511
 VERSION AM045511.1 GI:75968795
 KEYWORDS EST.

SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 24)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC18g01.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 938

AM046329

LOCUS AM046329 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM046329 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC20a08.q1k, mRNA sequence.

ACCESSION AM046329
 VERSION AM046329.1 GI:75970408
 KEYWORDS EST.

SOURCE Schistosoma mansoni
 ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 24)

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
 TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC20a08.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 939

AM048042/c

LOCUS AM048042 24 bp mRNA linear EST 20-SEP-2005
 DEFINITION AM048042 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC18f02.q1k, mRNA sequence.

ACCESSION AM048042

VERSION AM048042.1 GI:75967816

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
 Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

TITLE Microarray analysis identifies genes preferentially expressed in
 the lung schistosomulum of Schistosoma mansoni

JOURNAL Unpublished (2005)

COMMENT Contact: Ivens AC
 Pathogen Microarrays Group
 Wellcome Trust Sanger Institute
 Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
 source 1..24
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SmlC18f02.q1k"
 /dev_stage="lung schistosomulum"
 /clone_lib="Schistosoma mansoni lung schistosomulum"
 /note="country: Puerto Rico"

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 940

BG670391

LOCUS BG670391 24 bp mRNA linear EST 30-APR-2001
 DEFINITION DRNBAF06 Rat DRG Library Rattus norvegicus cDNA clone DRNBAF06 5',
 mRNA sequence.

ACCESSION BG670391

VERSION BG670391.1 GI:13892490

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,
 Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,
 Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

TITLE Identification of gene expression profile of dorsal root ganglion
 in the rat peripheral axotomy model of neuropathic pain

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

PUBMED 12060780

COMMENT Contact: Zhang Xu

Laboratory of Sensory System

Institute of Neuroscience

320 Yue Yang Road, Shanghai 200031, P.R.China

```

Tel: 86-21-64748700-121
Fax: 86-21-64713446
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
PCR Primers
FORWARD: T3
BACKWARD: T7
Seq primer: T3
POLYA=No.
Location/Qualifiers
1. .24
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNBAF06"
/sex="male"
/tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 941
BX554611/c
LOCUS
DEFINITION
BX554611 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse16d06_pic, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, W.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL
PUBMED
14519198
Genome Biol. 4 (10), R63 (2003)
COMMENT
Contact: Hall N
The Sanger Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
Location/Qualifiers
1. .24
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse16d06_pic"

FEATURES
source

```

```

/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 942
CF276855
LOCUS
DEFINITION
CF276855 24 bp mRNA linear EST 14-AUG-2003
Oryza sativa Japonica cultivar-group) cDNA clone 14ETL--02-C19,
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa Japonica cultivar-group)
Oryza sativa Japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .24
/organism="Oryza sativa Japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--02-C19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 943
CF301561/c
LOCUS
DEFINITION
CF301561 24 bp mRNA linear EST 15-AUG-2003
7LEAF--06-H15 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa Japonica cultivar-group) cDNA clone 7LEAF--06-H15, mRNA
sequence.
ACCESSION

```


RESULT 946	CN545307	24 bp	mRNA	linear	EST 30-APR-2004
LOCUS	EST 17251	Green Grape Skin Triplex2 Library	Vitis vinifera	CDNA	
DEFINITION	Clone B3CS00GL006E12 3', mRNA sequence.				
ACCESSION	CN545307				
VERSION	CN545307.1	GI:46909932			
KEYWORDS	EST.				
SOURCE	Vitis vinifera				
ORGANISM	Vitis vinifera				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.				
AUTHORS	1 (bases 1 to 24)				
	Abbal,P., Agasse,A., Ageorges,A., Atanasova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.				
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Hamdi S.				
	UMR 619 - Equipe Biologie de la Vigne				
	Universite de Bordeaux I, Institut National de la Recherche Agronomique				
	71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France				
	Tel: 00-33-(0)5-57-12-25-50				
	Fax: 00-33-(0)5-57-12-25-48				
	Email: s.hamdi@bordeaux.inra.fr				
	Seq primer: T7.				

```

FEATURES
source
seq primer: 171
Location/Qualifiers
1. .24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL006E12"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site 1:
SfiIA; Site 2: SfiIB; Oriented library"

```

Query Match	0.9%	Score 24;	DB 1;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 6.8e+02;		
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

	Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2732
	Dd	24	AAAAAAAAAAAAAAAAAAAAA	1

RESULT	947	CN545657	24 bp	mRNA	linear	EST 30-APR-2004
CN545657/c		EST 17601	Ripe Grape Skin	Triplex2 Library	<i>Vitis vinifera</i>	cDNA
LOCUS		clone B3CS00RL004E09	3'	mRNA sequence.		
DEFINITION						

VERSION	CNS45657.1	GI:46910282
KEYWORDS	EST.	
SOURCE	<i>Vitis vinifera</i>	
ORGANISM	<i>Vitis vinifera</i>	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.	
REFERENCE	1 (bases 1 to 24)	
AUTHORS	Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glisseant, D., Grimpiet, J., Hamdi, S., Romieu, C. and Terrier, N.	
TITLE	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages	
JOURNAL	Unpublished (2002)	
COMMENT	Contact: Hamdi S.	

UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seg primer: T7.

```

FEATURES
source
seq primer: 17:
Location/Qualifiers
1. .24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL004E09"
/dev_stage="ripening stage"
/clone_lfb="Ripe Grape Skin Triple2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site 2: SfiIB; Oriented library"

```

Query Match	0.9%	Score 24;	DB 1;	Length 24;
Best Local Similarity	100.0%;	Pred. No. 6.8e+02;		
Matches 24;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;

Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2732
Db	24	AAAAAAAAAAAAAAAAAAAAA	1

RESULT	948
CN545784/c	
LOCUS	
DEFINITION	CN545784 24 bp mRNA linear EST 30-APR-2004 EST 17728 ripe Grape Skin Triplex2 Library Vitis vinifera cDNA clone B3CS00RL005H06 3', mRNA sequence.
ACCESSION	CN545784
VERSION	CN545784.1 GI:46910409
KEYWORDS	EST.
SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera

REFERENCE AUTHORS	TITLE
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romeu, C. and Terrier, N.	Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
	Unpublished (2002)
	Contact: Hamdi S.

UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, Bp 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr

```

FEATURES
source
key primer: Location/Qualifiers
1..24
    /organism="Vitis vinifera"
    /mol_type="mRNA"
    /cultivar="Cabernet Sauvignon"
    /db_xref="taxon:29760"
    /clone="B3CS00RL005H06"
    /dev_stage="ripening stage"
    /clone_lib="Ripe Grape Skin Triplex2 Library"
    /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
    SfiA; Site_2: SfiTB; Oriented library"

```

Query Match 0.9%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 949
CN546689/c
LOCUS
DEFINITION EST 18460 Turning Grape Berry Lambda Triplex2 Library Vitis
vinifera cDNA clone B3C537B007F12 3', mRNA sequence.
ACCESSION CN546689.1 GI:46911314
VERSION
KEYWORDS
SOURCE
ORGANISM Vitis vinifera

REFERENCE
AUTHORS Abbal,P., Agasse,A., Agorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Handi,S., Ronieu,C. and Terrier,N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)
CONTACT: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

TITLE
JOURNAL
COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 24)
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

FEATURES
source
1. .24
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3C537B007F12"
/dev_stage="veraison stage"
/clone_lib="Turning Grape Berry Lambda Triplex2 Library"
/note="Organ: Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 950
DR073080/c
LOCUS
DEFINITION ik85902.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073080.1 GI:67050929
VERSION
KEYWORDS
SOURCE
ORGANISM Ginkgo biloba (maidenhair tree)

REFERENCE
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 24)
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1. .24
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

FEATURES
source
1. .24

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 951
DR074082/c
LOCUS
DEFINITION ik95a04.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074082.1 GI:67052028
VERSION
KEYWORDS
SOURCE
ORGANISM Ginkgo biloba (maidenhair tree)

REFERENCE
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1. .24
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

FEATURES
source
1. .24

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

FEATURES
source
1. .24

RESULT 950
DR073080/c
LOCUS
DEFINITION ik85902.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073080.1 GI:67050929
VERSION
KEYWORDS
SOURCE
ORGANISM Ginkgo biloba (maidenhair tree)

REFERENCE
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 24)
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 952

AZ328848

LOCUS

DEFINITION 24 bp DNA linear GSS 29-SEP-2000
 clone UUGC1M0052M17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ328848

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0052 row: M column: 17
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.

Location/Qualifiers
 1..24

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0052M17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 953

AZ363562

LOCUS

DEFINITION 24 bp DNA linear GSS 02-OCT-2000
 clone UUGC1M0109G10 F, genomic survey sequence.

ACCESSION

AZ363562

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: G column: 10
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

Location/Qualifiers
 1..24

source

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0109G10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

```

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 954
AZ386491 24 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0145D02 R, genomic survey sequence.
ACCESSION AZ386491
VERSION AZ386491.1 GI:10500191
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: D column: 02
Seq primer: CACACGAGNACGTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

```

```

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 955
AZ390642 24 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0152H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0152H07 F, genomic survey sequence.
ACCESSION AZ390642
VERSION AZ390642.1 GI:10505685
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: H column: 07
Seq primer: CGTGTAAAGCAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0152H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0152H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;

```

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 956
 AZ459280/c
 LOCUS
 DEFINITION 24 bp DNA linear GSS 04-OCT-2000
 1M0264A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0264A05 F, genomic survey sequence.

ACCESSION AZ459280
 VERSION A2459280.1 GI:10617405
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (Bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0264 row: A column: 05
 Seq primer: CGTTGTAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0264A05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 957
 AZ644621/c
 LOCUS
 DEFINITION 24 bp DNA linear GSS 14-DEC-2000
 1M0508F12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0508F12 R, genomic survey sequence.

ACCESSION AZ644621
 VERSION AZ644621.1 GI:11773331
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (Bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0508 row: F column: 12
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES
 source
 1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0508F12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 958
 A2834990
 LOCUS
 DEFINITION 2M0129A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0129A05 F, genomic survey sequence.
 ACCESSION A2834990
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0129 row: A column: 05
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

1. 24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0129A05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 959
 A2970038
 LOCUS
 DEFINITION 2M0243J02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0243J02 F, genomic survey sequence.
 ACCESSION A2970038
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0243 row: J column: 02
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers

FEATURES

1. 24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0243J02"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 960

AZ984490

LOCUS 24 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0266H05F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0266H05 F, genomic survey sequence.

ACCESSION AZ984490

VERSION AZ984490.1 GI:13855717

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0266 row: H column: 05

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0266H05"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.9%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 961

AZ993423/c

LOCUS 24 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0278019F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0278019 F, genomic survey sequence.

ACCESSION AZ993423

VERSION AZ993423.1 GI:13864650

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0278 row: O column: 19

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1..24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0278019"
 /sex="Female"
 /lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.9%; Score 24; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

```

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 962
DU829467/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS004P08, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 24)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone
KBrS004P08
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS004P08"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 963
DU830197/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS006E20, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 24)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone
KBrS049J13
Seq primer: T7
Class: BAC ends.

```

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 24)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006E20
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS006E20"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 964
DX047568/c
LOCUS
DEFINITION
subsp. pekinensis genomic clone KBrS049J13, genomic survey
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 24)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS049J13
Seq primer: T7
Class: BAC ends.

```


FEATURES		Location/Qualifiers	
source	1. .24	/organism="Brassica rapa subsp. pekinensis" /mol_type="genomic DNA" /cultivar="Chiifu" /sub_species="pekinensis" /db_xref="taxon:51351" /clone="KBrB049J13" /lab_host="E.coli DH10B" /note=vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa spp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."	
Query Match		0.9%	Score 24; DB 1; Length 24;
Best Local Similarity		100.0%	Pred. No. 6.8e+02;
Matches	24; Conservative	0; Mismatches	0; Indels
		0; Gaps	0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732	
Db	24	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1	
RESULT 965			
DX049347/c			
LOCUS			
DEFINITION			
DX049347 24 bp DNA linear GSS 10-JAN-2006 KBrB051P01f KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB051P01, genomic survey sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Brassica rapa subsp. pekinensis Brassica rapa subsp. pekinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
REFERENCE			
AUTHORS			
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S. End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005) Contact: Beom-Seok Park Brassica Genomics Team National Institute of Agricultural Biotechnology 225 Seodun-Dong, Suwon, 441-707, Korea Tel: +82-31-299-1670 Fax: +82-31-299-1672 Email: pbeom@da.go.kr BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone KBrB051P01			
Seq primer: T7			
Class: BAC ends.			
FEATURES		Location/Qualifiers	
source	1. .24	/organism="Brassica rapa subsp. pekinensis" /mol_type="genomic DNA" /cultivar="Chiifu" /sub_species="pekinensis" /db_xref="taxon:51351" /clone="KBrB051P01" /lab_host="E.coli DH10B" /clone_lib="KBrB, Brassica rapa BamHI BAC library" /note=vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa spp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."	
Query Match		0.9%	Score 24; DB 1; Length 24;
Best Local Similarity		100.0%	Pred. No. 6.8e+02;
Matches	24; Conservative	0; Mismatches	0; Indels
		0; Gaps	0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 2732	

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB081p14

Seq primer: T7
Class: BAC ends.

FEATURES source

```

1. .24
/organism="Brassica rapa subsp. pekinensis"
/cultivar="Chiifu"
/mol_type="genomic DNA"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081p14"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 968
DX080492 24 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB093A19R KBrB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrB093A19, genomic survey
sequence.

ACCESSION DX080492
VERSION DX080492.1 GI:84774788
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 24)

REFERENCE Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
AUTHORS Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB093A19

Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .24
/organism="Brassica rapa subsp. pekinensis"

FEATURES source

```

1. .24
/organism="Brassica rapa subsp. pekinensis"
```

```

/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB093A19"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 969
DX082296/c 24 bp DNA linear GSS 10-JAN-2006
LOCUS KBrB095I16F KBrB, Brassica rapa BamHI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrB095I16, genomic survey
sequence.

ACCESSION DX082296
VERSION DX082296.1 GI:84776592
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 24)
REFERENCE Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
AUTHORS Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB095I16

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095I16"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

FEATURES source

```

1. .24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095I16"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 970
TA169D12P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 169d12, forward sequence,
genomic survey sequence.
ACCESSION
AL478922
VERSION
AL478922.1 GI:11840452
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
1. .24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="169d12"

REFERENCE
1 (bases 1 to 24)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1. .24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="169d12"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 971
TA27B08Q
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 27b08, reverse sequence,
genomic survey sequence.
ACCESSION
AL453584
VERSION
AL453584.1 GI:11850982
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
1. (bases 1 to 24)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),

```

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

```

1. .24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="27b08"

```

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 972

TA354C06P

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 354c06, forward sequence,

genomic survey sequence.

ACCESSION

AL494439

VERSION

AL494439.1 GI:11870896

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

REFERENCE

1 (bases 1 to 24)

AUTHORS

Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,

Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE

Direct Submission

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

```

1. .24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="354c06"

```

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 973
LOCUS TA371F11P 24 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 371f11, forward sequence,
genomic survey sequence.
ACCESSION AL495622
VERSION AL495622.1 GI:11871906
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
location/Qualifiers
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="371f11"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 975
LOCUS AL587648/c 25 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587648 BP Chicken Brain Library Gallus gallus cdna clone
ROS060C07, mRNA sequence.
ACCESSION AL587648
VERSION AL587648.1 GI:13192682
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoeauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
location/Qualifiers
1..25
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060C07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_hosts="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="vector: pSPORT1; Site1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 974
LOCUS TA95B08P 24 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 95b08, forward sequence,
genomic survey sequence.
ACCESSION AL459003
VERSION AL459003.1 GI:11861374
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajadream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

```

```

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
location/Qualifiers
1..24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="95b08"

Query Match 0.9%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 24

RESULT 975
LOCUS AL587648/c 25 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587648 BP Chicken Brain Library Gallus gallus cdna clone
ROS060C07, mRNA sequence.
ACCESSION AL587648
VERSION AL587648.1 GI:13192682
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archoeauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 25)
AUTHORS Murray,F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
location/Qualifiers
1..25
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS060C07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_hosts="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="vector: pSPORT1; Site1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from

```

```

Clonetechn (*6854-1)"

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 976
CF317007/c
LOCUS
DEFINITION
HD--06-114-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-114, mRNA sequence.
CF317007
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
Clade; Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 977
CF638767
LOCUS
DEFINITION
D06_G05 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
CF638767
ACCESSION
VERSION
KEYWORDS
SOURCE
Ustilago maydis

Clonetechn (*6854-1)"

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 976
CF317007/c
LOCUS
DEFINITION
HD--06-114-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-114, mRNA sequence.
CF317007
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BAP
Clade; Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 25 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 978
N33150/c
LOCUS
DEFINITION
YV06G01.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone
IMAGE:270480 3' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE
(HUMAN);, mRNA sequence.
N33150
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 25)
Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marr,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

ORGANISM
Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE
1 (bases 1 to 25)
Nugent,K.G., Choffe,K. and Saville,B.J.
Gene expression during Ustilago maydis diploid filamentous growth:
EST library creation and analyses
Fungal Genet. Biol. 41 (3), 349-360 (2004)
14761795
COMMENT
Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-006-UTM row: 05 column: G
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"
/notes="Vector: pSPORT; mRNA was extracted from diploid
mycelia. A cDNA library was constructed and
unidirectionally cloned into pSPORT plasmid, with the use
of the Superscript II cDNA Library Construction Kit."

Query Match      0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 978
N33150/c
LOCUS
DEFINITION
YV06G01.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone
IMAGE:270480 3' similar to gb:D29805 N-ACETYLACTOSAMINE SYNTHASE
(HUMAN);, mRNA sequence.
N33150
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 25)
Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marr,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

```

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880122"
/db_xref="taxon:9606"
/clone="IMAGE:270480"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NBHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTCGAGCGCGCGACGTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaído. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match 0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 25 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 979

AZ381039
LOCUS
DEFINITION
1M0137N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0137N18 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0137 row: N column: 18
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1..25
/organism="Mus musculus"

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0137N18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GII4732114]gb[AP129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.9%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 980

CF639306
LOCUS
DEFINITION
D14_A02 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Ustilago maydis
Ustilago maydis
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
REFERENCE
1 (bases 1 to 26)
Nugent,K.G., Choffe,K. and Saville,B.J.
TITLE
Gene expression during Ustilago maydis diploid filamentous growth: EST library creation and analyses
JOURNAL
PUBMED
Fungal Genet. Biol. 41 (3), 349-360 (2004)
14761795
COMMENT
Contact: Barry J. Saville
Saville Lab
University of Toronto
3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada
Tel: 905 569 4702
Fax: 905 828 3792
Email: bsaville@utoronto.ca
Plate: UTM-UM-D126/7-014-UTM row: 02 column: A
Seq primer: T7 Reverse (5' GAGTAATACGACTCACTATAGG 3')
High quality sequence stop: 26.
Location/Qualifiers
1..26
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"

FEATURES

source
1..26
/organism="Ustilago maydis"
/mol_type="mRNA"
/strain="FBD12"
/db_xref="taxon:5270"
/cell_type="Mycelia"
/dev_stage="Filamentous diploid"
/clone_lib="Filamentous Forced Diploid"


```

Query Match          0.9%; Score 24; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
    |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 983
CF299084/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P02, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--08-B07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match          0.9%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 7.4e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2735
    |||||
Db 1 AAAAAAAAAACCAAAAAAAAAAAAAA 27

RESULT 985
R59382/c
LOCUS
DEFINITION
Yh17e07.g1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:37726 3' similar to gb:M65131 METHYLMALONYL-COA MUTASE
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 27)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfs,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality

Query Match          0.9%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 7.4e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2735
    |||||
Db 27 AAACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 984
CF318113
LOCUS
DEFINITION
HD--08-B07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--08-B07, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

```


Possible reversed clone: polyT not found

Seq primer: SP6

High quality sequence stop: 1.

FEATURES

source

```
1. .27
  /location/Qualifiers
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="GDB:410267"
  /db_xref="taxon:9606"
  /clone="IMAGE:37726"
  /sex="female"
  /dev_stage="73 days post natal"
  /lab_host="DH108 (ampicillin resistant)"
  /clone_lib="Soares infant brain INIB"
  /notes="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
  I; Site_2: Hind III; 1st strand cDNA was primed with a Not
  I - oligo(dT) primer [5',
  AACTGGAAGATTTCGGCGCGCAGGAATTTTCTTTTCTTTT 3'];
  double-stranded cDNA was ligated to Hind III adaptors
  (Pharmacia), digested with Not I and directionally cloned
  into the Not I and Hind III sites of the Lfamid BA vector.
  Library went through one round of normalization. Library
  constructed by Bento Soares and M.Fatima Bonaldo."
```

Query Match 0.9%; Score 23.8; DB 1; Length 27;
Best Local Similarity 92.6%; Pred. No. 7.4e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2707 CTAAGAAAAA 2733

Db 27 CTTGAAAAA 1

RESULT 986

LOCUS

DEFINITION CZ914142 28 bp DNA linear GSS 08-AUG-2005
4013005F10.2EL_xl 4013 - RescueMu Grid O Zea mays genomic, genomic
survey sequence.

ACCESSION CZ914142

VERSION CZ914142.1 GI:71930586

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 28)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)

COMMENT

Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4013005 row: F column: 10
Class: transposon-tagged.

FEATURES

source

```
1. .28
  /location/Qualifiers
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /cultivar="mixed background w23/A188/B73/K55"
  /db_xref="taxon:4577"
  /tissue_type="leaf"
  /dev_stage="adult"
  /lab_host="DH108"
  /clone_lib="4013 - RescueMu Grid O"
  /note="Organ: leaf; Vector: RescueMu (engineered from
  pBluescript backbone); Site_1: BamHI; Site_2: BglII;
```

RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH108 cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.8%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 2735

Db 1 AAAAAA 27

RESULT 987

LOCUS DX071727/c

DEFINITION DX071727 28 bp DNA linear GSS 10-JAN-2006

LOCUS KBr0801124F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBr0801124, genomic survey
sequence.

ACCESSION DX071727

VERSION DX071727.1 GI:84766023

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)

COMMENT

Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBr0801124
Seq primer: T7
Class: BAC ends.

FEATURES

source

```
1. .28
  /location/Qualifiers
  /organism="Brassica rapa subsp. pekinensis"
  /mol_type="genomic DNA"
  /cultivar="Chiifu"
  /sub_species="pekinensis"
  /db_xref="taxon:51351"
  /clone="KBr0801124"
  /lab_host="E.coli DH108"
  /clone_lib="KBrB, Brassica rapa BamHI BAC library"
  /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
  pekinensis var. Chiifu BAC library (KBrB BAC) is provided
  by Yong-Pyo Lim (CNU)."
```

Query Match 0.9%; Score 23.8; DB 1; Length 28;
Best Local Similarity 92.6%; Pred. No. 7.5e+02;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 2735

Db 28 AAAAAA 2


```

TITLE
JOURNAL
COMMENT
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS013P19
Seq primer: T7
Class: BAC ends
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013P19"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: PCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chilfu BAC library (KBrS BAC) is
available at NIAH."

Query Match
Best Local Similarity 0.9%; Score 23.4; DB 1; Length 25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 991
CF299646/c
LOCUS
DEFINITION
26 bp mRNA linear EST 15-AUG-2003
7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L24, mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BIP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-L24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

FEATURES
source
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013P19"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: PCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chilfu BAC library (KBrS BAC) is
available at NIAH."

Query Match
Best Local Similarity 0.9%; Score 23.4; DB 1; Length 26;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 25 ATTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 992
AZ316353
LOCUS
DEFINITION
26 bp DNA linear GSS 29-SEP-2000
1M0034D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0034D09 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: D column: 09
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0034D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to

```

RESULT 994	AU257468/c	AU257468	28 bp	mRNA	linear	EST 25-APR-2002
LOCUS	AU257468/3'	AU257468	3'-directed mouse	CDNA library	Mus musculus	
DEFINITION	BD0010669	3'	mRNA sequence.			
ACCESSION	AU257468					
VERSION	AU257468.1	GI:20322117				
KEYWORDS	EST.					

```

direction
Seq primer: -21m13UnivRev.
FEATURES
    Location/Qualifiers
        1..29
            /organism="Ginkgo biloba"
            /mol_type="mRNA"
            /db_xref="taxon:3311"
            /sex="Female"
            /clone_lib="Ginkgo megasporophyll (NYBG)"
            /note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
            xho1; Site2: Eco RI; Stragene ZAP Express cDNA
            Synthesis Kit. The library was size-fractionated to enrich

```

REFERENCE 1 (bases 1 to 29)

NATIONAL HUMAN GENOME RESEARCH INSTITUTE
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA

```

Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
Seq primer: M13 Forward.
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTBCael6e07"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site 1: EcoRI; Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR)."

Query Match
Best Local Similarity 0.8%; Score 23.2; DB 1; Length 28;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2704 GTACTAAAAA 2731
Db 28 GCACGAGAAAAA 1

RESULT 999
CF314795/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzoae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .29
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--03-H09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAD1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match
Best Local Similarity 0.8%; Score 23.2; DB 1; Length 29;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
Seq primer: M13 Forward.
Location/Qualifiers
1. .28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTBCael6e07"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site 1: EcoRI; Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR)."

Query Match
Best Local Similarity 89.3%; Pred. No. 8.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2702 TTGTACTAAAAA 2729
Db 29 TTTTAAAAA 2

RESULT 1000
DR074680/c
LOCUS
DEFINITION
ik98h02.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR074680
EST.
VERSION
DR074680.1 GI:67052674
KEYWORDS
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 29)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballia,V., Martensen,R.A., McCombie,R.W.,
Bentley,P., Coruzzi,G. and Stevenson,D.
O'Shaughnessy,A.L., Ballia,V., Martensen,R.A., McCombie,R.W.,
Bentley,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction.
Seq primer: -21M13UnivRev.
Location/Qualifiers
1. .29
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."

Query Match
Best Local Similarity 89.3%; Pred. No. 8.2e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2701 TTGTACTAAAAA 2728
Db 28 TTTTAAAAA 1

RESULT 1001
AZ827060/c
LOCUS
DEFINITION
AZ827060 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0103F17 F, genomic survey sequence.
ACCESSION
AZ827060.1 GI:12996968
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

```


SmaI: Single pass sequencing. Normalised library constructed from bovine ovary."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1004

AJ747297 23 bp mRNA linear EST 07-JUL-2004
LOCUS AJ747297 reverse - unstimulated minus stimulated macrophage Sus
DEFINITION scrofa cDNA clone R_1_D05, mRNA sequence.

ACCESSION AJ747297

VERSION AJ747297.1 GI:49917514

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 23)
Hopwood,P.A., Zhang,F., Lowden,S., Talbot,R., Burt,D., Archibald,A.
and Dixon,L.

TITLE Development of a porcine cDNA microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Hopwood PA

Dept. of Preclinical Veterinary Sciences

Royal School for Veterinary Studies

Summerhall, Edinburgh, EH9 1QH, UNITED KINGDOM

Sequencing was performed by ARK Genomics. This clone is available from ARK- Genomics, Roslin Institute, Roslin, Midlothian EH25 9PS, UK. See www.ark-genomics.org or contact info@arkgenomics.org.

FEATURES

source

1..23
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="R_1_D05"
/tissue_type="lung"
/cell_type="macrophage"
/clone_lib="reverse - unstimulated minus stimulated macrophage"

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1005

AM044732 23 bp mRNA linear EST 20-SEP-2005
LOCUS AM044732 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC30h01.q1k, mRNA sequence.

ACCESSION AM044732

VERSION AM044732.1 GI:75967222

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE 1 (bases 1 to 23)

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 23)
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni
Unpublished (2005)

CONTACT: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

source

1..23
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC30h01.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1006

AM047142 23 bp mRNA linear EST 11-AUG-2005

LOCUS AM047142 Schistosoma mansoni lung schistosomulum Schistosoma
DEFINITION mansoni cDNA clone SmlC26b06.q1k, mRNA sequence.

ACCESSION AM047142

VERSION AM047142.1 GI:72293133

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE 1 (bases 1 to 23)

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 23)

Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

CONTACT: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES

source

1..23
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="SmlC26b06.q1k"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="Country: Puerto Rico"

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1007

CF279238/c

LOCUS CF279238

DEFINITION 14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ORyza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12,

mRNA sequence.

ACCESSION CF279238

CF279238 23 bp mRNA linear EST 14-AUG-2003
14ETL--05-H12.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORyza sativa (japonica cultivar-group) cDNA clone 14ETL--05-H12,
mRNA sequence.
CF279238


```

CF297943.1 GI:33656624
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--05-H12"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice ciliated leaf plasmid cdna library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1008
CF297943/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2
```

```

RESULT 1010
CF319212/c
LOCUS
DEFINITION
HD--09-K06.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-K06, mRNA sequence.
ACCESSION
CF319212
VERSION
CF319212.1 GI:33690973
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eriartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="HD--09-K06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="HD--09-K06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1011
CF322953
LOCUS
DEFINITION
HDN--02-109.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
clone HDN--02-109, mRNA sequence.
ACCESSION
CF322953
VERSION
CF322953.1 GI:33794126
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eriartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

```

```

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="HDN--02-109"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

FEATURES
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="HDN--02-109"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="Vector: pBluescript SK(+); Site.1: EcoRI; Site.2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1012
CF329042
LOCUS
DEFINITION
NACL--04-D14.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-D14, mRNA
sequence.
ACCESSION
CF329042
VERSION
CF329042.1 GI:33806320
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eriartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="NACL--04-D14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

```

SOURCE	Vitis vinifera
ORGANISM	Vitis vinifera
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

FEATURES
SOURCE

UMR 619 - Equipe Biologie de la Vigne
Université de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.
Location/Qualifiers
1 23

```

/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS57RB007H08"
/dev_stage="ripe stage"
/clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
/clone_org="Fruit without seeds; Vector: Lambda
Triplex2; Site_1: SfiA; Site_2: SfiB; Oriented library"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1016
COS77495/c
LOCUS TVEST077D06 TV30236_PT cDNA Library Trichomonas vaginalis cDNA 5',
DEFINITION mRNA sequence.
ACCESSION COS77495
VERSION COS77495.1 GI:50407891
KEYWORDS EST.
SOURCE Trichomonas vaginalis
ORGANISM Trichomonas vaginalis
Eukaryota; Parabasalides; Trichomonada; Trichomonadida;
Trichomonadidae; Trichomonadinae; Trichomonas.
1 (bases 1 to 23)
Zhou,Y., Shu,W.M., Huang,S.C.C., Huang,K.Y. and Tang,P.
Analysis of Gene Expression Profile in Trichomonas vaginalis by EST
Sequencing
Unpublished (2003)
Contact: Tang, P.
Molecular Regulation and Bioinformatics Laboratory, College of
Medicine
Chang Gung University
259 Wenhsia 1st. Road, Kweishan, Taoyuan 333, Taiwan
Tel: +886 3 3283016 EXT5136
Fax: +886 3 3283031
Email: petang@mail.cgu.edu.tw
PCR Primers
FORWARD: T7
BACKWARD: T3
Seq primer: T3.
FEATURES
source
Location/Qualifiers
1..23
/organism="Trichomonas vaginalis"
/mol_type="mRNA"
/db_xref="taxon:5722"
/cell_line="ATCC30236"
/dev_stage="Trophozoites at mid-log phase"
/lab_host="XLI Blue-MRF"
/clone_lib="TV30236 PT cDNA Library"
/notes="Vector: Lambda ZAP-Express (Stratagene); Site_1:
EcoRI; Site_2: XhoI"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1017
CX004980/c
LOCUS t122h08.b7 Brain - Cerebellum Library (DOEST8) Canis familiaris
DEFINITION

```

```

cDNA, mRNA sequence.
CX004980
VERSION CX004980.1 GI:56276396
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 23)
Balijs,V., Nascimento,L.U. and McCombie,W.R.
ESTs from Canis familiaris cerebellum (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.
FEATURES
source
Location/Qualifiers
1..23
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cerebellum"
/dev_stage="3 month old normal canine"
/lab_host="XLI0 Gold"
/clone_lib="Brain - Cerebellum Library (DOEST8)"
/notes="Organ: Brain; Vector: pBluescript II SK; Site_1:
EcoRI; Site_2: XhoI; Library constructed using pBluescript
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1018
DR063413
LOCUS ip65a09.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION sequence.
ACCESSION DR063413
VERSION DR063413.1 GI:66986981
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balijs,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo megasporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

```

```

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="Female"
/clone_lib="Ginkgo megasporophyll (NYBG)"
/notes="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1019
DR072928      23 bp mRNA linear EST 08-JUN-2005
LOCUS ik79h04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION
DR072928
VERSION
DR072928.1 GI:67050776
KEYWORDS
SOURCE
ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/notes="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1020
DR072928
LOCUS ik79h04.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION
DR072928
VERSION
DR072928.1 GI:67051937
KEYWORDS
SOURCE
ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/notes="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1020
DR073135
LOCUS ik86h10.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION
DR073135
VERSION
DR073135.1 GI:67050986
KEYWORDS
SOURCE
ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"

```

```

ACCESSION
DR073135
VERSION
DR073135.1 GI:67050986
KEYWORDS
SOURCE
ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/notes="Organ: leaf; Vector: :pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1021
DR074008/c
LOCUS ik92a08.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
sequence.
ACCESSION
DR074008
VERSION
DR074008.1 GI:67051937
KEYWORDS
SOURCE
ORGANISM
Ginkgo biloba (maidenhair tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 23)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES
source      Location/Qualifiers
1. .23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"

```


inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1024
AZ312314/c
LOCUS AZ312314 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0028006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0028006 F, genomic survey sequence.

ACCESSION AZ312314
VERSION AZ312314.1 GI:10356138
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0028 row: 0 column: 06
Seq primer: CGTTGTAACGACGGCCACT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
1. .23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0028006"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1025
AZ313922/c
LOCUS AZ313922 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0030A02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0030A02 R, genomic survey sequence.

ACCESSION AZ313922
VERSION AZ313922.1 GI:10359299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0030 row: A column: 02
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES
source
1. .23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0030A02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1026

AZ351354

LOCUS AZ351354 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089D19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089D19 F, genomic survey sequence.

ACCESSION AZ351354

VERSION AZ351354.1 GI:10430591

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: D column: 19

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089D19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1027

AZ357645

LOCUS AZ357645 23 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0095C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0095C23 F, genomic survey sequence.

ACCESSION AZ357645

VERSION AZ357645.1 GI:10471345

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: C column: 23

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0095C23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1028

AZ419236/c

LOCUS AZ419236 23 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0195H07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0195H07 R, genomic survey sequence.

ACCESSION AZ419236

VERSION AZ419236.1 GI:10543249

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0195 row: H column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. .23

Location/Qualifiers

source

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0195H07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1029

AZ461220

LOCUS

DEFINITION AZ461220 23 bp DNA linear GSS 04-OCT-2000
1M0267D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0267D05 F, genomic survey sequence.

ACCESSION AZ461220

VERSION AZ461220.1 GI:10619345

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0267 row: D column: 05

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

Location/Qualifiers

source

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0267D05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1030
AZ465327/c
LOCUS
DEFINITION 23 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0275K12 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0275 row: K column: 12
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0275K12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1031

AZ481702/c
LOCUS
DEFINITION 23 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0306E11 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0306 row: E column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers

FEATURES
source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0306E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1032

AZ593540/C

LOCUS

DEFINITION AZ593540 23 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0396024 F, genomic survey sequence.

ACCESSION

AZ593540

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0396 row: 0 column: 24

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0396024"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1033

AZ593540/C

LOCUS

DEFINITION AZ593540 23 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0405C07 F, genomic survey sequence.

ACCESSION

AZ593540

VERSION

GSS.

KEYWORDS

Mus musculus (house mouse)

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A., and Wright, D. Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0405 row: C column: 07

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0405C07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1034
AZ610785
LOCUS IM0436N07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0436N07 F, genomic survey sequence.
ACCESSION AZ610785
VERSION AZ610785.1 GI:11732975
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0436 row: N column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES
source
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0436N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1035
AZ647637/c
LOCUS AZ647637 23 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0514E09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0514E09 F, genomic survey sequence.
ACCESSION AZ647637
VERSION AZ647637.1 GI:11779301
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0514 row: E column: 09
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0514E09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES
source
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0514E09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1036
AZ654903
LOCUS
DEFINITION
1M0529D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529D03 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0529D03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1|4732114|gb|AF129072.1), a copy-number

FEATURES
source

source

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1037
AZ778751
LOCUS
DEFINITION
2M0014008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0014008 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 08
Seq primer: CGTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers

1. .23

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014008"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1|4732114|gb|AF129072.1), a copy-number

FEATURES
Location/Qualifiers

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014008"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23: Conservative 0; Mismatches 0; Indels

Qy 2709 AAAAAAAAAAAAAAAAAAAAAAAAAA 2731
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1038

Accession	LOCUS	DEFINITION	23 bp	DNA	linear	GSS 16-FEB-2001
AZ787184	LOCUS	DEFINITION	AZ787184	2M0033C07F	Mouse 10kb plasmid UUCG1M library	Mus musculus genomic
				clone UUCG2M0033C07 F.	genomic survey sequence.	

ACCESSION AZ787184
 VERSION AZ787184.1 GI:12925692
 KEYWORDS GSS.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (pages 1 to 23)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Neidhausen, A. and Wright, D. Weists, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0033 row: C column: 07
Seq primer: CGTTGTAAACGACGGCCAGT

High quality sequence stop: 23.

```
source
1. 23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U9GC2M033C07"
/accession="J06"
```

/seq/maile
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGc1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114|ab/AP129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1039

AZ792751/c	AZ792751	23 bp	DNA	linear	GSS 16-FEB-2001
LOCUS	2M0045K24F	Mouse	10kb	plasmid	UUGC1M library
DEFINITION	clone UUGC2M0045K24 F.	genomic survey sequence.			

ACCESSION AZ792751
VERSION AZ792751.1 GI:12937005
KEYWORDS GSS.

Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts

JOURNAL Unpublished (2000)

CONTACT: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: K column: 24
Seq primer: CGTTGTAACGACGGCCAGT

High quality sequence stop: 23.

```

FEATURES
source
1. 23
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/accession="UUGC2M045K24"
/sex="Male"

```

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UUGCLM library"
/note="vector: PWD42n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi_47322114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1040

AZ859570 23 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0165B14 F, genomic survey sequence.

ACCESSION AZ859570
VERSION AZ859570.1 GI:13054022

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 23)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0165 row: B column: 14

Seq primer: CGTTGTAAACGACGCCACT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0165B14"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1041

AZ939608 23 bp DNA linear GSS 26-APR-2001
LOCUS 2M0198I07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0198I07 R, genomic survey sequence.

ACCESSION AZ939608
VERSION AZ939608.1 GI:13800390

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 23)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

JOURNAL
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0198 row: I column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0198I07"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT	1043
DU830086/c	
LOCUS	
DEFINITION	DU830086 23 bp DNA linear GSS 22-DEC-2005 KBR006B23F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBR006B23, genomic survey sequence.

ACCESSION	DU830086
VERSION	DU830086.1
KEYWORDS	GI:83866682
SOURCE	GSS.
ORGANISM	Brassica rapa subsp. pe
	Brassica rapa subsp. pe

ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassical

REFERENCE
AUTHORS
1 (bases 1 to 23)
Yang, T. J., Kwon, S. J., Kim, J. A., Kim, J. S., Lim, K. B., Jin, M.,
Park, J. Y., Lim, M. H., Kim, H. I., Choi, B. S., Seol, Y. J., Park, D. S.,
Hahn, J. H. and Park, B. S.

TITLE
JOURNAL
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)

CONTACT: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672

Email: pbeom@rda.go.kr
BAC end sequence of *Brassica rapa* ssp. *pekinensis* Sau3AI BAC clone
KBrS006B23
Seq primer: T7
Class: BAC ends.
Location/Qualifiers

```
source
1. .23
/organ
```

```

/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS006B23"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAB."

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. NO. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    2709 AAAAAAAAAAAAAAAAAAAAAA 2731
       |||
Db    23  AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1044
DUB34017/c
LOCUS          DUB834017        23 bp     DNA     linear      GSS 22-DEC-2005

```



```

DEFINITION   KBrS013E12R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS013E12, genomic survey
              sequence.
ACCESSION    DU834017
VERSION      DU834017.1 GI:83870613
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
ORGANISM     Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pheom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
              KBrS013E12
              Seq primer: M13 Reverse
              Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..23
                     /organism="Brassica rapa subsp. pekinensis"
                     /mol_type="genomic DNA"
                     /cultivar="Chiifu"
                     /sub_species="pekinensis"
                     /db_xref="taxon:51351"
                     /clone="KBrS013E12"
                     /lab_host="E. coli DH10B"
                     /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
                     /notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
                     ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
                     available at NIAB."

Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db   23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1045
LOCUS    DX071679/c
DEFINITION   KBrS081H24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
              subsp. pekinensis genomic clone KBrS081H24, genomic survey
              sequence.
ACCESSION    DX071679
VERSION      DX071679.1 GI:84765975
KEYWORDS     GSS.
SOURCE       Brassica rapa subsp. pekinensis
ORGANISM     Brassica rapa subsp. pekinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE        End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
              Brassica Genomics Team

```

```

National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pheom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrS081H24
Seq primer: T7
Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..23
                     /organism="Brassica rapa subsp. pekinensis"
                     /mol_type="genomic DNA"
                     /cultivar="Chiifu"
                     /sub_species="pekinensis"
                     /db_xref="taxon:51351"
                     /clone="KBrS081H24"
                     /lab_host="E. coli DH10B"
                     /clone_lib="KBrB, Brassica rapa BamHI BAC library"
                     /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
                     pekinensis var. Chiifu BAC library (KBrB BAC) is provided
                     by Yong-Pyo Lim (CNU)."

Query Match          0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db   23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1046
LOCUS    TA151C02Q
DEFINITION   T. brucei sheared genomic DNA clone 151c02, reverse sequence,
              genomic survey sequence.
ACCESSION    AL473028
VERSION      AL473028.1 GI:11838301
KEYWORDS     GSS.
SOURCE       Trypanosoma brucei
ORGANISM     Trypanosoma brucei
              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
              Trypanosoma.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
              Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
              Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
              project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
              Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
              nh@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
              Rockville, MD. Genomic DNA isolated from a cloned population of
              Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
              to give a tight size distribution (
              4 kb). The v + i method used for the library construction is
              described in detail in Smith, H. and Venter, J.C. (Making small
              insert libraries for whole genome shotgun sequencing projects. In
              Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
              Barrell, Oxford University Press, 1999).
              Email: nelsayed@tigr.org
              Details of T. brucei sequencing at the Sanger Centre are available
              at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES             Location/Qualifiers
     source           1..23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="151c02"

```

```

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1047
TA274B03P/c
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 274b03, forward sequence,
genomic survey sequence.
ACCESSION
AL484584
VERSION
AL484584.1 GI:11851281
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274b03"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1048
TA353A10P
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION
AL494456
VERSION
AL494456.1 GI:11870913
KEYWORDS
GSS.
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,

```

```

Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="353a10"

Query Match      0.8%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1049
AZ786257
LOCUS
DEFINITION
2M0031H11R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG2M0031H11 R, genomic survey sequence.
ACCESSION
AZ786257
VERSION
AZ786257.1 GI:12923835
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"

```

```

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1051
AZ386891
LOCUS
DEFINITION
  LM0146A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0146A08 F, genomic survey sequence.
ACCESSION
  AZ386891
VERSION
  AZ386891.1 GI:10500591
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
TITLE
  Contact: Robert B. Weiss
JOURNAL
  University of Utah Genome Center
COMMENT
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0146 row: A column: 08
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 25.
  Location/Qualifiers
    1..25
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0146A08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 2 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1050
CF301712/c
LOCUS
DEFINITION
  7LEAF--06-K21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--06-K21, mRNA
  sequence.
ACCESSION
  CF301712
VERSION
  CF301712.1 GI:33673473
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 25)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnaem@ggbio.com, bhnaem@bio.myongji.ac.kr.
  Location/Qualifiers
    1..25
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="7LEAF--06-K21"
      /tissue type="leaf"
      /dev stage="7 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

Query Match      0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 24 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1051
AZ386891
LOCUS
DEFINITION
  LM0146A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0146A08 F, genomic survey sequence.
ACCESSION
  AZ386891
VERSION
  AZ386891.1 GI:10500591
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
TITLE
  Contact: Robert B. Weiss
JOURNAL
  University of Utah Genome Center
COMMENT
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0146 row: A column: 08
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 25.
  Location/Qualifiers
    1..25
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0146A08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1052

AZ832800/c

LOCUS AZ832800 25 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0113M21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0113M21 F, genomic survey sequence.

ACCESSION AZ832800

VERSION AZ832800.1 GI:13002708

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0113 row: M column: 21

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

FEATURES

source

1..25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0113M21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
DB 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1053

BQ583199/c

LOCUS BQ583199 26 bp mRNA linear EST 06-DEC-2002
DEFINITION E012097-024-006-E10-SP6 MP1Z-ADIS-024-Inflorance Beta vulgaris cDNA clone 024-006-E10 5-PRIME, mRNA sequence.

ACCESSION BQ583199

VERSION BQ583199.1 GI:26112776

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

1 (bases 1 to 26)
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

JOURNAL

COMMENT

Contact: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaa@mpiz-koeln.mp9.de

Insert Length: 26 Std Error: 0.00

Plate: 6 row: E column: 10

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

source

1..26
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:183502"
/db_xref="taxon:161934"
/clone="024-006-E10"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-Inflorance"
/note="Vector: PCWVSP0R76; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAA 2729
|||||
DB 23 CTAATAAAAAAAAAAAAAAAAAA 1

```

RESULT 1054
R26779/c
LOCUS
DEFINITION
  R26779          26 bp      mRNA          linear      EST 24-APR-1995
  YH44f06.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
  IMAGE:132611 3' similar to gb:M85164 SERUM RESPONSE FACTOR
  ACCESSORY PROTEIN 1A (HUMAN);, mRNA sequence.
ACCESSION
R26779          R26779.1  GI:782914
VERSION
R26779.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 26)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1384 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES
source
1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
/clone="IMAGE:132611"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAAGATTCTGGCGCGCAGGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
Query Match          0.8%; Score 23; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2730
Db 23 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1055
N29432/c
LOCUS
DEFINITION
  N29432          27 bp      mRNA          linear      EST 05-JAN-1996
  YH13c06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
  IMAGE:271114 3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR
  (HUMAN);, mRNA sequence.
ACCESSION
N29432
VERSION
N29432.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

```

```

DEFINITION
yw86h10.s1 Soares placenta 8to9weeks 2NbHP8to9W Homo sapiens cDNA
Clone IMAGE:259171 3' similar to gb:X64559 TETRAPECTIN PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
N29432
VERSION
N29432.1  GI:1147952
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 27)
AUTHORS
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.
FEATURES
source
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3888877"
/db_xref="taxon:9606"
/clone="IMAGE:259171"
/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta 8to9weeks 2NbHP8to9W"
/notes="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCGCGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
Query Match          0.8%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1056
N34459/c
LOCUS
DEFINITION
  N34459          27 bp      mRNA          linear      EST 16-JAN-1996
  YH13c06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
  IMAGE:271114 3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR
  (HUMAN);, mRNA sequence.
ACCESSION
N34459
VERSION
N34459.1  GI:1155601
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisan,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 16
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 16.
FEATURES
source
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3880756"
/db_xref="taxon:9606"
/clone="IMAGE:271114"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="PH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/notes="Vector: pT7T3D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; let strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCAATCTAGTGGAGCGCGCGATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
Query Match 0.8%; Score 23; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1057
AJ922998/c
LOCUS AJ922998 Theileria annulata piroplasm Theileria annulata cDNA clone
DEFINITION TAC20g08_gika, mRNA sequence.
ACCESSION AJ922998
VERSION AJ922998.1 GI:67493340
KEYWORDS EST.
SOURCE Theileria annulata
ORGANISM Theileria annulata
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
Theileria.
REFERENCE 1 (bases 1 to 28)
AUTHORS Pain,A., Renaud,H., Berriman,M., Murphy,L., Yeats,C.A., Weir,W.,
Kerhornou,A., Aslett,M., Bishop,R., Bouchier,C., Cochet,M.,
Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Foster,N.,
Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F.,
Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,P.,
Nene,V., O'Neil,S., Price,C., Quail,M.A., Rabinowitsch,E.,
Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T.,
Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J.,
Dobelaere,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D.,
Shiels,B., Tait,A., Barrell,B. and Hall,N.
The genome of the host-cell transforming parasite Theileria
annulata and a comparison with T. parva
Contact: Pain A
Contact: Pain A
The Pathogen Sequencing Unit
The Wellcome Trust Sanger Institute
Genome Campus, CB10 1SA, UNITED KINGDOM
Piroplasm cDNA library: Frank Katzer and Brian Shiels, Division of
Veterinary Infection and Immunity, ICM, University of Glasgow, UK.
FEATURES
source
1..28
/organism="Theileria annulata"
/mol_type="mRNA"
/isolate="Ankara (clone D7)"
/db_xref="taxon:5874"
/clone="TAC20g08_gika"
/dev_stage="piroplasm"
/lab_host="Bos taurus (cow)"
/clone_lib="Theileria annulata piroplasm"
/notes="country: Turkey;Ankara"
Query Match 0.8%; Score 23; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1058
DX072773
LOCUS DX072773 28 bp DNA linear GSS 10-JAN-2006
DEFINITION KBR082023F KBRB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBR082023, genomic survey
sequence.
ACCESSION DX072773
VERSION DX072773.1 GI:84767069
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 28)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBRB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBR082023
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chilfu"
/sub_species="pekinensis"
/db_xref="taxon:51351"

```

pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yongq-Pyo Lim (CNU)."

conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAAAAAAAAAAAAAAA 23

282.R1 CSEQFL36 fetal brain Sus scrofa cDNA, mRNA 26 bp mRNA linear EST 27-FEB-2002

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

David L. Adelson
Breeding and Genetics
University
Science Dept., TAMU-2471, College Station, TX 77843-2471,

430370
vid.adelson@tamu.edu.

```

/organism="Sus scrofa"
/mol_type="mrna"
/db_xref="taxon:9823"
/dev_stages="fetal"
/clone_lib="CSQFXL36_fetal brain"
/notes="Organ: brain; Vector: plusscript SK+; Site_1:
NotI; Site_2: EcoRI; sequence 5' of the insert
(5'-NNN...NNNNNNNN)"
GGCAATTGGAGCTCCACCGCGTGGCGCGCGCTCGAG. Sequence 3' of
the inserts (AAGATTCGATCAAGCTTCATCGACCTCGACCTCGAG.
non-normalized library, sequenced 3' with M13 primer."

```

ervative 0; Mismatches 2; Indels 0; Gaps 0;

AAAAAAAAAGAGAAAAAA 1

26 bp mRNA linear EST 10-OCT-2003
Glossina morsitans morsitans adult infected gut Glossina
morsitans cDNA clone Tse6fe05 plc, mRNA sequence.

morsitans morsitans

Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene Trap.

FEATURES

source

Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="A015.B4"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/note="Vector: pFLIP1"

Query Match 0.8%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 8.2e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAA 2733

|||||
Db 26 TAACAATAAAAAA 1

RESULT 1062

CZ908520

LOCUS CZ908520 27 bp DNA linear GSS 08-AUG-2005
DEFINITION 4018003G05.2EL_y1 4018 - RescueMu Grid X Zea mays genomic, genomic survey sequence.

ACCESSION

VERSION

CZ908520

KEYWORDS

GSS.

SOURCE

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 27)

Walbot.V.

Maize genomic sequences found using engineered RescueMu transposon

Contact: Walbot V

Unpublished (2001)

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence.

Plate: 4018003 row: G column: 05

Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1..27
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="4018 - RescueMu Grid X"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid X was grown at UCSD in 2003. DNA was extracted from leaf

strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 22.8; DB 1; Length 27;
Best Local Similarity 92.3%; Pred. No. 8.4e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAGAAAAA 2734

|||||
Db 1 AAAAAATAAGAAAAA 26

RESULT 1063

CV091538/c

LOCUS CV091538 28 bp mRNA linear EST 26-AUG-2004
DEFINITION NAI103.R cDNA non acclimated Bluecrop library Vaccinium corymbosum cDNA 3', mRNA sequence.

ACCESSION

VERSION

CV091538

KEYWORDS

EST.

SOURCE

Vaccinium corymbosum

Vaccinium corymbosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; Ericales; Ericaceae; Vaccinioideae; Vaccinieae;

Vaccinium.

1 (bases 1 to 28)

Dhanaraj,A.L., Alkharouf,N.W., Beard,H.S., Chouikha,I.B.,

Matthews,B.F. and Rowland,L.J.

Monitoring gene expression changes during cold acclimation of

blueberry (Vaccinium corymbosum L.) using a cDNA microarray

Unpublished (2004)

JOURNAL

COMMENT

Contact: Rowland, L.J.

Fruit Lab

US Department of Agriculture (USDA), ARS, PSI

Bldg 010A, 10300 Baltimore avenue, BARC West, Beltsville, MD

20705-2350, USA

Tel: 301-504-6654

Fax: 301-504-5653

Email: rowlandj@ba.ars.usda.gov.

Location/Qualifiers

1..28

/organism="Vaccinium corymbosum"

/mol_type="mRNA"

/cultivar="Bluecrop"

/db_xref="taxon:69266"

/tissue_type="Flower buds including bud scales"

/dev_stage="Mature plants"

/clone_lib="cDNA non acclimated Bluecrop library"

/note="Vector: pBluescript SK-; cDNA clones from Vaccinium

corymbosum cv. Bluecrop, RNA for preparation of library

was extracted from flower buds collected in the fall from

non acclimated plants"

FEATURES

source

Query Match 0.8%; Score 22.8; DB 1; Length 28;
Best Local Similarity 85.7%; Pred. No. 8.5e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2709 AAAAAAAGAAAAA 2736

|||||
Db 28 ANAAAAAGTNAAAAAA 1

RESULT 1064

TA327D04P/c

LOCUS TA327D04P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 327d04, forward sequence, genomic survey sequence.

ACCESSION

VERSION

AL497297

KEYWORDS

GSS.

SOURCE

Trypanosoma brucei

ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 28)

REFERENCE
AUTHORS Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M. A. and Barrell, B. G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nalsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source Location/Qualifiers
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="327d04"

Query Match 0.8%; Score 22.8; DB 1; Length 28;
Best Local Similarity 92.3%; Pred. No. 8.5e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2701 TTGTGCTACTAAAAA 24 bp mRNA linear EST 14-AUG-2003
||||| 26 TTTTAAATAAAAAA 2726
Db

RESULT 1065
CF281313/c
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--08-F05,
mRNA sequence.
ACCESSION CF281313.1 GI:33658700
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 24)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source Location/Qualifiers
1..24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"

/clone="14ETL--08-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAA 24 bp mRNA linear EST 07-JAN-2000
||||| 24 AAAAAAGAAAAA 2732
Db

RESULT 1066
AW247159/c
LOCUS
DEFINITION 2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
mRNA sequence.
ACCESSION AW247159
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 24)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819627.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
[www-bio.llnl.gov/bbrp/image/image.html](http://bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu/LowQualitySequence>: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LiCM2 row: B column: 12
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819627"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

FEATURES
source

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1067

LOCUS AZ438069 24 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0228A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0228A10 F, genomic survey sequence.

ACCESSION AZ438069

VERSION AZ438069.1 GI:10562178

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Place: 0228 row: A column: 10

Seq primer: CTTGTAAACACGCGCAGT

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0228A10"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1068

LOCUS AZ458112 24 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261E24 R, genomic survey sequence.

ACCESSION AZ458112

VERSION AZ458112.1 GI:10616237

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0261 row: E column: 24

Seq primer: CACACAGAAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261E24"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1069

AZ607198

LOCUS

DEFINITION 24 bp DNA linear GSS 13-DEC-2000
1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0429G03 R, genomic survey sequence.

ACCESSION

AZ607198

VERSION

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0429 row: G column: 03

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (G1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

source

FEATURES

source

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0429G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Ad

adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
|||||
DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1071

DU835497/C

LOCUS 24 bp DNA linear GSS 22-DEC-2005
DEFINITION KBrS016M18F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa subsp. pekinensis genomic clone KBrS016M18, genomic survey sequence.

ACCESSION DU835497
VERSION DU835497.1
SOURCE GI:83872093

ORGANISM Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 24)

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J. H. and Park, B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone KBrS016M18

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..24

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrS016M18"

/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"

/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrS BAC) is available at NIAH."

Query Match

Best Local Similarity 0.8%; Score 22.4; DB 1; Length 24;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

|||||

DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1072

DX045709/C

LOCUS

DEFINITION KBrB047B17F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB047B17, genomic survey sequence.

ACCESSION

VERSION

DX045709.1 GI:84740006

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone KBrB047B17

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..24

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB047B17"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."

Query Match

Best Local Similarity 0.8%; Score 22.4; DB 1; Length 24;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732

|||||

DB 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1073

LOCUS

DEFINITION

N27663 25 bp mRNA linear EST 30-DEC-1995
YW50906.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255706 3', similar to gb:J05032 ASPARTYL-TRNA SYNTHETASE (HUMAN); mRNA sequence.

ACCESSION

VERSION

N27663

GI:1142144

EST

EST

Source

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 25)

AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,

Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,

and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

PUBMED 8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="CDB:3866115"
/db_xref="taxon:9606"
/clone="IMAGE:255706"
/sex="Female"
/tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOIR cells (kanamycin resistant)"
/clone_lib="Weizmann Olfactory Epithelium"
/notes="Organ: nose; Vector: pBluescript SK-; Site 1:
ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Olfactory epithelium, normal. Average insert
size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N.
Walker, D. Lancet, Weizmann Institute of Science. ~5'
adaptor sequence: 5' GAATTCGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match

Best Local Similarity 95.8%; Score 22.4; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAATAAAAAAAAAAAAAA 2730

Db 24 CTCAAAAAATAAAAAAAAAAAAAA 1

RESULT 1074

CF310745 27 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-J07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-J07, mRNA sequence.

CF310745.1 GI:33682506

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 27)

REFERENCE

AUTHORS Kim J.S., Jun K.M., Cheong P.J., Kim M.J., Lee T.H., Shin Y.C.,

Song S.I., Kim J.K., Kim Y.-K. and Nahm B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--05-J07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: ECORI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 22.4; DB 1; Length 27;

Best Local Similarity 95.8%; Pred. No. 8.8e+02;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAATAAAAAAAAAAAAAA 2730

Db 4 CCAAAAAAATAAAAAAAAAAAAAA 27

RESULT 1075

AL039138

LOCUS

DEFINITION DKF2p566L164.r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKF2p566L164, mRNA sequence.

ACCESSION AL039138

VERSION AL039138.1

GI:49682258

KEYWORDS

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo

Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and

Wiemann, S.

EST (Bloecker, et al.)

Unpublished (1999)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

1. .28

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKF2p566L164"

/tissue_type="kidney"

/dev_stage="fetal"

/lab_host="Xl-2blue"

/clone_lib="566 (synonym: hfkd2)"

/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.8%; Score 22.4; DB 1; Length 28;

Best Local Similarity 95.8%; Pred. No. 8.9e+02;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2704 GTACTAAAAAATAAAAAAAAAA 2727

Db 5 GTAATAAAAAAATAAAAAAAAAA 28

RESULT 1076

DX082097

LOCUS

DEFINITION DX082097 28 bp DNA linear GSS 10-JAN-2006
KBrB095E02F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB095E02, genomic survey
sequence.

ACCESSION DX082097

VERSION DX082097.1

GI:84776393

```

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 28)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.U., Park, D.S.,
Hahn, J.H. and Park, B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB095E02
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..28
/organism="Brassica rapa subsp. pekinensis"
/mol_type="Genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095E02"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22.4; DB 1; Length 28;
Best Local Similarity 95.8%; Pred. No. 8.9e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTTAAAAAATTTAAAAA 2730
|||
5 CTTAAAAAATTTAAAAA 28

Db

RESULT 1077
CF298133/c
LOCUS
DEFINITION
27 bp mRNA linear EST 15-AUG-2003
7LEAF--01-G09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA
sequence.
ACCESSION
CF298133
VERSION
CF298133.1 GI:33669894
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
FEATURES
source
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-009"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAATTTAAAAA 2735
|||
27 AAAAAAATTTAAAAA 1

Db

RESULT 1078
CF328811/c
LOCUS
DEFINITION
27 bp mRNA linear EST 18-AUG-2003
NACL--03-009.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--03-009, mRNA
sequence.
ACCESSION
CF328811
VERSION
CF328811.1 GI:33805864
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 27)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers
FEATURES
source
1..27
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--03-009"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22.2; DB 1; Length 27;
Best Local Similarity 88.9%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAAATTTAAAAA 2735
|||
27 AAAAAAATTTAAAAA 1

Db

```


		/clone="7LEAF--04-G19"	
		/tissue_type="leaf"	
		/dev_stage="7 days after germination"	
		/lab_host="E.coli DH10B"	
		/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"	
		/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	
Query Match		0.8%; Score 22; DB 1; Length 22;	
Best Local Similarity		100.0%; Pred. No. 8.5e+02;	
Matches		22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2730	
Db	22	AAAAAAAAAAAAAAAAAAAAA 1	
RESULT 1085			
CF310366/c			
LOCUS			
DEFINITION			
ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--04-P14, mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Oryza sativa (japonica cultivar-group)			
Oryza sativa (japonica cultivar-group)			
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.			
REFERENCE			
1 (bases 1 to 22)			
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.			
Large-scale Sequencing Analysis of Rice ESTs			
Unpublished (2003)			
Contact: Nahm B.H.			
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University			
Yongin, Gyeonggi, Korea			
Tel: 82 31 330 6193			
Fax: 82 31 321 6355			
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.			
Location/Qualifiers			
1. .22			
/organism="Oryza sativa (japonica cultivar-group)"			
/mol_type="mRNA"			
/cultivar="Nackdong"			
/db_xref="taxon:39947"			
/clone="ABF--04-P14"			
/tissue_type="leaf"			
/dev_stage="14 days after germination"			
/lab_host="E.coli DH10B"			
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"			
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."			
Query Match		0.8%; Score 22; DB 1; Length 22;	
Best Local Similarity		100.0%; Pred. No. 8.5e+02;	
Matches		22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2730	
Db	22	AAAAAAAAAAAAAAAAAAAAA 1	
RESULT 1086			
CF311269/c			

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-B13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1088
CF312498/c
LOCUS
DEFINITION
ABF--08-E15.g1 ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-H22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1090
CF333430/c
LOCUS
DEFINITION
JMT--02-F04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-F04, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-E15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1088
CF312498
LOCUS
DEFINITION
ABF--08-E15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-E15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-E15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1088
CF312498
LOCUS
DEFINITION
ABF--08-E15.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-E15, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1. .22
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--06-H22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1090
CF333430/c
LOCUS
DEFINITION
JMT--02-F04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-F04, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--02-F04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match

Best Local Similarity 0.8%; Score 22; DB 1; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1091

CF334781/c

LOCUS

JMT--04-D05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--04-D05, mRNA sequence.

CF334781

CF334781.1 GI:33817904

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1. .22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--04-D05"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match

Best Local Similarity 0.8%; Score 22; DB 1; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1092

CF336250/c

LOCUS

JMT--06-D20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

JMT--06-D20, mRNA sequence.

CF336250

CF336250.1 GI:33820891

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 22)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

source

1. .22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--06-D20"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

Query Match

Best Local Similarity 0.8%; Score 22; DB 1; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1093

CF337580

LOCUS CF337580 22 bp mRNA linear EST 18-AUG-2003
 DEFINITION JMT--08-B11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--08-B11, mRNA sequence.

ACCESSION

CF337580

VERSION

CF337580.1 GI:33823547

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

REFERENCE

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="JMT--08-B11"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis jasmonate Carboxyl

methyltransferase overexpression line."

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1094

CF338524/c

LOCUS

CF338524 22 bp mRNA linear EST 18-AUG-2003

RCL1--01-P07.g1 Regenerated callus lambda phage cDNA library (RCL1)

Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-P07,

mRNA sequence.

ACCESSION

CF338524

VERSION

CF338524.1 GI:33825436

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 22)

REFERENCE

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

FEATURES

source

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="RCL1--01-P07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli SOLR"

/clone_lib="Regenerated callus lambda phage cDNA library

(RCL1)"

/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'

end with SstI and 3' end with XhoI site. Callus was

induced on 2N6 media for 30 days and cultured for 36hrs on

regenerated media"

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||

Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1095

AW332181/c

LOCUS

AW332181 22 bp mRNA linear EST 31-JAN-2000

DEFINITION SSC7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.

ACCESSION AW332181

VERSION AW332181.1 GI:6828538

KEYWORDS EST.

SOURCE Pneumocystis carinii

ORGANISM Pneumocystis carinii

Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;

Pneumocystidaceae; Pneumocystis.

1 (bases 1 to 22)

Edman, J.C., Kovacs, J. and Cushion, M.

Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,

Expressed sequence tags from Pneumocystis carinii

Unpublished (2000)

Contact: Staben C

School of Biological Sciences

University of Kentucky

101 Morgan Building, University of Kentucky, Lexington, KY

40506-0225, USA

Tel: 606 257 2161

Fax: 606 257 1717

Email: staben@pop.uky.edu.

Location/Qualifiers

1..22

/organism="Pneumocystis carinii"

/db_xref="taxon:4754"

/lab_host="E. coli"

/clone_lib="AGS-1"

/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;

P. carinii organisms (3x10e9) from a single rat (99-1-6,

sacrificed on 3/17/99) at Cincinnati VA facilities.

Trizol extracted RNA. Oligo dr priming, standard

conditions described by vendor, Stratagene. Further

details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.8%; Score 22; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 8.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

```

Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 1096
LOCUS   AW332399/c              22 bp  mRNA  linear  EST 31-JAN-2000
DEFINITION   SBA2 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION   AW332399
VERSION     AW332399.1  GI:6828756
KEYWORDS    EST.
SOURCE      Pneumocystis carinii
            Pneumocystis carinii
ORGANISM    Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
            Pneumocystidaceae; Pneumocystis.
REFERENCE   1  (bases 1 to 22)
AUTHORS     Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
            Edman,J.C., Kovacs,J. and Cushion,M.
TITLE       Expressed sequence tags from Pneumocystis carinii
JOURNAL     Unpublished (2000)
COMMENT     Contact: Staben C
            School of Biological Sciences
            University of Kentucky
            101 Morgan Building, University of Kentucky, Lexington, KY
            40506-0225, USA
            Tel: 606 257 2161
            Fax: 606 257 1717
            Email: staben@pop.uky.edu.

FEATURES             source
   source
   1..22
   /organism="Pneumocystis carinii"
   /mol_type="mRNA"
   /db_xref="taxon:4754"
   /lab_host="E. coli"
   /clone_lib="AGS-1"
   /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
P. carinii organisms (3x10e9) from a single rat (99-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dt priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709  AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1097
LOCUS   CN545550/c              22 bp  mRNA  linear  EST 30-APR-2004
DEFINITION   EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL003D05 3', mRNA sequence.
ACCESSION   CN545550
VERSION     CN545550.1  GI:46910175
KEYWORDS    EST.
SOURCE      Vitis vinifera
            Vitis vinifera
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 22)
AUTHORS     Abbai,P., Agase,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne

Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709  AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1097
LOCUS   CN545550/c              22 bp  mRNA  linear  EST 30-APR-2004
DEFINITION   EST 17494 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
            clone B3CS00RL003D05 3', mRNA sequence.
ACCESSION   CN545550
VERSION     CN545550.1  GI:46910175
KEYWORDS    EST.
SOURCE      Vitis vinifera
            Vitis vinifera
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 22)
AUTHORS     Abbai,P., Agase,A., Ageorges,A., Atanassova,R., Barrieu,F.,
            Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
            Hamdi,S., Romieu,C. and Terrier,N.
TITLE       Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
            or seeds) at Various Developmental Stages
JOURNAL     Unpublished (2002)
COMMENT     Contact: Hamdi S.
            UMR 619 - Equipe Biologie de la Vigne

```

```

Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES             source
   source
   1..22
   /organism="Vitis vinifera"
   /mol_type="mRNA"
   /cultiivar="Cabernet Sauvignon"
   /db_xref="taxon:29760"
   /clone="B3CS00RL003D05"
   /dev_stage="ripening stage"
   /clone_lib="Ripe Grape Skin Triplex2 Library"
   /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709  AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db      22  AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1098
LOCUS   DN955212                22 bp  mRNA  linear  EST 04-MAY-2005
DEFINITION   it83g12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
            sequence.
ACCESSION   DN955212
VERSION     DN955212.1  GI:63027350
KEYWORDS    EST.
SOURCE      Gnetum gnemon
            Gnetum gnemon
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetales; Gnetum.
REFERENCE   1  (bases 1 to 22)
AUTHORS     Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE       Expressed tag sequences from Gnetum female cone (NYBG)
JOURNAL     Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.

FEATURES             source
   source
   1..22
   /organism="Gnetum gnemon"
   /mol_type="mRNA"
   /db_xref="taxon:3382"
   /sex="female"
   /clone_lib="Gnetum female cone (NYBG)"
   /note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]


```

DEFINITION ik79e05.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073458
VERSION DR073458.1 GI:67051333
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 22)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
FEATURES             source
    source
        1..22
        /organism="Ginkgo biloba"
        /mol_type="mRNA"
        /db_xref="taxon:3311"
        /sex="female"
        /clone_lib="Ginkgo female leaf (NYBG)"
        /note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
        Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
        The library was size-fractionated to enrich for large
        inserts."
Query Match          0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1106
LOCUS DR074014/c
DEFINITION ik92d03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074014
VERSION DR074014.1 GI:67051943
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 22)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
    source
        1..22
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clones="UUGC1M0018D18"
        /sex="Male"
        /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The

```

```

1..22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo male leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2:
Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large
inserts."
Query Match          0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1107
LOCUS AZ310066/c
DEFINITION AZ310066 22 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0018D18 R, genomic survey sequence.
ACCESSION AZ310066
VERSION AZ310066.1 GI:10351682
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: D column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES             source
    source
        1..22
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clones="UUGC1M0018D18"
        /sex="Male"
        /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The

```


adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1108
AZ351527
LOCUS 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089E07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0089E07 R, genomic survey sequence.

ACCESSION AZ351527
VERSION AZ351527.1 GI:10430764
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: E column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089E07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1109
AZ357630
LOCUS 22 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0099M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0099M15 F, genomic survey sequence.

ACCESSION AZ357630
VERSION AZ357630.1 GI:10471318
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: M column: 15

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099M15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1110

AZ398103

LOCUS

DEFINITION AZ398103 22 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0147N14 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0147N14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1111

AZ401908/c

LOCUS

DEFINITION AZ401908 22 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0169P24 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0169P24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1112
AZ424307/c
LOCUS
DEFINITION
1M0203A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0203A24 R, genomic survey sequence.

ACCESSION
AZ424307
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 22.
FEATURES
Location/Qualifiers
1..22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0203A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1113
AZ428818/c
LOCUS
DEFINITION
1M0212A05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0212A05 R, genomic survey sequence.

ACCESSION
AZ428818
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0212 row: A column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 22.
FEATURES
Location/Qualifiers
1..22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0212A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.8%;	Score 22;	DB 1;	Length 22;
Best Local Similarity	100.0%;	Pred. No. 8.5e+02;		
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAA	2730	
Db	22	AAAAAAAAAAAAAAAAAAAAA	1	

RESULT	1115
AZ463503/c	
LOCUS	
DEFINITION	AZ463503 22 bp DNA linear GSS 04-OCT-2000 clonote UUGC1M7E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M027E24 F, genomic survey sequence.
ACCESSION	AZ463503
VERSION	AZ463503
KEYWORDS	AZ463503.1 GI:10621628
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus

REFERENCE
1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

**JOURNAL
COMMENT**

*Presented and
Unpublished (2000)*
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Email: doum@genetics.ucan.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0272 row: E column: 24
Seq primer: CGTTGAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 22.

```

FEATURES
    source
        Location/Qualifiers
            1..22
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0272E24"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

```

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1116
 AZ463652/c
 LOCUS
 DEFINITION 22 bp DNA linear GSS 04-OCT-2000
 clone UUGC1M0272E12 R, genomic survey sequence.
 ACCESSION
 VERSION AZ463652.1 GI:10621777
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0272 row: E column: 12
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 source
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0272E12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1117
 AZ582403
 LOCUS
 DEFINITION 22 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0374J15 R, genomic survey sequence.
 ACCESSION
 VERSION AZ582403
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0374 row: J column: 15
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 source
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0374J15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1118

AZ607658 22 bp DNA linear GSS 13-DEC-2000
LOCUS IM0430A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0430A13 F, genomic survey sequence.

ACCESSION AZ607658
VERSION AZ607658.1 GI:11729848

KEYWORDS

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0430 row: A column: 13

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0430A13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1119

AZ654691 22 bp DNA linear GSS 14-DEC-2000
LOCUS IM0529D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0529D05 F, genomic survey sequence.

ACCESSION AZ654691

VERSION AZ654691.1 GI:11791837

KEYWORDS

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: D column: 05

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0529D05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1120
AZ760533
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0554A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0554A24 F, genomic survey sequence.

ACCESSION AZ760533
VERSION AZ760533.1 GI:12868477
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1121
AZ779844/c
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0016112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0016112 R, genomic survey sequence.

ACCESSION AZ779844
VERSION AZ779844.1 GI:12910910
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: I column: 12
Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0016112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1122

AZ785019/c

LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0028504R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0028E04 R, genomic survey sequence.

ACCESSION AZ785019

VERSION AZ785019.1 GI:12921341

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: E column: 04

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0028E04"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1123

AZ787098/c

LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0033A05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0033A05 F, genomic survey sequence.

ACCESSION AZ787098

VERSION AZ787098.1 GI:12925520

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 22)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0033 row: A column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0033A05"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1124
AZ787606/c
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0034G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0034G12 F, genomic survey sequence.

ACCESSION AZ787606
VERSION AZ787606.1 GI:12926565
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0034 row: G column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034G12"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1125
AZ792704/c
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0045A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045A24 F, genomic survey sequence.

ACCESSION AZ792704
VERSION AZ792704.1 GI:12936911
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: A column: 24

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045A24"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1126

AZ810674/c

LOCUS

DEFINITION 2M0076E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076E19 F, genomic survey sequence.

ACCESSION

AZ810674

VERSION

AZ810674.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: E column: 19

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0076E19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1127

AZ820439/c

LOCUS

DEFINITION 2M0092K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0092K13 R, genomic survey sequence.

ACCESSION

AZ820439

VERSION

AZ820439.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: K column: 13

Seq primer: CACACGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0092K13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1128

AZ841661

LOCUS

AZ841661 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0139118 R, genomic survey sequence.

ACCESSION

AZ841661

VERSION

AZ841661.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: I column: 18

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0139118"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1129

AZ843514/c

LOCUS

AZ843514 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0142124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142124 F, genomic survey sequence.

ACCESSION

AZ843514

VERSION

AZ843514.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0142 row: I column: 24

Seq primer: CGTTGTAAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0142124"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1130

AZ946102 22 bp DNA linear GSS 27-APR-2001
LOCUS 2M0207D13R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0207D13 R, genomic survey sequence.

ACCESSION AZ946102
VERSION
KEYWORDS
SOURCE GI:13812911
GSS.

Mus musculus
Mus musculus (house mouse)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0207 Row: D Column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0207D13"
/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWB42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1131

DUB34428 22 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS014E07F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS014E07, genomic survey
sequence.

ACCESSION DUB34428
VERSION
KEYWORDS
SOURCE GI:83871024
GSS.

ORGANISM
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seo, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.

TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL
COMMENT Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670
Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis Sau3AI BAC clone

KBrS014E07

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..22

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrS014E07"

/lab_host="E. coli DH10B"

/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"

/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa

subsp pekinensis var. Chiifu BAC library (KBrS BAC) is

available at NIAS."

available at NIAS."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

```

RESULT 1132
DUB35320
LOCUS
DEFINITION
  KBrS016H03F KBrS, Brassica rapa Sau3AI BAC library GSS 22-DEC-2005
  subsp. pekinensis genomic clone KBrS016H03, genomic survey
sequence.
ACCESSION
DUB35320
VERSION
DUB35320.1 GI:83871916
SOURCE
GSS.
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 22)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
  Unpublished (2005)
  Contact: Beom-Seok Park
  Brassica Genomics Team
  National Institute of Agricultural Biotechnology
  225 Seodun-Dong, Suwon, 441-707, Korea
  Tel: +82-31-299-1670
  Fax: +82-31-299-1672
  Email: pbeom@da.go.kr
  BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
  KBrS016H03
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..22
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBrS016H03"
      /lab_host="E. coli DH10B"
      /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
      /note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa
      ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
      available at NTAB."

Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred.No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1133
DUB35320/c
LOCUS
DEFINITION
  KBrB031121R KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
  subsp. pekinensis genomic clone KBrB031121, genomic survey
sequence.
ACCESSION
DUB35320
VERSION
DUB35320.1 GI:84728217
SOURCE
GSS.
ORGANISM
  Brassica rapa subsp. pekinensis
  Brassica rapa subsp. pekinensis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 22)
  Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
  Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
  Hahn,J.H. and Park,B.S.
  End sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
  KBrB031121
  Seq primer: T7
  Class: BAC ends.
  Location/Qualifiers
    1..22
      /organism="Brassica rapa subsp. pekinensis"
      /mol_type="genomic DNA"
      /cultivar="Chiifu"
      /sub_species="pekinensis"
      /db_xref="taxon:51351"
      /clone="KBrB031121"
      /lab_host="E. coli DH10B"
      /clone_lib="KBrB, Brassica rapa BamHI BAC library"
      /note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa ssp
      pekinensis var. Chiifu BAC library (KBrB BAC) is provided
      by Yong-Pyo Lim (CNU)."
```

```

/db_xref="taxon:51351"
/clone="KBrB047K13"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1135
DX056961/C

LOCUS
DEFINITION KBrB062A19f KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB062A19, genomic survey
sequence.

ACCESSION
VERSION DX056961
KEYWORDS
SOURCE GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 22)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
KBrB079A22
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB079A22"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1137
DX080494

LOCUS
DEFINITION KBrB093A20R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB093A20, genomic survey
sequence.

ACCESSION
VERSION DX080494
KEYWORDS
SOURCE GSS.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 22)
AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J.H. and Park, B.S.
TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park

```

Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB093A20
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
    source
        1..22
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBrB093A20"
            /lab_host="E.coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1138
 AG194579
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-072N05.TJ, genomic survey
 sequence.
 ACCESSION AG194579
 VERSION AG194579.1 GI:45226755
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pan.

REFERENCE 1
 AUTHORS Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
 Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
 BAC end sequences of Library RP-43
 Unpublished
 2 (bases 1 to 22)
 TITLE Pan troglodytes (chimpanzee)
 JOURNAL Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
 Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
 (E-mail: redstone@mail.krribb.re.kr, URL: http://phs.grc.krribb.re.kr/,
 Tel: 82-42-866-7181, Fax: 82-42-860-4409)
 COMMENT Clones are derived from the chimpanzee BAC library RP-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: TJ
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..22
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"

FEATURES
 source

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1140
 TA329F10P
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,
 genomic survey sequence.
 ACCESSION AL492691
 VERSION AL492691.1 GI:11868830
 KEYWORDS GSS.

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1139
 TA329F10P
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,
 genomic survey sequence.
 ACCESSION AL464164
 VERSION AL464164.1 GI:11834427
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (
 4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 source
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="131b09"

Query Match 0.8%; Score 22; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
 |||||||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1140
 TA329F10P
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,
 genomic survey sequence.
 ACCESSION AL492691
 VERSION AL492691.1 GI:11868830
 KEYWORDS GSS.

```

/db_xref="taxon:9598"
/clone="RP43-072N05.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

Query Match 0.8%; Score 22; DB 1; Length 22;  

Best Local Similarity 100.0%; Pred. No. 8.5e+02;  

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730  

    |||||||||||||||||||||||||  

    Db 1 AAAAAAAAAAAAAAAAAAAAAA 22



RESULT 1139  

    TA329F10P  

    LOCUS  

    DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,  

    genomic survey sequence.  

    ACCESSION AL464164  

    VERSION AL464164.1 GI:11834427  

    KEYWORDS GSS.  

    SOURCE Trypanosoma brucei  

    ORGANISM  

    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  

    Trypanosoma.  

    1 (bases 1 to 22)  

    AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  

    Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  

    Melville, S.E., Rajandream, M.A. and Barrell, B.G.  

    TITLE Direct Submission  

    JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  

    project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  

    Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  

    nh@sanger.ac.uk  

    COMMENT Constructed at the Institute for Genomic Research (TIGR),  

    Rockville, MD. Genomic DNA isolated from a cloned population of  

    Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  

    to give a tight size distribution (  

    4 kb). The v + i method used for the library construction is  

    described in detail in Smith, H. and Venter, J.C. (Making small  

    insert libraries for whole genome shotgun sequencing projects. In  

    Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  

    Barrell, Oxford University Press, 1999).  

    Email: nelsayed@tigr.org  

    Details of T. brucei sequencing at the Sanger Centre are available  

    at http://www.sanger.ac.uk/Projects/T_brucei/.



FEATURES  

    source  

    1..22  

    /organism="Trypanosoma brucei"  

    /mol_type="genomic DNA"  

    /strain="TREU927"  

    /db_xref="taxon:5691"  

    /clone="131b09"



Query Match 0.8%; Score 22; DB 1; Length 22;  

    Best Local Similarity 100.0%; Pred. No. 8.5e+02;  

    Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730  

    |||||||||||||||||||||||||  

    Db 1 AAAAAAAAAAAAAAAAAAAAAA 22



RESULT 1140  

    TA329F10P  

    LOCUS  

    DEFINITION T. brucei sheared genomic DNA clone 329f10, forward sequence,  

    genomic survey sequence.  

    ACCESSION AL492691  

    VERSION AL492691.1 GI:11868830  

    KEYWORDS GSS.


```

```

SOURCE      Trypanosoma brucei
ORGANISM    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   source
            1..22
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="329F10"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 1141
TA35C12Q/c
LOCUS      TA35C12Q 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 35c12, reverse sequence,
            genomic survey sequence.
ACCESSION  AL454256
VERSION    AL454256.1 GI:11855060
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   source
            1..22
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="329F10"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 1141
TA35C12Q/c
LOCUS      TA35C12Q 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 35c12, reverse sequence,
            genomic survey sequence.
ACCESSION  AL454256
VERSION    AL454256.1 GI:11855060
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   source
            1..22
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="329F10"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 1142
TA380A07P
LOCUS      TA380A07P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 380a07, forward sequence,
            genomic survey sequence.
ACCESSION  AL497713
VERSION    AL497713.1 GI:11873435
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 22)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES   source
            1..22
            /organism="Trypanosoma brucei"
            /mol_type="genomic DNA"
            /strain="TREU927"
            /db_xref="taxon:5691"
            /clone="35c12"
Query Match      0.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 1143
CF329694/c
LOCUS      CF329694 23 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-B19.b1 Rice callus plasmid cDNA library (NACL) Oryza

```



```

sativa (japonica cultivar-group) cDNA clone NACL--05-B19, mRNA
sequence.
ACCESSION CF329694
VERSION CF329694.1 GI:33807601
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..23
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--05-B19"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA...AAAAAAAAA 2729
Db 22 TAAAAA...AAAAAAAAA 1

RESULT 1144
CF32379/c
LOCUS CF32379 23 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-N21.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--08-N21, mRNA
sequence.
ACCESSION CF32379
VERSION CF32379.1 GI:33812983
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    Location/Qualifiers

```

```

    source
        1..23
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="NACL--08-N21"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7e-02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA...AAAAAAAAA 2729
Db 22 TAAAAA...AAAAAAAAA 1

RESULT 1145
DT495201
LOCUS DT495201 23 bp mRNA linear EST 29-AUG-2005
DEFINITION WS0112_BR_L03 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0112_L03
5', mRNA sequence.
ACCESSION DT495201
VERSION DT495201.1 GI:73892463
KEYWORDS EST.
SOURCE Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids 1; Malpighiales; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaliff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglass,C., Ritland,K. and
Bohlmann,J.
TITLE The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
JOURNAL Unpublished (2004)
COMMENT Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0112 row: L column: 03
High quality sequence stop: 132
POLYA=Yes.

FEATURES
    Location/Qualifiers
        1..23
            /organism="Populus trichocarpa"
            /mol_type="mRNA"
            /cultivar="383-2499 (Nisqually-1)"
            /db_xref="taxon:3694"
            /clone="WS0112_L03"
            /sex="Female"
            /lab_host="E. coli DH10B T1 phage resistant cells"
            /clone_lib="PT-P-FL-A-2"
            /note="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
            end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
            cambium from 8 year old trees harvested within the Boise
            Cascade region of Washington state on May 15th, 2001. cDNA
            was prepared from 20 micrograms of mRNA according to the
            full-length cDNA library construction method described by

```

Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector digested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation."

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 8.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2708 TAAAAA 2730
|||||
Db 1 TAAAAA 23

RESULT 1146

AZ425710 23 bp DNA linear GSS 03-OCT-2000
LOCUS IM0205123R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0205123 R, genomic survey sequence.

ACCESSION AZ425710
VERSION AZ425710.1 GI:10549723
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0205 row: L column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 23.

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0205123"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAA 2730
|||||
Db 2 AAAAAA 23

RESULT 1147

AZ801003 23 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0059J16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UGC2M0059J16 F, genomic survey sequence.

ACCESSION AZ801003
VERSION AZ801003.1 GI:12953326
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: J column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES

source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0079 row: A column: 23
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

Location/Qualifiers
 1. .24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0079A23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWP42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI-. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 TRACE considered overall poor quality
 Seq primer: ml3 -40 forward
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1. .25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3905397"
 /db_xref="taxon:9606"
 /clone="IMAGE:289557"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares multiple sclerosis 2NBHMSp"
 /note="Vector: pT7T3D (Pharmacia) with a modified polylinker V-type: phagemid; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5', TGTACCAATCTGAAGTGGCGGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."

Query Match 0.8%; Score 22; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 9e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 22 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1152
 CZ914626/c
 LOCUS CZ914626 25 bp mRNA linear EST 23-FEB-1996
 DEFINITION 4013007H05.2EL.y1 4013 - RescueMu Grid O Zea mays genomic, genomic survey sequence.
 ACCESSION CZ914626
 VERSION CZ914626.1 GI:71931353
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 25)

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

REFERENCE
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

FEATURES

Location/Qualifiers
 1. .25

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4013 - RescueMu Grid O"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid O was grown at Stanford in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1153

CZ916641

LOCUS

DEFINITION 4021002C08.2EL.Y1 4021 - RescueMu Grid V Zea mays genomic, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 4021002 row: C column: 08
Class: transposon-tagged.
Location/Qualifiers
1..25

FEATURES

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="4021 - RescueMu Grid V"
/notes="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription

units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
Db 4 TAAAAAAAAAAAAAAAAAAAAA 25

RESULT 1154

TA154D03P/C

LOCUS

DEFINITION T. brucei sheared genomic DNA clone 154d03, forward sequence, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 25)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="154d03"

Query Match 0.8%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 1155

AM046273

LOCUS

DEFINITION AM046273 Schistosoma mansoni lung schistosomulum Schistosoma mansoni cDNA clone SmlC32a10.q1k, mRNA sequence.

ACCESSION

AM046273


```

RESULT 1158
AW249476/c
LOCUS
DEFINITION      25 bp mRNA linear EST 07-JAN-2000
                  2821131.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821131 3',
                  mRNA sequence.
ACCESSION
VERSION          AW249476
KEYWORDS
SOURCE
ORGANISM         Homo sapiens (human)

REFERENCE
AUTHORS          NIH-MGC http://mgc.nci.nih.gov/
TITLE            National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL          Unpublished (1999)
COMMENT          Other_ESTs: 2821131.5prime
                  Contact: Robert Strausberg, Ph.D.
                  Email: cgapbs-r@mail.nih.gov
                  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
                  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
                  Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
                  project Clone distribution: MGC clone distribution information can
                  be found through the I.M.A.G.E. Consortium/LNL at:
                  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
                  Scores: PHRED from University of Washington Genome Center. Vector
                  Trimming: cross match from University of Washington Genome Center
                  PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
                  Drosophila Genome Project. University of Washington Genome Center:
                  http://www.genome.washington.edu Low Quality Sequence: 25
                  contiguous PHRED high quality bases followed vector sequence. Very
                  Low Quality Sequence: Trace file contained 25 contiguous distinct
                  peaks following vector sequence. Polyadenylation: Based upon the
                  presence of a XhoI site followed by a run of 14 or more T residues
                  at the beginning of the sequence, this cDNA insert was
                  polyadenylated.
                  Plate: L1CM6 row: A column: 4
                  High quality sequence stop: 25.
                  Location/Qualifiers
                    1..25
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2821131"
                      /tissue_type="small cell carcinoma"
                      /cell_line="MGC3"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH MGC 7"
                      /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                      EcoRI; cDNA made by oligo-dT priming. Directionally
                      cloned into EcoRI/XhoI sites using the following 5'
                      adaptor: GGACGAG(G). Size-selected >500bp for average
                      insert size 1.8kb. Library constructed by Ling Hong in
                      the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      0.8%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 9.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAGAAATAAAAAAAAA 1

RESULT 1159
DN954014
LOCUS
DEFINITION      25 bp mRNA linear EST 04-MAY-2005
                  DN954014
                  1t67e09.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
```

```

sequence.
DN954014
VERSION          DN954014.1 GI:63026152
KEYWORDS
SOURCE
ORGANISM         Gnetum gnemon
                  Gnetum gnemon
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Gnetaophyta; Gnetales; Gnetales; Gnetales; Gnetales;
                  1 (bases 1 to 25)
                  Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
                  O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McComb, R.W.,
                  Bentley, P., Coruzzi, G. and Stevenson, D.
                  Expressed tag sequences from Gnetum female cone (NYBG)
                  Unpublished (2003)
                  Contact: W. Richard McComb
                  Lita Annenberg Hazen Genome Sequencing Center
                  Cold Spring Harbor Laboratory
                  PO Box 100, Cold Spring Harbor, NY 11724, USA
                  Tel: 516 367 8884
                  Fax: 516 367 8874
                  Email: mccomb@cschl.org
                  Seq primer: -21M13UnivRev,
                  Location/Qualifiers
                    1..25
                      /organism="Gnetum gnemon"
                      /mol_type="mRNA"
                      /db_xref="taxon:3382"
                      /sex="female"
                      /clone_lib="Gnetum female cone (NYBG)"
                      /notes="Organ: mature, unfertilized reproductive strobili;
                      Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
                      Completed 02/11/02, submitted for sequencing 02/12/02.
                      Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                      library was size-fractionated to enrich for large inserts.
                      Sample: NYBG accession number #436/84"

Query Match      0.8%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 9.2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2704 GTACTAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 GTTATAAAAAAAAAAAAAAAAAAAAAA 25

RESULT 1160
AZ330737
LOCUS
DEFINITION      25 bp DNA linear GSS 29-SEP-2000
                  1M0056F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                  clone UUGC1M0056F09 F, genomic survey sequence.
ACCESSION
VERSION          AZ330737.1 GI:10392737
KEYWORDS
SOURCE
ORGANISM         Mus musculus (house mouse)
                  Mus musculus
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                  Sciurognathi; Muridae; Muridae; Muridae; Muridae;
                  1 (bases 1 to 25)
                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
                  Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
                  Niederhausern, A. and Wright, D., Weiss, R.
                  Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
                  Unpublished (2000)
                  Contact: Robert B. Weiss
                  University of Utah Genome Center
                  University of Utah
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                  84112, USA
                  Tel: 801 585 5606
                  Fax: 801 585 7177
```

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0056 row: F column: 09
 Seq primer: CATTGTAAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

```
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.8%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 9.2e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2705 TACTAAAAAATTTAAAAA 2729
 ||| |
 Db 1 TATTAAAAAATTTAAAAA 25

RESULT 1161

AZ442170
 LOCUS 1M0234H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0234H18 R, genomic survey sequence.
 ACCESSION AZ442170
 VERSION AZ442170.1 GI:10566183
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 REFERENCE Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0234 row: H column: 18
 Seq primer: CACACGAAACACGTATGACC
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers

FEATURES

source

```
1..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0234H18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.8%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 9.2e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAATTTAAAAA 2733
 ||| |
 Db 1 AAAAAAATTTAAAAA 25

RESULT 1162

DX053323/c
 LOCUS DX053323 25 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBRB057C20R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBRB057C20, genomic survey sequence.
 ACCESSION DX053323
 VERSION DX053323.1 GI:84747620
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 25)
 REFERENCE Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hahn, J.H. and Park, B.S.
 End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
 TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone
 JOURNAL
 COMMENT Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr
 BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone


```

KBrB057C20
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB057C20"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 0.8%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1163
CF337311/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--07-L06.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--07-L06, mRNA sequence.
CF337311.1 GI:33823014
1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 26;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

KBrB057C20
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB057C20"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match
Best Local Similarity 0.8%; Score 21.8; DB 1; Length 25;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1163
CF337311/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--07-L06.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--07-L06, mRNA sequence.
CF337311.1 GI:33823014
1. .25
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 26;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2733
Db 25 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1164
CF334077/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) EST 18-AUG-2003
JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
JMT--03-D17, mRNA sequence.
CF334077.1 GI:33816466
1. .23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-D17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 95.7%; Score 21.4; DB 1; Length 23;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1165
DR072900/c
LOCUS
DEFINITION
Ginkgo biloba (maidenhair tree) EST 08-JUN-2005
ik78f03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR072900.1 GI:67050748
1. .23
/organism="Ginkgo biloba (maidenhair tree)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--07-L06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 1; Length 26;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Expressed tag sequences from Ginkgo female leaf (NYBG)

TITLE
JOURNAL
COMMENT

Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers

FEATURES
source

1..23
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."
Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAATAAAAAAAAAAAAAAAAAAAAAA 2730

Db 23 TAAATAAAAAAAAAAAAAAAAAAGAAAA 1

RESULT 1166

DT501689 23 bp mRNA linear EST 29-AUG-2005
WS01313.BR M18 PTX-D-IL-FL-A-4 Populus trichocarpa x Populus
deltoides cDNA clone WS01313_M18 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DT501689.1 GI:73898951

Populus trichocarpa x Populus deltoides

Populus trichocarpa x Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;
rosids; eurosids 1; Malpighiales; Salicaceae; Populus.

REFERENCE
AUTHORS

1 (bases 1 to 23)
Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
Bohmann, J.

The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries

TITLE
JOURNAL
COMMENT

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS01313 row: M column: 18
High quality sequence stop: 123
POLYA=Yes.

FEATURES
source

1..23
Location/Qualifiers
/organism="Populus trichocarpa x Populus deltoides"
/mol_type="mRNA"
/cultivar="Hil-11"
/db_xref="taxon:3695"
/clone="WS01313_M18"
/sex="Male"

/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTX-D-IL-FL-A-4"
/note="Vector: pBluescript II SK (+) XR; Site 1: SetI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
one metre in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caged
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 4 hours, 8 hours and 24
hours after the onset of treatment. Mature leaves were
also collected above the caged region (systemic response)
4 hours, 12 hours and 48 hours after the onset of
treatment. mRNA was isolated from each tissue source
independently and equal quantities of mRNA from each
tissue were then pooled. cDNA was prepared from 20
micrograms of mRNA according to the full-length cDNA
library construction method described by Carninci P. et
al. (2000), Genome Research 10(10):1617-1630 and
directionally ligated into the pBluescript II SK (+) XR
vector digested with SetI (5' end) and XhoI (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (invitrogen) for propagation."

Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2706 ACTATAAAAAAAAAAAAAAAAAAAAAA 2728

Db 1 ATTAATAAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1167

AZ382013

LOCUS

DEFINITION

clone UUGC1M0138M14 R, genomic survey sequence.

ACCESSION

AZ382013

VERSION

AZ382013.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

AUTHORS

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0138 row: M column: 14

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0138M14"

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 23

```

```

RESULT 1168
AZ486853/c
LOCUS      23 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION      1M0315M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315M14 R, genomic survey sequence.

```

```

ACCESSION      AZ486853
VERSION        AZ486853.1 GI:10654033
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315M14"

```

```

FEATURES
source

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
      ||||| ||||| ||||| |||||
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 1169
AZ627841/c
LOCUS      23 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474E01 F, genomic survey sequence.

```

```

ACCESSION      AZ627841
VERSION        AZ627841.1 GI:11750127
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

```

JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

```

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: E column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474E01"

```

```

FEATURES
source

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAATAAAAAAAAAAAAA 1

```

RESULT 1170

```

AZ645254/c
LOCUS      23 bp      DNA      linear      GSS 14-DEC-2000
DEFINITION mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0510005 R, genomic survey sequence.

```

```

ACCESSION  AZ645254
VERSION     AZ645254.1  GI:11774572
KEYWORDS   GSS.
SOURCE     Mus musculus
           Mus musculus (house mouse)

```

ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

REFERENCE

```

1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.

```

```

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

```

TITLE

```

Unpublished (2000)

```

JOURNAL

```

Contact: Robert B. Weiss

```

COMMENT

```

University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 595 5606
Fax: 801 595 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0510 row: 0 column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

```

FEATURES

```

source

```

```

1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0510005"

```

```

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
DB 23 AAAAAAAAAAGAAAAAAAAAAAA 1

```

RESULT 1171

```

CL693171
LOCUS      23 bp      DNA      linear      GSS 10-JUL-2004
DEFINITION PRI0160b_B06_2 - PRI0160b.BR (23) Note: Recurring String Mixed
            stage fosmid library of P. pacificus var. California Pristionchus
            pacificus genomic, genomic survey sequence.

```

```

ACCESSION  CL693171
VERSION     CL693171.1  GI:50215079
KEYWORDS   GSS.
SOURCE     Pristionchus pacificus
           Pristionchus pacificus

```

ORGANISM

```

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

```

REFERENCE

```

1 (bases 1 to 23)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus

```

```

Nucleic Acids Res. 32 (1), D421-D422 (2004)

```

```

14681447

```

```

Contact: Sommer RJ

```

```

Evolutionary Biology

```

```

Max-Planck-Institute for Developmental Biology

```

```

Spemannstr. 37-39, Tuebingen D-72076, Germany

```

```

Tel: 00497071601371

```

```

Fax: 00497071601498

```

```

Email: ralf.sommer@tuebingen.mpg.de

```

```

This library was generated at Caltech, Pasadena, USA and end

```

```

sequenced at Vancouver, Canada.

```

```

Seq primer: T7

```

```

Class: fosmid ends.

```

```

Location/Qualifiers

```

FEATURES

```

source

```

```

1..23
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="vector: pEpifos-5 Fosmid vector"

```

```

Query Match      0.8%; Score 21.4; DB 1; Length 23;

```

```

Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAAACAAAAAAAAA 23

RESULT 1172
DU828758/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

DU828758 23 bp DNA linear GSS 22-DEC-2005
KBrS003116F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS003116, genomic survey
sequence.
DU828758
DU828758.1 GI:83865354
GSS.
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 23)
Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS003116
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..23
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS003116"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NTAB."

Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 23 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1173
TA55C06P
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

TA55C06P 23 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 55c06, forward sequence,
genomic survey sequence.
AL455778
AL455778.1 GI:11856729
GSS.
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

```

```

Trypanosoma.
1 (bases 1 to 23)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strains="TREU927"
/db_xref="taxon:5691"
/clone="55c06"

Query Match 0.8%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 9.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
Db 1 AAAAAAAAAATAAAAAAAAAA 23

RESULT 1174
CD743368/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CD743368 24 bp mRNA linear EST 25-JUN-2004
IRB8_E10_IRB8_072 Infected Rat Blood-fed (IRB) An.gam. 30 hr
Abdomen Library Anopheles gambiae cDNA 5', mRNA sequence.
CD743368
CD743368.1 GI:49247179
EST.
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 24)
Dana, A.N., Lobo, N.F., Hillenmeyer, M.E. and Collins, F.H.
Hematophagy-associated gene expression patterns in adult female
Anopheles gambiae mosquitoes
Unpublished (2003)
Contact: Dana A.N.
Frank H. Collins Laboratory
University of Notre Dame
Center for Tropical Disease
Sci., Notre Dame, IN 46556, USA
Tel.: 574 - 631 - 3241
Fax: 574 - 631 - 3996
Email: adana@nd.edu
PCR Primers
FORWARD: ctccggaagcgccattgtgttg
BACKWARD: ataccgactcatagggaattgc
Seq primer: ctccggaagcgccattgtgttg.
Location/Qualifiers
1..24
/organism="Anopheles gambiae"
/mol_type="mRNA"

```

```

/strain="4Arr"
/db_xref="taxon:7165"
/sex="female"
/tissue_type="Abdomens"
/dev_stage="Female adult 5-7 days post eclosion"
/lab_host="E. coli XLI-Blue"
/clone_lib="Infected Rat Blood-fed (IRB) An.gam. 30 hr
Abdomen Library"
/notes="Vector: lambdaTriplEx2 (Clontech); Site 1: Sfi IA;
Site 2: Sfi IB; Plasmidium berghel-infected rat blood-fed
adult female An. gambiae mosquitoes were flash frozen
after a 30 hour incubation of adult mosquitoes at 19
degrees Celsius. Total RNA extracted from abdomens
separated from remaining carcasses. cDNA inserts >500 bp
cloned directionally into IriplEx2; Sfi IA site is 5'.
Non-normalized and Non-amplified phagemid library. Single
pass sequencing reactions from 5' end."

```

Query Match 0.8%; Score 21.4; DB 1; Length 24;
 Best Local Similarity 91.7%; Pred. No. 9.5e+02;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||||||
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1175
 CF292725/c
 LOCUS
 DEFINITION 24 bp mRNA linear EST 14-AUG-2003
 30DGS--01-K12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 sativa (japonica cultivar-group) cDNA clone 30DGS--01-K12, mRNA
 sequence.

ACCESSION CF292725
 VERSION CF292725.1 GI:33661758
 KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. 24

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="30DGS--01-K12"

/tissue_type="leaf"

/dev_stage="30 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.8%; Score 21.4; DB 1; Length 24;
 Best Local Similarity 95.7%; Pred. No. 9.5e+02;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2702 TTGTACTAAAAAAAAAAAAA 2724

Db 23 TTGTCTAAAAAAAAAAAAA 1
 |||||||||

RESULT 1176
 AZ404871

LOCUS

DEFINITION

AZ404871 24 bp DNA linear GSS 03-OCT-2000

clone UGCGIM0173J14 R, genomic survey sequence.

ACCESSION AZ404871

VERSION AZ404871.1 GI:10528884

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhauser, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0173 row: J column: 14

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. 24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGIM0173J14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGIM library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.8%; Score 21.4; DB 1; Length 24;

Best Local Similarity 95.7%; Pred. No. 9.5e+02;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2707 CTAAAAAAAAAAAAAAAAAAAA 2729

```

Db      2  CTCAAAAAAAAAAAAAAAAAAAA 24

RESULT 1177
LOCUS   AZ486788
DEFINITION 1M031512F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM031512 F, genomic survey sequence.
ACCESSION AZ486788
VERSION   AZ486788.1 GI:10653906
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus

REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0315 row: I column: 22
          Seq Primer: CGTGTAAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 24.
          Location/Qualifiers
            source
              1. .24
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGCM0315122"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UGCM library"
                /notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA was hydronamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 [G14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.8%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 9.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAAAAAA 2730

```

```

Db      23 TAAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1178
LOCUS   AU265663/c
DEFINITION AU265663 VS Dictyostelium discoideum cDNA clone VSF713 5', mRNA sequence.
ACCESSION AU265663
VERSION   AU265663.1 GI:20524461
KEYWORDS  EST.
SOURCE    Dictyostelium discoideum
ORGANISM  Dictyostelium discoideum

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
TITLE    1 (bases 1 to 25)
AUTHORS  Uruehigahara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H., Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE    Analyses of cDNAs from growth and slug stages of Dictyostelium discoideum
JOURNAL  Nucleic Acids Res. 32 (5), 1647-1653 (2004)
PUBMED   15010511
COMMENT  Contact: Hideko Urushihara
          Institute of Biological Sciences
          University of Tsukuba
          1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
          Tel: 81-298-53-4664
          Fax: 81-298-53-6614
          Email: hideko@biol.tsukuba.ac.jp.
          Location/Qualifiers
            source
              1. .25
                /organism="Dictyostelium discoideum"
                /mol_type="mRNA"
                /strain="AX4"
                /db_xref="taxon:44689"
                /clone="VSF713"
                /sex="mat A"
                /dev_stage="vegetative"
                /clone_lib="VS"

Query Match      0.8%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2731

Db      24 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1179
LOCUS   AV737092
DEFINITION AV737092 CB Homo sapiens cDNA clone CBFB11 5', mRNA sequence.
ACCESSION AV737092
VERSION   AV737092.1 GI:10854673
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
TITLE    1 (bases 1 to 25)
AUTHORS  Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
TITLE    Homo sapiens CB library cDNA clones
JOURNAL  Unpublished (2000)
COMMENT  Shanghai Institute of Hematology, Rui-Jin Hospital
          197 Rui-Jin II Road, Shanghai 200025, P. R. China
          Tel: 86-21-64740490
          Fax: 86-21-64743206
          Email: mbshi@ms.stn.sh.cn
          This clone is available at Shanghai Hematology Institute in

```

```

Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES
  source
    1..25
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CBFBIB11"
      /tissue_type="cord blood"
      /cell_type="CD34+ hematopoietic stem/progenitor cell"
      /lab_host="BM25.8"
      /clone_lib="CB"
      /note="Vector: pBluescript; Site 1: EcoRI; The insert is
        cloned randomly with the EcoRI digestion"
    Query Match      0.8%; Score 21.4; DB 1; Length 25;
    Best Local Similarity 88.0%; Pred. No. 9.7e+02;
    Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2707 CTAAAAAAGAAAAAAGAAAAA 2731
Db 1 CNAANAAAAACAAAAAAGAAAAA 25

RESULT 1180
CG726337/C
LOCUS
DEFINITION
  1119089E12.2EL.Y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
  survey sequence.
ACCESSION
  CG726337
VERSION
  CG726337.1 GI:37764992
KEYWORDS
  GSS.
SOURCE
  Zea mays
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
    clade; Panicoideae; Andropogoneae; Zea.
  1 (bases 1 to 25)
REFERENCE
  Walbot,V.
  Maize genomic sequences found using engineered RescueMu transposon
  Unpublished (2001)
  Contact: Walbot V
  Department of Biological Sciences
  Stanford University
  855 California Ave, Palo Alto, CA 94304, USA
  Tel: 650 723 2227
  Fax: 650 725 8221
  Email: walbot@stanford.edu
  Possible ligation site of ends cut by 2 different endonucleases.
  Reverse complemented post-ligation sequence from source sequence.
  Plate: 1119089 row: E column: 12
  Class: transposon-tagged.
  Location/Qualifiers
    1..25
      /organism="Zea mays"
      /mol_type="genomic DNA"
      /cultivar="mixed background W23/Al88/B73/K55"
      /db_xref="taxon:4577"
      /tissue_type="leaf"
      /dev_stage="adult"
      /lab_host="DH10B"
      /clone_lib="1119 - RescueMu Grid AA"
      /note="Organ: leaf; Vector: RescueMu (engineered from
        pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
        RescueMu is a 4.9 kb, modified maize Mu transposon
        designed to allow plasmid rescue from total genomic DNA.
        Mu elements insert preferentially into transcription
        units. For more information on RescueMu, go to the web
        site 'www.zmndb.iaatate.edu' and follow the links for
        'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
        was extracted from leaf strips, double digested using
        BamHI and BglII, and ligated to form circular plasmids.

```

```

DH10B cells were transformed and then screened on LB
plates with ampicillin."
    Query Match      0.8%; Score 21.4; DB 1; Length 25;
    Best Local Similarity 95.7%; Pred. No. 9.7e+02;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAGAAAAAAGAAAAA 2729
Db 24 CCAAAAAAAGAAAAAAGAAAAA 2

RESULT 1181
AG194089
LOCUS
DEFINITION
  AG194089 Pan troglodytes DNA, clone: RP43-071013.TJ, genomic survey
  sequence.
ACCESSION
  AG194089
VERSION
  AG194089.1 GI:45226265
KEYWORDS
  GSS.
SOURCE
  Pan troglodytes (chimpanzee)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Pan.
  1
REFERENCE
  Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
  Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  BAC end sequences of Library RP-43
  Unpublished
  2 (bases 1 to 26)
REFERENCE
  Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
  Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  Direct Submission
  Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
  Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
  52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
  (E-mail:redtcons@mail.krrib.re.kr, URL:http://phs.grc.krrib.re.kr/,
  Tel:82-42-866-7181, Fax:82-42-860-4409)
  Clones are derived from the chimpanzee BAC library RP-43 This BAC
  end was generated during the R&D process and may have higher chance
  of clone tracking errors.
  PRIMERS
    Sequencing: TJ
  LIBRARY
    Vector : pBACe3.6
    R.Site 1 : EcoRI
    R.Site 2 : EcoRI.
  Location/Qualifiers
    1..26
      /organism="Pan troglodytes"
      /mol_type="genomic DNA"
      /db_xref="taxon:9598"
      /clone="RP43-071013.TJ"
      /sex="male"
      /cell_type="lymphocytes"
      /clone_lib="RP-43 Chimpanzee Male BAC Library"
    Query Match      0.8%; Score 21.4; DB 1; Length 26;
    Best Local Similarity 95.7%; Pred. No. 9.9e+02;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAAAGAAAAA 2730
Db 4 TAAAAAAGAAAAAAGAAAAA 26

RESULT 1182
AM043942
LOCUS
DEFINITION
  AM043942 Schistosoma mansoni lung schistosomulum Schistosoma
  mansoni cDNA clone SmC11B03.glk, mRNA sequence.
ACCESSION
  AM043942

```



```

VERSION AM043942.1 GI:72292305
KEYWORDS
SOURCE Schistosoma mansoni
ORGANISM Schistosoma mansoni

REFERENCE
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,
Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.
Microarray analysis identifies genes preferentially expressed in
the lung schistosomulum of Schistosoma mansoni
JOURNAL Unpublished (2005)
COMMENT Contact: Ivens AC
Pathogen Microarrays Group
Wellcome Trust Sanger Institute
Hinxton, CB10 1SA, UNITED KINGDOM.

FEATURES
source
1..26
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="Smlc1lb03.glk"
/dev_stage="lung schistosomulum"
/clone_lib="Schistosoma mansoni lung schistosomulum"
/note="country: Puerto Rico"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2701 TTGTACTAAAAA 2726
Db 1 TTTTTCCTAAAAA 1

RESULT 1184
CF280688/c
LOCUS 26 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--07-H09-g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ORYZA SATIVA (japonica cultivar-group) cDNA clone 14ETL--07-H09,
mRNA sequence.
ACCESSION CF280688
VERSION CF280688.1 GI:33658074
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-H09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"

/Note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2703 TGTACTAAAAA 2728
Db 26 TTTTCCAAAAA 1

RESULT 1184
AW333508/c
LOCUS 26 bp mRNA linear EST 31-JAN-2000
DEFINITION S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW333508
VERSION AW333508.1 GI:6829865
KEYWORDS EST.
ORGANISM Pneumocystis carinii
SOURCE Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 26)
Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..26
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"

/Note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat (59-1-6,
sacrificed on 3/17/99) at Cincinnati VA facilities.
Trioxol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 88.5%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 2701 TTTTACTAAAAA 2726
Db 26 TTTTTCCTAAAAA 1

RESULT 1185
AZ358846/c
LOCUS 26 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0101M24F Mouse 10kb plasmid UUG1M library Mus musculus genomic
clone UUG1M0101M24 F, genomic survey sequence.
ACCESSION AZ358846
VERSION AZ358846.1 GI:10472546
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 26)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,R., Stokes,R., Tingley,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0101 row: M column: 24
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 26.
FEATURES
source
              1..26
              /location/Qualifiers
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUC1M0101M24"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      0.8%; Score 21.2; DB 1; Length 26;
              Best Local Similarity 88.5%; Pred. No. 1e+03;
              Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2703 TCTACTAAAAA 2728
Db 26 TTTTAAAAA 1
              RESULT 1186
              C2917639
              LOCUS      C2917639      26 bp      DNA      linear      GSS 08-AUG-2005
              DEFINITION 4021006D11.2EL Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
              survey sequence.
              ACCESSION  C2917639
              VERSION     C2917639.1 GI:71936614
              KEYWORDS    GSS.
              SOURCE      Zea mays
              ORGANISM   Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 26)
              Walbot,V.
TITLE        Maize genomic sequences found using engineered RescueMu transposon
              Unpublished (2001)
JOURNAL
COMMENT      Contact: Walbot V
              Department of Biological Sciences
              Stanford University
              855 California Ave, Palo Alto, CA 94304, USA
              Tel: 650 723 2227
              Fax: 650 725 8221
              Email: walbot@stanford.edu
              Possible ligation site of ends cut by 2 different endonucleases.
              Reverse complemented post-ligation sequence from source sequence.
              Plate: 4021006 row: D column: 11
              Class: transposon-tagged.
FEATURES
source
              1..26
              /location/Qualifiers
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /cultivar="mixed background W23/A188/B73/K55"
              /db_xref="taxon:4577"
              /tissue_type="leaf"
              /dev_stage="adult"
              /lab_host="DH10B"
              /clone_lib="4021 - RescueMu Grid V"
              /note="Organ: leaf; Vector: RescueMu (engineered from
              pBluescript backbone); Site 1: BamHI; Site 2: BglII;
              RescueMu is a 4.9 kb, modified maize Mu transposon
              designed to allow plasmid rescue from total genomic DNA.
              Mu elements insert preferentially into transcription
              units. For more information on RescueMu, go to the web
              site 'http://www.mutransposon.org/project/RescueMu/'. Grid
              V was grown at University of Arizona in 2003. DNA was
              extracted from leaf strips, double digested using BamHI
              and BglII, and ligated to form circular plasmids. DH10B
              cells were transformed and then screened on LB plates with
              ampicillin."
              Query Match      0.8%; Score 21.2; DB 1; Length 26;
              Best Local Similarity 88.5%; Pred. No. 1e+03;
              Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2709 AAAAAA 2734
Db 1 AAAAAA 26
              RESULT 1187
              AJ658282
              LOCUS      AJ658282      21 bp      mRNA      linear      EST 28-JUN-2004
              DEFINITION AJ658282 KN277 Sus scrofa cDNA clone C0005212_D02, mRNA sequence.
              ACCESSION  AJ658282
              VERSION     AJ658282.1 GI:49342351
              KEYWORDS    EST.
              SOURCE      Sus scrofa (pig)
              ORGANISM   Sus scrofa
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.
              1 (bases 1 to 21)
              Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
              Development of cDNA and EST resources for studying reproduction and
              embryo development in pigs and cattle
              Unpublished (2004)
              Contact: Anderson SI
              Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
              Single pass sequencing. Bases called and trimmed with phred
              v0.020425.c. Vector identified by cross_match with the -minscore 20
              and -mismatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI
              R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
              from pooled early embryos, from 8- cell stage to blastocysts.

```

Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

```

source
1. .21
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005212_D02"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1188

```

AJ666203
LOCUS
DEFINITION
AJ666203 CSQRAN09 Sus scrofa cDNA clone C000033_C15, mRNA
sequence.

```

ACCESSION AJ666203

VERSION AJ666203.1 GI:49350654

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 21)

REFERENCE
 AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

```

source
1. .21
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000033_C15"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/notes="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1189

AL048777

LOCUS

DEFINITION
 AL048777 21 bp mRNA linear EST 04-SEP-2003
 DKFZP566N053_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZP566N053, mRNA sequence.

VERSION AL048777

KEYWORDS AL048777.1 GI:4727848

SOURCE EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominiidae; Homo.

1 (bases 1 to 21)

REFERENCE

AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.

TITLE EST (Koehrer, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source

```

1. .21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566N053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1190

AM047262/c

LOCUS

DEFINITION
 AM047262 Schistosoma mansoni lung schistosomulum Schistosoma
 mansoni cDNA clone SmlC23B06.gik, mRNA sequence.

ACCESSION AM047262

VERSION AM047262.1 GI:72293372

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 21)

REFERENCE

AUTHORS Dillon,G.P., Feltwell,T., Skelton,J.P., Ashton,P.D., Coulson,P.S.,

Nikolaïdou-Katsaridou,N., Quail,M.A., Wilson,R.A. and Ivens,A.C.,

Microarray analysis identifies genes preferentially expressed in

the lung schistosomulum of Schistosoma mansoni

Unpublished (2005)

CONTACT: Ivens AC

Pathogen Microarrays Group

Wellcome Trust Sanger Institute

Hinxton, CB10 1SA, UNITED KINGDOM.

Location/Qualifiers

1. .21

/organism="Schistosoma mansoni"

/mol_type="mRNA"

/db_xref="taxon:6183"

/clone="SmlC23B06.gik"

/dev_stage="lung schistosomulum"

/clone_lib="Schistosoma mansoni lung schistosomulum"

```

/note="Country: Puerto Rico"

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1191
CF282216      21 bp mRNA linear EST 14-AUG-2003
LOCUS 14ETL--09-K01.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-K01,
mRNA sequence.
ACCESSION CF282216.1 GI:33659603
VERSION CF282216
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1192
CF292703/c
LOCUS CF292703
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--01-K01, mRNA
sequence.
ACCESSION CF292703.1 GI:33661736
VERSION CF292703
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--01-K01"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1193
CF295642/c
LOCUS CF295642
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 30DGS--05-K20, mRNA
sequence.
ACCESSION CF295642.1 GI:33664675
VERSION CF295642
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--05-K20"
/tissue_type="leaf"

```



```

/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--05-G20"
/tissue_type="leaf"
/dev stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1197
 CF312715 21 bp mRNA linear EST 15-AUG-2003
 LOCUS ABP--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABP--08-J10, mRNA sequence.

ACCESSION CF312715 GI:33684476
 VERSION
 KEYWORDS

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 21)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .21

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABP--08-J10"

/tissue_type="leaf"

/dev stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1198
 CF316073/c

LOCUS

DEFINITION

HD--05-D16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa (japonica cultivar-group) cDNA clone

HD--05-D16, mRNA sequence.

CF316073

ACCESSION CF316073.1 GI:33687834

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .21

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--05-D16"

/tissue_type="callus"

/dev stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(200m) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1199
 CF326952/c

LOCUS

DEFINITION

NACL--01-D20.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--01-D20, mRNA

sequence.

CF326952

ACCESSION CF326952.1 GI:33802159

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-01-D20"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1200

CF327391
LOCUS
DEFINITION
NACL--01-N18.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--01-N18, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-01-N18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1201

CF32956
LOCUS
DEFINITION
JMT--01-K14.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT-01-K14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||

Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1202

CF338057
LOCUS
DEFINITION
JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

cDNA clone B3CS57RB007G04 3', mRNA sequence.
 CN546504
 EST 18739 RIPE Grape Berry Lambda Triplex2 Library Vitis vinifera
 CN546504.1 GI:46911129
 EST.
 SOURCE
 ORGANISM
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 21)
 Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
 Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
 source
 1. .21
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS57RB007G04"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /notes="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
 Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1206
 CN546595/c
 LOCUS
 DEFINITION
 EST 18739 RIPE Grape Berry Lambda Triplex2 Library Vitis vinifera
 cDNA clone B3CS58RB008G02 3', mRNA sequence.
 CN546595
 EST.
 CN546595.1 GI:46911220
 EST.
 SOURCE
 ORGANISM
 Vitis vinifera
 Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 21)
 Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
 Couture,C., Dedaldecamp,F., Delrot,S., Glissant,D., Grimplet,J.,
 Hamdi,S., Romieu,C. and Terrier,N.
 Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
 or seeds) at Various Developmental Stages
 Unpublished (2002)
 Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Université de Bordeaux I, Institut National de la Recherche
 Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
 France

Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.
 FEATURES
 source
 1. .21
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS58RB008G02"
 /dev_stage="ripe stage"
 /clone_lib="Ripe Grape Berry Lambda Triplex2 Library"
 /notes="Organ: Fruit without seeds; Vector: Lambda
 Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"
 Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1207
 CO779794/c
 LOCUS
 DEFINITION
 BL007D E05 6-Day Axolotl Tail Blastema (6DAXBL) Ambystoma mexicanum
 cDNA 5' similar to hypothetical protein, mRNA sequence.
 CO779794
 EST.
 CO779794.1 GI:50995774
 EST.
 SOURCE
 ORGANISM
 Ambystoma mexicanum (axolotl)
 Ambystoma mexicanum
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
 Ambystoma.
 1 (bases 1 to 21)
 Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
 Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
 An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
 expressed sequence tags from embryonic and regenerating blastema
 cDNA libraries
 Genome Biol. (2004) In press
 Contact: Elly M. Tanaka
 Tanaka Lab
 Max Planck Institute of Molecular Cell Biology and Genetics,
 Dresden
 Pfotenhauserstrasse 108,01307 Dresden, Germany
 Tel: 0049 351 210 2620
 Fax: 0049 351 210 1489
 Email: tanaka@mpi-cbg.de
 Plate: BL007D row: 05 column: E
 Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
 source
 1. .21
 /organism="Ambystoma mexicanum"
 /mol_type="mRNA"
 /db_xref="taxon:8296"
 /tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DAXBL)"
 /notes="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI;
 Unnormalized cDNA plasmid library prepared by Invitrogen.
 Size fractionated mRNA was polydt primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kB.
 TAG_LTB-6DAXBL"

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1208

DR063419/c
 LOCUS ip65b04.g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.
 ACCESSION DR063419 21 bp mRNA linear EST 06-JUN-2005
 VERSION DR063419.1 GI:66986987
 KEYWORDS EST.
 SOURCE Ginkgo biloba (maidenhair tree)
 ORGANISM Ginkgo biloba
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
 TITLE Expressed tag sequences from Ginkgo megasporophyll (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES

source
 1..21
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="Female"
 /clone_lib="Ginkgo megasporophyll (NYBG)"
 /note="Organ: megasporophyll; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1209

DR072918/c
 LOCUS ik79c11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION sequence.
 ACCESSION DR072918 21 bp mRNA linear EST 08-JUN-2005
 VERSION DR072918.1 GI:67050766
 KEYWORDS EST.
 SOURCE Ginkgo biloba (maidenhair tree)
 ORGANISM Ginkgo biloba
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballja,V., Martienssen,R.A., McCombie,R.W., Benfey,P., Coruzzi,G. and Stevenson,D.
 TITLE Expressed tag sequences from Ginkgo female leaf (NYBG)
 JOURNAL Unpublished (2005)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Seq primer: -21M13UnivRev.

FEATURES

source
 1..21
 Location/Qualifiers
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="female"
 /clone_lib="Ginkgo female leaf (NYBG)"
 /note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1210

AZ348593
 LOCUS AZ348593 21 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0085A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0085A13 F, genomic survey sequence.
 ACCESSION AZ348593
 VERSION AZ348593.1 GI:10427830
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0085 row: A column: 13
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source
 1..21
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0085A13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1211
AZ350611
LOCUS 21 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0088C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0088C14 F, genomic survey sequence.

ACCESSION AZ350611
VERSION AZ350611.1 GI:10429848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: C column: 14

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21
Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0088C14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1212

AZ386711

LOCUS

21 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0145016R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0145016 R, genomic survey sequence.

ACCESSION AZ386711

VERSION AZ386711.1 GI:10500411

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: O column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21
Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0145016"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1213

AZ386794

LOCUS

DEFINITION AZ386794 21 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0145022 R, genomic survey sequence.

ACCESSION

AZ386794

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0145 row: 0 column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0145022"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1214

AZ389287

LOCUS

DEFINITION AZ389287 21 bp DNA linear GSS 02-OCT-2000
clone UUGC1M0149A13 R, genomic survey sequence.

ACCESSION

AZ389287

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0149 row: A column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0149A13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1215
AZ389687
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ389687 21 bp DNA linear GSS 02-OCT-2000
1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B10 R, genomic survey sequence.

ACCESSION
AZ389687
VERSION
AZ389687.1 GI:105033395
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1216
AZ406936/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ406936 21 bp DNA linear GSS 03-OCT-2000
1M0176E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0176E24 F, genomic survey sequence.

ACCESSION
AZ406936
VERSION
AZ406936.1 GI:10530949
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: E column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0176E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source

1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0176E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1217
A2412739/c
LOCUS
DEFINITION
1M0186023F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0186023 F, genomic survey sequence.

ACCESSION A2412739
VERSION A2412739.1 GI:10536752
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: D column: 23
Seq primer: CGTTGTAAACACGCGCAGT

Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186023"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1218
A2412931/c
LOCUS
DEFINITION
1M0186N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0186N08 R, genomic survey sequence.

ACCESSION A2412931
VERSION A2412931.1 GI:10536944
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0186 row: N column: 08
Seq primer: CACACGAAACACGTATGACC

Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0186N08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1219

AZ415029
LOCUS 21 bp DNA linear GSS 03-OCT-2000
DEFINITION IM0189M07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0189M07 R, genomic survey sequence.

ACCESSION AZ415029
VERSION AZ415029.1 GI:105339042
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0189 row: M column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0189M07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1220

AZ465890/C

LOCUS 21 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0276F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0276F07 F, genomic survey sequence.

ACCESSION AZ465890

VERSION AZ465890.1 GI:10624015

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0276 row: F column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0276F07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||||
DB 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1221

AZ611116

LOCUS

DEFINITION AZ611116 21 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0436N02 R, genomic survey sequence.

ACCESSION

AZ611116

VERSION

AZ611116.1

GI:11733306

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0436 row: N column: 02

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0436N02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1222

AZ6111423

LOCUS

DEFINITION AZ6111423 21 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0437E13 R, genomic survey sequence.

ACCESSION

AZ6111423

VERSION

AZ6111423.1

GI:11733613

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0437 row: E column: 13

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0437E13"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1223
AZ615628/c
LOCUS
DEFINITION
1M0444M19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0444M19 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ615628
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: M column: 19
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
1. . 21

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0444M19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1224
AZ627843/c

LOCUS
DEFINITION
1M0474H03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474H03 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AZ627843
GSS.
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: H column: 03
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

Location/Qualifiers
1. . 21

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474H03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1225

AZ627845/c
LOCUS AZ627845 21 bp DNA linear GSS 13-DEC-2000
DEFINITION M0474G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474G11 F, genomic survey sequence.

ACCESSION AZ627845
VERSION AZ627845.1 GI:11750131
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: G column: 11

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0474G11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1226

AZ657727
LOCUS AZ657727 21 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0534B07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0534B07 F, genomic survey sequence.

ACCESSION AZ657727
VERSION AZ657727.1 GI:11794873
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

1 (bases 1 to 21)

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: B column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0534B07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1227
AZ766552
LOCUS 21 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0564011F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0564011 F, genomic survey sequence.
ACCESSION AZ766552
VERSION AZ766552.1 GI:12883741
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0564 row: 0 column: 11
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0564011"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1228
AZ769976
LOCUS 21 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0571111F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0571111 F, genomic survey sequence.
ACCESSION AZ769976
VERSION AZ769976.1 GI:12890681
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0571 row: L column: 11
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0571111"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

FEATURES
source

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1229

AZ793486/c
LOCUS
DEFINITION 21 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0046G18 R, genomic survey sequence.

ACCESSION AZ793486
VERSION
KEYWORDS
SOURCE GSS.
GI:12938487

ORGANISM
Mus musculus
(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0046 row: G column: 18

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0046G18"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1230

AZ799327
LOCUS
DEFINITION 21 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0056C09 R, genomic survey sequence.

ACCESSION AZ799327
VERSION
KEYWORDS
SOURCE GSS.
GI:12950331

ORGANISM
Mus musculus
(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: C column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056C09"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1231
AZ810054
LOCUS AZ810054 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0074E19 F, genomic survey sequence.
ACCESSION AZ810054
VERSION AZ810054.1 GI:12976935
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: E column: 19
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0074E19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1232
AZ815424
LOCUS AZ815424 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0083H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0083H1 R, genomic survey sequence.
ACCESSION AZ815424
VERSION AZ815424.1 GI:12985332
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: H column: 11
Seq primer: CACACAGGAACAGGTATGACC
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
1..21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0083H1"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: FW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1233

AZ819181
LOCUS AZ819181 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0089110 R, genomic survey sequence.

ACCESSION AZ819181
VERSION AZ819181.1 GI:12989089
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: 1 column: 10

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0089110"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1234

AZ832198
LOCUS AZ832198 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0112P20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0112P20 F, genomic survey sequence.

ACCESSION AZ832198
VERSION AZ832198.1 GI:13002106
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0112 row: P column: 20

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0112P20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1235

AZ843603
LOCUS 21 bp DNA linear GSS 20-FEB-2001
DEFINITION ZM0142106R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0142106 R, genomic survey sequence.

ACCESSION AZ843603
VERSION AZ843603.1 GI:13013511
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0142 row: I column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1. .21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0142106"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1236

AZ960063
LOCUS 21 bp DNA linear GSS 27-APR-2001
DEFINITION ZM0228A01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0228A01 F, genomic survey sequence.

ACCESSION AZ960063

VERSION AZ960063.1 GI:13831290

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: A column: 01

Seq primer: CGTTGTAAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1. .21
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0228A01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1237
BH000837 21 bp DNA linear GSS 27-APR-2001
LOCUS 2M0288020R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION Clone UUGC2M0288020 R, genomic survey sequence.

ACCESSION BH000837
VERSION BH000837.1 GI:13872063
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0288 row: 0 column: 20

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0288020"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

source

Query Match 0.8%; Score 21; DB 1; Length 21;

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1238
DU828985/c

LOCUS DU828985

DEFINITION DU828985

subsp. pekinensis genomic clone KBR5004C05, genomic survey

sequence.

ACCESSION DU828985

VERSION DU828985.1 GI:83865581

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 21)

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

JOURNAL

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone

KBrS004C05

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .21

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrS004C05"

/lab_host="E. coli DH10B"

/clone_lib="KBrS Brassica rapa Sau3AI BAC library"

/note="Vector: pCUGIBAC1; Site_1: Sau3AI; Brassica rapa

ssp pekinensis var. Chiifu BAC library (KBrS BAC) 18

available at NIAB."

Query Match 0.8%; Score 21; DB 1; Length 21;


```

Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1239
DUB30099 21 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS006C07R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS006C07, genomic survey
sequence.
ACCESSION DUB30099
VERSION DUB30099.1 GI:83866695
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS006C07
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1..21
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS006C07"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIB."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1240
DUB32906 21 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS011B18R KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS011B18, genomic survey
sequence.
ACCESSION DUB32906
VERSION DUB32906.1 GI:83869502
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS011B18
Seq primer: T7

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS011B18
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1..21
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS011B18"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chifu BAC library (KBrS BAC) is
available at NIB."

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1241
DUB34573 21 bp DNA linear GSS 22-DEC-2005
LOCUS KBrS014K05F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION subsp. pekinensis genomic clone KBrS014K05, genomic survey
sequence.
ACCESSION DUB34573
VERSION DUB34573.1 GI:83871169
KEYWORDS GSS.
SOURCE Brassica rapa subsp. pekinensis
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 21)
AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
Hahn,J. H. and Park,B.S.
TITLE End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL Unpublished (2005)
COMMENT Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS014K05
Seq primer: T7

```

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

REFERENCE
AUTHORS      1 (bases 1 to 21)
              Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
              Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
              Hahn,J.H. and Park,B.S.
TITLE
JOURNAL      End sequence of Brassica rapa BamHI (KBrB) BAC clone
COMMENT      Unpublished (2005)
              Contact: Beom-Seok Park
              Brassica Genomics Team
              National Institute of Agricultural Biotechnology
              225 Seodun-Dong, Suwon, 441-707, Korea
              Tel: +82-31-299-1670
              Fax: +82-31-299-1672
              Email: pbeom@da.go.kr
              BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
              KBrB052P02
              Seq primer: T7
              Class: BAC ends.
FEATURES
source       Location/Qualifiers
              1..21
              /organism="Brassica rapa subsp. pekinensis"
              /mol_type="genomic DNA"
              /cultivar="Chiifu"
              /sub_species="pekinensis"
              /db_xref="taxon:51351"
              /clone="KBrB052P02"
              /lab_host="E.coli DH10B"
              /clone_lib="KBrB, Brassica rapa BamHI BAC library"
              /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
              pekinensis var. Chiifu BAC library (KBrB BAC) is provided
              by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
DB      1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1245
LOCUS   DX056929/c
DEFINITION
KBrB061P24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB061P24, genomic survey
sequence.
ACCESSION
VERSION  DX056929.1 GI:84751226
KEYWORDS
SOURCE    GSS.
ORGANISM  Brassica rapa subsp. pekinensis
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
           Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
           Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
           Brassica Genomics Team
           National Institute of Agricultural Biotechnology
           225 Seodun-Dong, Suwon, 441-707, Korea
           Tel: +82-31-299-1670
           Fax: +82-31-299-1672
           Email: pbeom@da.go.kr
           BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
           KBrB061P24
           Seq primer: T7
           Class: BAC ends.
FEATURES
source     Location/Qualifiers
            1..21
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBrB061P24"
            /lab_host="E.coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chiifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
DB      1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1245
LOCUS   DX056929/c
DEFINITION
KBrB061P24R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB061P24, genomic survey
sequence.
ACCESSION
VERSION  DX056929.1 GI:84751226
KEYWORDS
SOURCE    GSS.
ORGANISM  Brassica rapa subsp. pekinensis
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
           Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
           Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
           Brassica Genomics Team
           National Institute of Agricultural Biotechnology
           225 Seodun-Dong, Suwon, 441-707, Korea
           Tel: +82-31-299-1670
           Fax: +82-31-299-1672
           Email: pbeom@da.go.kr
           BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
           KBrB061P24
           Seq primer: T7
           Class: BAC ends.
FEATURES
source     Location/Qualifiers
            1..21
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBrB061P24"
            /lab_host="E.coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chiifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB061P24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
DB      1 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1246
LOCUS   DX059939/c
DEFINITION
KBrB066A01F KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB066A01, genomic survey
sequence.
ACCESSION
VERSION  DX059939.1 GI:84754235
KEYWORDS
SOURCE    GSS.
ORGANISM  Brassica rapa subsp. pekinensis
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
           rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS   Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
           Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
           Hahn,J.H. and Park,B.S.
TITLE     End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL   Unpublished (2005)
COMMENT   Contact: Beom-Seok Park
           Brassica Genomics Team
           National Institute of Agricultural Biotechnology
           225 Seodun-Dong, Suwon, 441-707, Korea
           Tel: +82-31-299-1670
           Fax: +82-31-299-1672
           Email: pbeom@da.go.kr
           BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
           KBrB066A01
           Seq primer: T7
           Class: BAC ends.
FEATURES
source     Location/Qualifiers
            1..21
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBrB066A01"
            /lab_host="E.coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chiifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
DB      1 AAAAAAAAAAAAAAAAAAAAAA 1
```

RESULT 1247

DX075742

LOCUS

DEFINITION

21 bp DNA linear GSS 10-JAN-2006
 KBrB086M24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB086M24, genomic survey
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DX075742.1 GI:84770038

GSS.

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

KBrB086M24

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21

Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB086M24"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp

pekinensis var. Chiifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match

Best Local Similarity 0.8%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709

1

AAAAAAAAAAAAAAAAAAAAA 2729

|||||

AAAAAAAAAAAAAAAAAAAAA 21

RESULT 1248

DX082155/c

LOCUS

DEFINITION

21 bp DNA linear GSS 10-JAN-2006
 KBrB095F12F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB095F12, genomic survey
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DX082155.1 GI:84776451

GSS.

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

TITLE

JOURNAL

COMMENT

Hahn, J.H. and Park, B.S.
 End sequence of Brassica rapa BamHI (KBrB) BAC clone
 Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB095F12

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21

Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB095F12"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp

pekinensis var. Chiifu BAC library (KBrB BAC) is provided

by Yong-Pyo Lim (CNU)."

Query Match

Best Local Similarity 0.8%; Score 21; DB 1; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709

1

AAAAAAAAAAAAAAAAAAAAA 2729

|||||

AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1249

DX082624

LOCUS

DEFINITION

21 bp DNA linear GSS 10-JAN-2006
 KBrB095P24F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB095P24, genomic survey
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

DX082624.1 GI:84776920

GSS.

Brassica rapa subsp. pekinensis

Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 21)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB095P24

Seq primer: T7

Class: BAC ends.

FEATURES

source

1. .21

Location/Qualifiers

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

```

/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB095924"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.8%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1250

AL038477

LOCUS DXFZp566C1646_r1 566 (synonym: hfk42) Homo sapiens cDNA clone
DEFINITION DXFZp566C1646, mRNA sequence.

ACCESSION AL038477

VERSION AL038477.1 GI:49692139

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 22)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES
source
1..22
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566C1646"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfk42)"
/notes="Vector: pAMF1; Site 1: NotI; Site 2: SalI"

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 2 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1251

CF282024/c

LOCUS 14ETL--09-F13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F13,
mRNA sequence.

ACCESSION CF282024

VERSION CF282024.1 GI:33659411

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 22)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--09-F13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 22 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1252

CO778290

LOCUS CO778290 22 bp mRNA linear EST 05-AUG-2004
DEFINITION BL003B_H01 6-Day Axolotl Tail Blastema (GDAXBL) Ambystoma mexicanum
cDNA 5' similar to hypothetical protein, mRNA sequence.

ACCESSION CO778290

VERSION CO778290.1 GI:50994270

KEYWORDS EST.

SOURCE Ambystoma mexicanum (axolotl)

ORGANISM Ambystoma mexicanum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
Ambystoma.
1 (bases 1 to 22)
Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Pehike,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfothenhauserstrasse 108,01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: BL003B row: 01 column: H
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
source
1..22
Location/Qualifiers
/organism="Ambystoma mexicanum"
/mol_type="mRNA"
/db_xref="taxon:8296"

/tissue_type="Tail Blastema"
 /cell_type="regenerating tail blastema"
 /clone_lib="6-Day Axolotl Tail Blastema (6DaxBL)"
 /note="Vector: pCMVSPORT6; Site_1: NOT1; Site_2: SalI;
 Unnormalized cDNA plasmid library prepared by invitrogen.
 Size fractionated mRNA was polydT primed and cloned into
 NotI-SalI site of pCMVSPORT6. Bacterial host is
 EMDH10B-TONA. Average insert size is 1.67 kb.
 TAG_LIB=6DAXBL"

Query Match 0.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1253
 AZ304806
 LOCUS 22 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0005K17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0005K17 F, genomic survey sequence.

ACCESSION AZ304806
 VERSION AZ304806.1 GI:10341191

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0005 row: K column: 17

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0005K17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gil4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 |||||
 DB 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1254

AZ374487

LOCUS 22 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0127H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0127H16 F, genomic survey sequence.

ACCESSION AZ374487

VERSION AZ374487.1 GI:10488187

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0127 row: H column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0127H16"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1255
AZ505769
LOCUS 22 bp DNA linear GSS 05-OCT-2000
DEFINITION lM0346A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ505769
VERSION 1 GI:10687085
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0346 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0346A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
Db 2 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1256
AZ823875
LOCUS 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0098K07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ823875
VERSION 1 GI:12993795
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

REFERENCE
AUTHORS
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: K column: 07
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0098K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

FEATURES
source

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [GI:4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.8%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
|||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1257

AL048776
LOCUS
DEFINITION
23 bp mRNA linear EST 04-SEP-2003
DKFZp566N213_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566N213, mRNA sequence.

ACCESSION
AL048776
VERSION
AL048776.1 GI:4727847

KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE

1 (bases 1 to 23)
AUTHORS
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehrer, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1. .23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N213"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pMPL; Site_1: NotI; Site_2: Sali"

Query Match 0.8%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 3 TAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1258

DT503381
LOCUS
DEFINITION
23 bp mRNA linear EST 29-AUG-2005
WS0136.BR_G19 PTXD-IL-FL-A-4 Populus trichocarpa x Populus
deltoides cDNA clone WS0136_G19 5', mRNA sequence.

ACCESSION
DT503381
VERSION
DT503381.1 GI:73900643

KEYWORDS

EST.

SOURCE

Populus trichocarpa x Populus deltoides
Populus trichocarpa x Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Populus.

REFERENCE

AUTHORS

1 (bases 1 to 23)
Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
Bohlmann, J.

TITLE

The poplar transcriptome: Analysis of expressed sequence tags from

multiple cDNA libraries

JOURNAL

COMMENT

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0136 row: G column: 19
High quality sequence stop: 104
POLYA=Yes.

FEATURES

source

1. .23
Location/Qualifiers
/organism="Populus trichocarpa x Populus deltoides"
/mol_type="mRNA"
/cultivar="Hil-11"
/db_xref="taxon:3695"
/clone="WS0136_G19"
/sex="Male"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTXD-IL-FL-A-4"
/note="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
one metre in height and grown under greenhouse conditions
were exposed to continuous feeding by Malacosoma disstria
Hubner (forest tent caterpillar) mid-instar larvae caged
on the sapling using mesh bags. Mature leaves from within
the caged region were collected 4 hours, 8 hours and 24
hours after the onset of treatment. Mature leaves were
also collected above the caged region (systemic response)
4 hours, 12 hours and 48 hours after the onset of
treatment. mRNA was isolated from each tissue source
independently and equal quantities of mRNA from each
tissue were then pooled. cDNA was prepared from 20
micrograms of mRNA according to the full-length cDNA
library construction method described by Carninci P. et
al. (2000). Genome Research 10(10):1617-1630 and
directionally ligated into the pBluescript II SK (+) XR
vector digested with SstI (5' end) and XhoI (3'). Plasmid
DNA was then transformed by electroporation into DH10B
cells (Invitrogen) for propagation."

Query Match 0.8%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
|||||
DB 3 TAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1259

AL037096
LOCUS
DEFINITION
26 bp mRNA linear EST 06-JUL-2004
DKFZp564I2164_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKFZp564I2164, mRNA sequence.

ACCESSION
AL037096

VERSION
AL037096.1 GI:49681938

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;


```

REFERENCE
AUTHORS      Hominidae; Homo.
              1 (bases 1 to 26)
TITLE        Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
              Wiemann, S.
JOURNAL      EST (Duesterhoeft, et al.)
COMMENT      Unpublished (1999)
              Contact: MIPS
              MIPS

FEATURES
source       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
              1..26
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="DKFZP564L2164"
                /tissue_type="brain"
                /dev_stage="fetal"
                /lab_host="X1-2blue"
                /clone_lib="564 (synonym: hibr2)"
                /note="Vector: pAMP1; Site_1: NotI; Site_2: Sali"

Query Match      0.8%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches          21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      6 AAAAAAAAAAAAAAAAAAAAAA 26

RESULT 1260
TA321G11P
LOCUS      TA321G11P
DEFINITION T. brucei sheared genomic DNA clone 321g11, forward sequence,
            genomic survey sequence.
ACCESSION  AL492371
VERSION     AL492371.1 GI:11867375
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
ORGANISM    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma
            1 (bases 1 to 26)
REFERENCE   Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
            Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
            Melville, S.E., Rajandream, M.A. and Barrell, B.G.
            Direct Submission
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source       Location/Qualifiers
              1..26
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clone="321g11"

Query Match      0.8%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;

```

```

Matches          21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1261
AZ626101/c
LOCUS      AZ626101
DEFINITION 1M0466J07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0466J07 F, genomic survey sequence.
ACCESSION  AZ626101
VERSION     AZ626101.1 GI:11748291
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
            1 (bases 1 to 24)
REFERENCE   Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0466 row: J column: 07
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.

FEATURES
source       Location/Qualifiers
              1..24
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0466J07"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03;

```

Matches	22;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	2709	AAAAAAAAAAAAAAAAAAAAAA 							
Db	24	AAAAAAAAAAAAAAAAAAAAAAGAA 1							
RESULT 1262									
AZ627850 A2627850 24 bp DNA linear GSS 13-DEC-2000									
LOCUS									
DEFINITION M0474N20F Mouse 10kb plasmid UUCG1M library Mus musculus genomic									
Clone UUGC1M0474N20 F, genomic survey sequence.									
ACCESSION A2627850									
VERSION A2627850.1 GI:11750136									
KEYWORDS GSS.									
SOURCE Mus musculus (house mouse)									
ORGANISM									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C., Islam.H., Longacre.S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes.R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: dduun@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0474 row: N column: 20 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24. Location/Qualifiers 1 . 24 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0474N20" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UUCG1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW42 [gi1473114 gbAFI29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."									
FEATURES									
source									
Query Match 0.8%; Score 20.8; DB 1; Length 24; Best Local Similarity 91.7%; Pred.No. 1e+03;									

```

Hahn, J. H. and Park, B. S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeon@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS004M04
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. .24
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS004M04"
/lab_host="E. coli DH10B"
/clone_lib="KBrS Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGTBAC1; Site_1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAH."

Query Match      0.8%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1265
AZ476141/c
LOCUS
DEFINITION
1M0294M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0294M10 R, genomic survey sequence.
ACCESSION
AZ476141
VERSION
AZ476141.1 GI:10634266
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0294 row: M column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25

TITLE
JOURNAL
COMMENT

```

```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0294M10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.8%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 1e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
Db 24 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1266
CZ910207
LOCUS
DEFINITION
C4012001F09.1EL_Y1 4012 - RescueMu Grid BB Zea mays genomic, genomic
survey sequence.
ACCESSION
CZ910207
VERSION
CZ910207.1 GI:71923665
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 25)
Walbot V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 4012001 row: F column: 09
Class: transposon-tagged
Location/Qualifiers
1. .25
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"

FEATURES
source

```

/lab_host="DH10B"
 /clone_lib="4012 - RescueMu Grid BB"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid BB was grown at UC Berkeley in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 0.8%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2731
 |||||||||||||||||||||
 Db 1 TAAAAAAAAAAAAAAAAAACAG 24

RESULT 1267

CZ917081 25 bp DNA linear GSS 08-AUG-2005
 LOCUS 4021004807.2EL_Y1 4021 - RescueMu Grid V Zea mays genomic, genomic
 DEFINITION survey sequence.

ACCESSION CZ917081
 VERSION CZ917081.1 GI:71935617
 KEYWORDS GSS.

SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE Walbot,V.
 Maize genomic sequences found using engineered RescueMu transposon
 TITLE Unpublished (2001)
 JOURNAL Contact: Walbot V
 COMMENT Department of Biological Sciences

Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 4021004 row: B column: 07
 Class: transposon-tagged.

FEATURES

source

1. .25
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73/K55"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"

/clone_lib="4012 - RescueMu Grid v"
 /note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'http://www.mutransposon.org/project/RescueMu/'. Grid V was grown at University of Arizona in 2003. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with

ampicillin."

Query Match 0.8%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 1e+03;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2732
 |||||||||||||||||||||
 Db 1 AAAAAAAAAAAAAAAAAAGAGAAA 24

RESULT 1268

AZ437459/c

LOCUS AZ437459 26 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1W0225B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0225B15 R, genomic survey sequence.

ACCESSION AZ437459
 VERSION AZ437459.1 GI:10561472

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 26)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0225 row: B column: 15

Seg primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

Location/Qualifiers

1. .26

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0225B15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [gi4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0287 row: L column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source
Location/Qualifiers

1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0287L21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydronamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|95|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity 95.5%; Pred. No. 1e+03; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||
1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1274

DU835072/c

LOCUS

DEFINITION 22 bp DNA linear GSS 22-DRC-2005
subsp. pekinensis genomic clone KBrS015P15, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 22)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J. H. and Park, B.S.

End sequence of Brassica rapa Sau3AI (KBrS) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS015P15

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS015P15"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: PCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match

Best Local Similarity 95.5%; Pred. No. 1e+03; Length 22;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2730

|||||
22 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1275

DX060105

LOCUS

DEFINITION 22 bp DNA linear GSS 10-JAN-2006
KBrS066D14F KBrS, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrS066D14, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 22)

Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,

Hahn, J.H. and Park, B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrS066D14

Seq primer: T7

Class: BAC ends.

source

Location/Qualifiers

1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS066D14"
/lab_host="E. coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

```

Query Match      0.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
    |||||
Db 1 AAAAAAAAAAAAAAAAAACAAA 22

RESULT 1276
TA303G05P
LOCUS TA303G05P 22 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence,
genomic survey sequence.
ACCESSION AL497383
VERSION AL497383.1 GI:11865504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhi@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 Gutrat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
source
1..22
Location/Qualifiers
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="303g05"

Query Match      0.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
    |||||
Db 1 AAAAAAAAAAGAAAAAAAAA 22

RESULT 1277
AL038397
LOCUS AL038397 23 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp566N082_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566N082, mRNA sequence.
ACCESSION AL038397
VERSION AL038397.1 GI:49682109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

Query Match      0.7%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
    |||||
Db 1 AAAAAAAAAAGAAAAAAAAA 22

RESULT 1278
AL038592
LOCUS AL038592 23 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp566G1446_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566G1446, mRNA sequence.
ACCESSION AL038592
VERSION AL038592.1 GI:49682166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566G1446"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTATAAAAAAAAAAAAAAAAAA 2726
    |||
Db 2 TACAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1279
AL038609
LOCUS AL038609 23 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp566N082_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566N082, mRNA sequence.
ACCESSION AL038609
VERSION AL038609.1 GI:49682109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```

```

REFERENCE 1 (bases 1 to 23)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N082"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTATAAAAAAAAAAAAAAAAAA 2726
    |||
Db 2 TACAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1278
AL038592
LOCUS AL038592 23 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp566G1446_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566G1446, mRNA sequence.
ACCESSION AL038592
VERSION AL038592.1 GI:49682166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 23)
AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566G1446"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2705 TACTATAAAAAAAAAAAAAAAAAA 2726
    |||
Db 2 TACAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1279
AL038609
LOCUS AL038609 23 bp mRNA linear EST 06-JUL-2004
DEFINITION DKFZp566N082_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566N082, mRNA sequence.
ACCESSION AL038609
VERSION AL038609.1 GI:49682109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

```



```

SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, BEP
clade, Ehrhartoideae, Oryzeae, Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
Contact: Nahm B.H.
JOURNAL
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
source
1..23
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--05-P06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2730
Db 22 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 1283
DT496947 23 bp mRNA linear EST 29-AUG-2005
WS01125.BR A14 PT-P-FL-A-2 Populus trichocarpa cDNA clone
WS01125 A14 5', mRNA sequence.
DT496947
ACCESSION DT496947.1 GI:73894209
VERSION
KEYWORDS
SOURCE
ORGANISM
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Malpighiales, Salicaceae, Salicaceae, Populus.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Scott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Jones,S., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,
Holt,R., Moran,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Bohlmann,J.
The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2004)
TITLE
Contact: Joerg Bohlmann
JOURNAL
Genome BC forest genomics program
COMMENT
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@mel.ubc.ca
Plate: WS01125 row: A column: 14
High quality sequence stop: 108
POLYA=Yes.
FEATURES
Location/Qualifiers
source
1..23
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01125_A14"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/note="Vector: pBluescript II SK (+) XR; Site 1: SctI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000). Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SctI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."
Query Match 0.7%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
Db 2 TCAAAAAAAAAAAAAAAAAAAAA 23
RESULT 1284
AL048765 24 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION
DKFZps566M233.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
AL048765
ACCESSION
VERSION
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 24)
AUTHORS
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
Location/Qualifiers
source
1..24
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZps566M233"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2708 TAAAAAAAAAAAAAAAAAAAAA 2729
Db 1 |||||

```

```

Db      3  TCAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1285
CF326993
LOCUS   NACL--01-E17, g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone NACL--01-E17, mRNA
sequence.
ACCESSION CF326993
VERSION   1
KEYWORDS  24 bp mRNA linear EST 18-AUG-2003
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 24)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
AUTHORS   Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
TITLE     Contact: Nahm B.H.
JOURNAL   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT   of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..24
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--01-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2730
        |||||
Db      3  AAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1286
DT496307
LOCUS   WS01123_BR_A15 PT-P-FL-A-2 Populus trichocarpa cDNA clone
DEFINITION WS01123_A15 5', mRNA sequence.
ACCESSION DT496307
VERSION   1
KEYWORDS  24 bp mRNA linear EST 29-AUG-2005
SOURCE    Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM  Populus trichocarpa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Malpighiales; Salicaceae; Populus.
          1 (bases 1 to 24)
REFERENCE Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,
AUTHORS   Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
          Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
          Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
          Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
          Bohlmann, J.

TITLE     The poplar transcriptome: Analysis of expressed sequence tags from
JOURNAL   multiple cDNA libraries
COMMENT   Unpublished (2004)
          Contact: Joerg Bohlmann
          Genome BC forest genomics program
          University of British Columbia
          Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
          Vancouver, British Columbia, Canada, V6T 1Z3
          Tel: 1-604-822-0282
          Fax: 1-604-822-2114
          Email: bohlmann@mal.ubc.ca
          Plate: WS01123 row: A column: 15
          High quality sequence stop: 124
          POLYA=Yes.

FEATURES
source
1..24
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01123_A15"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SstI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

Query Match 0.7%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2707 CTAAAAAAAAAAAAAAAAAAAA 2728
        |||||
Db      3  CCAAAAAAAAAAAAAAAAAAAAA 24

RESULT 1287
CF310471/c
LOCUS   ABF--05-C07.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C07, mRNA sequence.
ACCESSION CF310471
VERSION   1
KEYWORDS  25 bp mRNA linear EST 15-AUG-2003
SOURCE    Oryza sativa (japonica cultivar-group)
ORGANISM  Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          clade; Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 25)
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
AUTHORS   Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
TITLE     Contact: Nahm B.H.
JOURNAL   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
COMMENT   of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..24
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS01123_A15"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SstI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

```

Query Match	0.7%	Score 20.4;	DB 1;	Length 25;
Best Local Similarity	95.5%	Pred. No. 1.1e+03;		

TITLE
JOURNAL

COMMENT
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
1..25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="12f02"

Query Match 0.7%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2701 TTGTACTAAAAA 2725
||| |||||
Db 1 TTTTAAAAA 25

RESULT 1293
AJ666402/c
LOCUS
DEFINITION
AJ666402
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AJ666402 20 bp mRNA linear EST 28-JUN-2004
AJ666402 CSEQRAN09 Sus scrofa CDNA clone C000033_C23, mRNA sequence.
AJ666402
AJ666402.1 GI:49350853
EST.
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 20)
Anderson S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..20
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000033_C23"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library

constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2709 AAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAA 1

RESULT 1294
AL038427
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL038427 20 bp mRNA linear EST 06-JUL-2004
DKFP566A1746_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038427
AL038427.1 GI:49682121
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566A1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="XI-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site 1: NotI; Site 2: SalI"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2708 TAAAAA 2727
|||||
Db 1 TAAAAA 20

RESULT 1295
AL038429
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL038429 20 bp mRNA linear EST 06-JUL-2004
DKFP566A1946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038429
AL038429.1 GI:49682123
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2708 TAAAAA 2727
|||||
Db 1 TAAAAA 20

RESULT 1295
AL038429
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL038429 20 bp mRNA linear EST 06-JUL-2004
DKFP566A1946_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038429
AL038429.1 GI:49682123
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Ottewaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Ottewaelder, et al.)
Unpublished (1999)
Contact: MIPS
MIPS

```

FEATURES
source
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566M1146"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA...AAAAAAAAA 2727
Db 1 TAAAAA...AAAAAAAAA 20

RESULT 1296
AL038570
LOCUS
DEFINITION
DKFP566F1746_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION
AL038570
VERSION
AL038570.1 GI:49682159
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 20)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS

FEATURES
source
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566F1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA...AAAAAAAAA 2727
Db 1 TAAAAA...AAAAAAAAA 20

RESULT 1297
AL038750
LOCUS
DEFINITION
DKFP566M1146_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION
AL038750
VERSION
AL038750.1 GI:49682199
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

```

```

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 20)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS

FEATURES
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566M1146"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAA...AAAAAAAAA 2728
Db 1 AAAAAA...AAAAAAAAA 20

RESULT 1298
CF280913
LOCUS
DEFINITION
14ETL--07-M07.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--07-M07,
mRNA sequence.
ACCESSION
CF280913
VERSION
CF280913.1 GI:33658299
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
Contact: Nahm B.H.
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--07-M07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

```

RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1299

CF282035 20 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,
 mRNA sequence.

ACCESSION CF282035 GI:33659422

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--09-F19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1300

CF282414 20 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ETL--09-F19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--09-F19,
 mRNA sequence.

ACCESSION CF282414 GI:33659801

VERSION EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ETL--09-F19"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice etiolated leaf plasmid cDNA library
 (14ETL)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1301

CF299822/c

LOCUS

DEFINITION

CF299822 20 bp mRNA linear EST 15-AUG-2003
 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--03-P22, mRNA
 sequence.

ACCESSION CF299822

VERSION CF299822.1 GI:33671583

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--03-P22"


```

/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1302
CF301720/c
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L01, mRNA
sequence.
ACCESSION  CF301720
VERSION     CF301720.1 GI:33673481
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1303
CF302027/c
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA
sequence.
ACCESSION  CF302027
VERSION     CF302027.1 GI:33673788
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--06-L01"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1303
CF302027/c
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-C16, mRNA
sequence.
ACCESSION  CF302027
VERSION     CF302027.1 GI:33673788
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

```

```

ACCESSION  CF302027
VERSION     CF302027.1 GI:33673788
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1304
CF310604
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-F14, mRNA sequence.
ACCESSION  CF310604
VERSION     CF310604.1 GI:33682365
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1304
CF310604
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-F14, mRNA sequence.
ACCESSION  CF310604
VERSION     CF310604.1 GI:33682365
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAA 2728
    |||||
Db 20 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 1304
CF310604
LOCUS      20 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-F14, mRNA sequence.
ACCESSION  CF310604
VERSION     CF310604.1 GI:33682365
KEYWORDS   Oryza sativa (japonica cultivar-group)
SOURCE     Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
ORGANISM   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
           clade; Ehrhartoideae; Oryzae; Oryza.
           1 (bases 1 to 20)
REFERENCE   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS     Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
           Location/Qualifiers
             1..20
               /organism="Oryza sativa (japonica cultivar-group)"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:39947"
               /clone="7LEAF--07-C16"
               /tissue_type="leaf"
               /dev_stage="7 days after germination"
               /lab_host="E.coli DH10B"
               /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
               /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
               with oligoribonucleotides and then used as templates for
               RT-PCR."

```

```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-05-F14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1305
CF313067
LOCUS
DEFINITION
HD--01-B02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-B02, mRNA sequence.
ACCESSION
CF313067
VERSION
CF313067.1 GI:33684828
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-B02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1306
CF313067
LOCUS
DEFINITION
HD--01-B02.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-B02, mRNA sequence.
ACCESSION
CF313067
VERSION
CF313067.1 GI:33684828
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-B02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1307
CF319133/c
LOCUS
DEFINITION
HD--09-I13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-I13, mRNA sequence.
ACCESSION
CF319133
VERSION
CF319133.1 GI:33690894
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

```

|||||
1 AAAAAAAAAAAAAAAAAAAAAA 20

Db

RESULT 1306
CF313569/c
LOCUS
DEFINITION
HD--01-L22.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--01-L22, mRNA sequence.
ACCESSION
CF313569
VERSION
CF313569.1 GI:33685330
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--01-L22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1307
CF319133/c
LOCUS
DEFINITION
HD--09-I13.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-I13, mRNA sequence.
ACCESSION
CF319133
VERSION
CF319133.1 GI:33690894
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

```

TITLE
JOURNAL
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-09-113"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1308
CF321721/c
LOCUS
DEFINITION

CF321721 20 bp mRNA linear EST 15-AUG-2003
HD-13-B05-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD-13-B05, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-13-B05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1309
CF328565
LOCUS
DEFINITION

CF328565 20 bp mRNA linear EST 18-AUG-2003
NACL-03-II4.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL-03-II4, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-03-II4"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1310
CF333173/c
LOCUS
DEFINITION

CF333173 20 bp mRNA linear EST 18-AUG-2003
JMT--01-P11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--01-P11, mRNA sequence.

ACCESSION CF333173
 VERSION CF333173.1 GI:33814617
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--01-P11"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."
 Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1311
 CF334170/c
 LOCUS
 DEFINITION JMT--03-F17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-F17, mRNA sequence.
 ACCESSION CF334170
 VERSION CF334170.1 GI:33816671
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--03-F17"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."
 Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1312
 CF33525/c
 LOCUS
 DEFINITION JMT--06-J21.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--06-J21, mRNA sequence.
 ACCESSION CF33525
 VERSION CF33525.1 GI:33821425
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.
 1 (bases 1 to 20)
 REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
 JOURNAL
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--06-J21"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."
 Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

```

Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
CF337494      20 bp mRNA linear EST 18-AUG-2003
JMT--07-P04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--07-P04, mRNA sequence.
CF337494
CF337494.1 GI:33823378
EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP.
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
source
Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1315
CN545446/c
LOCUS      20 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CS00GL005C02 3', mRNA sequence.
ACCESSION  CN545446
VERSION     CN545446.1 GI:46910071
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE      Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL    Unpublished (2002)
COMMENT    Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
Location/Qualifiers
source
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005C02"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match          0.7%; Score 20; DB 1; Length 20;

Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1314
AW334823/c
LOCUS      20 bp mRNA linear EST 31-JAN-2000
DEFINITION S39P5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION  AW334823
VERSION     AW334823.1 GI:6831180
KEYWORDS   EST.
SOURCE     Pneumocystis carinii
ORGANISM   Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.
TITLE      Expressed sequence tags from Pneumocystis carinii
JOURNAL    Unpublished (2000)
COMMENT    Contact: Staben C

```

```

School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers
source
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat [99-1-6,
sacrificed on 3/17/99] at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/project/Pneumocystis/"

Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No.1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||

RESULT 1315
CN545446/c
LOCUS      20 bp mRNA linear EST 30-APR-2004
DEFINITION EST 17390 Green Grape Skin Triplex2 Library Vitis vinifera CDNA
clone B3CS00GL005C02 3', mRNA sequence.
ACCESSION  CN545446
VERSION     CN545446.1 GI:46910071
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F.,
Couture,C., Dedaidechamp,F., Delrot,S., Glissant,D., Grimplet,J.,
Hamdi,S., Romieu,C. and Terrier,N.
TITLE      Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
JOURNAL    Unpublished (2002)
COMMENT    Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33- (0)5-57-12-25-50
Fax: 00-33- (0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: 17.
Location/Qualifiers
source
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005C02"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match          0.7%; Score 20; DB 1; Length 20;

```

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1316

CN545501/c
LOCUS DN954281/c
DEFINITION EST 17445 Green Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00GL005H02 3', mRNA sequence.

ACCESSION CN545501
VERSION
KEYWORDS
SOURCE CN545501.1 GI:46910126

ORGANISM

Vitis vinifera
Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 20)

REFERENCE

AUTHORS Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

JOURNAL

COMMENT UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France

Tel: 00-33-(0)5-57-12-25-50

Fax: 00-33-(0)5-57-12-25-48

Email: a.hamdi@bordeaux.inra.fr

Seq primer: T7

Location/Qualifiers

FEATURES

1..20
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00GL005H02"
/dev_stage="green stage"
/clone_lib="Green Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1317

CN545501/c
LOCUS DN953918
DEFINITION DN953918.1 GI:63026056
sequence.

ACCESSION DN953918

KEYWORDS

EST.

SOURCE

Gnetum gnetum
Gnetum gnetum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetum.
1 (bases 1 to 20)

REFERENCE

AUTHORS Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

FEATURES

source
1..20
/organism="Gnetum gnetum"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.7%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1318

CN545501/c
LOCUS DN954281/c
DEFINITION DN954281.1 GI:63026419
sequence.

ACCESSION DN954281

VERSION DN954281.1

KEYWORDS EST.

SOURCE Gnetum gnetum

ORGANISM Gnetum gnetum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetophyta; Gnetales; Gnetales; Gnetum.
1 (bases 1 to 20)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Gnetum female cone (NYBG)

Unpublished (2003)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

Location/Qualifiers

FEATURES

source
1..20
/organism="Gnetum gnetum"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1322
DR073130/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

DR073130 20 bp mRNA linear EST 08-JUN-2005
ik86h03.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR073130
DR073130.1 GI:67050981
EST.
Ginkgo biloba (maidenhair tree)
Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers

FEATURES
source
1..20
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: Leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stragene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1323
DT493556
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

DT493556 20 bp mRNA linear EST 29-AUG-2005
WS0111_BR_L11 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0111_L11
5', mRNA sequence.
DT493556
DT493556.1 GI:73890818
EST.
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
Populus trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 20)
Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stott,J., Barber,S., Yang,G.,
Babakaiff,R., Brown-John,M., Chand,S., Featherstone,R., Masson,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Ritland,C.E., Siddiqui,A.,

TITLE
JOURNAL
COMMENT

Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and
Bohlmann,J.
The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0111 row: L column: 11
High quality sequence stop: 139
POLYA=yes.

FEATURES
source
1..20

/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultiVar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS0111_L11"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"
/note="Vector: pluescript II SK (+) XR; Site 1: SacI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Phiom and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci,P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SclI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1324
TS0579/c

TS0579 20 bp mRNA linear EST 06-FEB-1995
Yb76d04.r1 Stragene ovary (#937217) Homo sapiens cDNA clone
IMAGE:77095 5' similar to contains L1 repetitive element, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

TS0579
TS0579.1 GI:652439
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 20)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
8889549
PUBMED

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source
1. .20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:506824"
/db_xref="taxon:9606"
/clone="IMAGE:77095"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR vector; ~5' adaptor sequence: 5'
GAATTCGGACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1325
AZ307671/c
LOCUS 20 bp DNA linear GSS 29-SBP-2000
DEFINITION 1M0009M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0009M20 R, genomic survey sequence.
ACCESSION AZ307671
VERSION AZ307671.1 GI:10346897
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: M column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0009M20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1326
AZ333980/c
LOCUS 20 bp DNA linear GSS 29-SBP-2000
DEFINITION 1M0063K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0063K10 F, genomic survey sequence.
ACCESSION AZ333980
VERSION AZ333980.1 GI:10400856
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0063 row: K column: 10
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0063K10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114[GB|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1327
A2341530
LOCUS
DEFINITION
A2341530 20 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0073N21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: N column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
Location/Qualifiers

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0076F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1329
AZ351273
LOCUS 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0089B18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0089B18 F, genomic survey sequence.
ACCESSION AZ351273
VERSION AZ351273.1 GI:10430510
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: B column: 18
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0089B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1330
AZ357623
LOCUS 20 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0099A20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0099A20 F, genomic survey sequence.
ACCESSION AZ357623
VERSION AZ357623.1 GI:10471335
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: A column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```



```

source      1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0145C11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1334
AZ396481
LOCUS      20 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0161K02 F, genomic survey sequence.
ACCESSION      AZ396481
VERSION      AZ396481.1 GI:10511553
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 02
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source      1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0161K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1333
AZ396481
LOCUS      20 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION      1M0161K02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0161K02 F, genomic survey sequence.
ACCESSION      AZ396481
VERSION      AZ396481.1 GI:10511553
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0161 row: K column: 02
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUGC1M0236B11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1335
A2463331/c
LOCUS
DEFINITION
IM0272006F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0272006 F, genomic survey sequence.
ACCESSION
A2463331.1 GI:10621456
VERSION
A2463331.1
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0272 row: 0 column: 06
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
location=1..20

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0297E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1337
AZ479464/c
LOCUS
DEFINITION
1M0300P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0300P01 F, genomic survey sequence.
ACCESSION
AZ479464
VERSION
AZ479464.1 GI:10638941
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: P column: 01
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.le+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1338
AZ486784/c
LOCUS
DEFINITION
1M0315C20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315C20 F, genomic survey sequence.
ACCESSION
AZ486784
VERSION
AZ486784.1 GI:10653898
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: C column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
FEATURES

```

source

```

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2708 TAAAAA 2727
Db 20 TAAAAA 1

```

```

RESULT 1339
AZ498625/c

```

```

LOCUS          AZ498625          20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION     IM0336E05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0336E05 F, genomic survey sequence.

```

```

ACCESSION      AZ498625
VERSION        AZ498625.1 GI:10676657
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

```

```

ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

```

REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts

```

```

JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah

```

```

                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA

```

```

                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0336 row: E column: 05
                Seq primer: CGTTGTAAACGACGCCAGT
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers

```

FEATURES

source

```

1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0336E05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAA 2728
Db 20 AAAAAA 1

```

```

RESULT 1340
AZ514729

```

```

LOCUS          AZ514729          20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION     IM0361E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0361E11 R, genomic survey sequence.

```

```

ACCESSION      AZ514729
VERSION        AZ514729.1 GI:10696045
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)

```

```

ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muridea; Muridae; Murinae; Mus.

```

```

REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts

```

```

JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah

```

```

                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA

```

```

                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0361 row: E column: 11
                Seq primer: CACACAGGAACACGTATGACC
                Class: plasmid ends
                High quality sequence stop: 20.
                Location/Qualifiers

```

FEATURES


```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0361E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
    ||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1341
AZ581208
LOCUS      20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0369P15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369P15 R, genomic survey sequence.
ACCESSION  AZ581208
VERSION     AZ581208.1 GI:11695991
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0369 row: P column: 15
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0369P15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
    ||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1342
AZ588011
LOCUS      20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0396A13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0396A13 F, genomic survey sequence.
ACCESSION  AZ588011
VERSION     AZ588011.1 GI:11710297
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0396 row: A column: 13
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0396A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1343
AZ607328
LOCUS
DEFINITION
clone UUGC1M0429A14 R, genomic survey sequence.
ACCESSION
AZ607328
VERSION
GI:11729518
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: A column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: A column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460K05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G[14732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1345
AZ623214/c
LOCUS
DEFINITION
1M0460L12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460L12 R, genomic survey sequence.
ACCESSION
VERSION AZ623214.1 GI:11745404
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0460L12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G[14732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1346
AZ643992
LOCUS
DEFINITION
1M0507D18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0507D18 R, genomic survey sequence.
ACCESSION
VERSION AZ643992
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: D column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0507D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1347
AZ645829/c
LOCUS
DEFINITION
20 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0511D03 R, genomic survey sequence.
ACCESSION
AZ645829
VERSION
GI:11775703
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0511 row: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0511D03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1348
AZ650271
LOCUS
DEFINITION
20 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0520C21 F, genomic survey sequence.
ACCESSION
AZ650271
VERSION
GI:11784588
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0520 row: C column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

```

```
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520C21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1349
AZ760838 20 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0554A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0554A24 R, genomic survey sequence.
ACCESSION AZ760838
VERSION AZ760838.1 GI:12869112
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

```
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0554A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1350
AZ764504 20 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0560M02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0560M02 R, genomic survey sequence.
ACCESSION AZ764504
VERSION AZ764504.1 GI:12879535
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: M column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560M02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1351
AZ765211/c
LOCUS
DEFINITION
  AZ765211 20 bp DNA linear GSS 16-FEB-2001
  clone UUGC1M0562H04 F, genomic survey sequence.
ACCESSION
  AZ765211
VERSION
  AZ765211.1 GI:12880970
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0562 row: H column: 04
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0562H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1352
AZ772091
LOCUS
DEFINITION
  AZ772091 20 bp DNA linear GSS 16-FEB-2001
  clone UUGC1M0574A13 R, genomic survey sequence.
ACCESSION
  AZ772091
VERSION
  AZ772091.1 GI:12895040
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0574 row: A column: 13
  Seq primer: CACACAGGAACACGTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

FEATURES
  Location/Qualifiers

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0574A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1353
AZ779425/c
LOCUS
DEFINITION
2M0015M18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0015M18 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: M column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0015M18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1354
AZ784041
LOCUS
DEFINITION
2M0026221F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0026B21 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: B column: 21
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

```

FEATURES

```

source
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0026B21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1355
AZ793467/c
LOCUS
DEFINITION
2M0046C16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0046C16 R, genomic survey sequence.
ACCESSION
AZ793467
VERSION
AZ793467.1 GI:12938450
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: C column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

source
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0046C16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1356
AZ798529/c
LOCUS
DEFINITION
2M0055G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0055G19 F, genomic survey sequence.
ACCESSION
AZ798529
VERSION
AZ798529.1 GI:12948718
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: G column: 19
Seq primer: CGTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

```



```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0055G19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1357
AZ805163
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0066L14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0066L14 F, genomic survey sequence.
ACCESSION  AZ805163
VERSION     AZ805163.1 GI:12965890
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0066 row: L column: 14
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0066L14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1358
AZ806521
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0068C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0068C08 R, genomic survey sequence.
ACCESSION  AZ806521
VERSION     AZ806521.1 GI:12969953
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0068 row: C column: 08
            Seq primer: CACACAGGAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0068C08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1359
AZ806585
LOCUS
DEFINITION
2M0068C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0068C15 R, genomic survey sequence.
ACCESSION
AZ806585
VERSION
AZ806585.1 GI:12970081
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0068 row: C column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUGC2M0068C15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1360
AZ809306
LOCUS
DEFINITION
2M0073D15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073D15 F, genomic survey sequence.
ACCESSION
AZ809306
VERSION
AZ809306.1 GI:12975468
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: D column: 15
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

```

```

source
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0073D15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1361
AZ810986
LOCUS
DEFINITION
2M0076120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076120 R, genomic survey sequence.
ACCESSION
VERSION AZ810986.1 GI:12978793
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: I column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076120"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1362
AZ813908
LOCUS
DEFINITION
2M0081F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0081F21 F, genomic survey sequence.
ACCESSION
VERSION AZ813908
KEYWORDS
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: F column: 21
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUGC2M0086C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/cloned_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1364
AZ817323
LOCUS
DEFINITION
2M0086C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0086C20 R, genomic survey sequence.
ACCESSION
AZ817323
VERSION
AZ817323.1 GI:12987327
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: C column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/cloned="UUGC2M0086C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/cloned_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1363
AZ817323
LOCUS
DEFINITION
2M0086C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0086C20 R, genomic survey sequence.
ACCESSION
AZ817323
VERSION
AZ817323.1 GI:12987327
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: C column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1365
AZ817467 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0086J15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0086J15 R, genomic survey sequence.
ACCESSION AZ817467
VERSION AZ817467.1 GI:12987291
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: J column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
```

```
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086J15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1366
AZ817608/20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0087K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0087K08 F, genomic survey sequence.
ACCESSION AZ817608
VERSION AZ817608.1 GI:12987516
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: K column: 08
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1367
AZ818489/c
LOCUS
DEFINITION
AZ818489 20 bp DNA linear GSS 20-FEB-2001
clone UUGC2M008K01 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0088 row: K column: 01
Seq primer: CACACAGAAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089M05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1369
AZ837491
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0132K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0132K13 R, genomic survey sequence.
ACCESSION  AZ837491
VERSION     AZ837491.1 GI:13007399
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0132 row: K column: 13
            Seq primer: CACACAGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source      1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0132K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1370
AZ841342
LOCUS      20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0139H16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0139H16 F, genomic survey sequence.
ACCESSION  AZ841342
VERSION     AZ841342.1 GI:13011250
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0139 row: H column: 16
            Seq primer: CGTTGTAAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
            Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139H16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1371
A2841558/c
LOCUS
DEFINITION
2M0139A10R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0139A10 R, genomic survey sequence.
ACCESSION
A2841558
VERSION
A2841558.1 GI:13011466
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139H16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1371
A2858052
LOCUS
DEFINITION
2M0163003F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGC2M0163003 F, genomic survey sequence.
ACCESSION
A2858052
VERSION
A2858052.1 GI:13050813
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: O column: 03
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
Location/Qualifiers

```



```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1373
AZ858419
LOCUS
DEFINITION
2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0163003 R, genomic survey sequence.
ACCESSION
AZ858419
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1374
AZ936914
LOCUS
DEFINITION
2M0193G23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0193G23 R, genomic survey sequence.
ACCESSION
AZ936914
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 20)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: G column: 23
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

```

```

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0193G23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1375
AZ949180/c
LOCUS
DEFINITION
  AZ949180 Mouse 10kb plasmid UUGC2M library Mus musculus genomic
  clone UUGC2M012102 R, genomic survey sequence.
ACCESSION
  AZ949180
VERSION
  AZ949180.1 GI:13820407
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0212 row: I column: 02
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0212I02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1376
AZ963973/c
LOCUS
DEFINITION
  AZ963973 Mouse 10kb plasmid UUGC2M library Mus musculus genomic
  clone UUGC2M0233J01 F, genomic survey sequence.
ACCESSION
  AZ963973
VERSION
  AZ963973.1 GI:13835200
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0233 row: J column: 01
  Seq primer: CGTTGTAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 20.
  Location/Qualifiers

```

```

1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0233J01"
/sex="female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```
Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT	1377				
CW979138					
LOCUS					
DEFINITION					
	CW979138	20 bp	DNA	linear	GSS 28-DEC-2004
	KBrH001K19	KBrH,	Brassica rapa	HindIII BAC library	Brassica rapa
	subsp. pekinensis	genomic clone	KBrH001K19,	genomic survey	

REFERENCE	1 (bases 1 to 20)
AUTHORS	Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Lim, Y.P. and Park, B.S.
TITLE	End sequence of <i>Brassica rapa</i> HindIII BAC library (KBrH)
JOURNAL	Unpublished (2004)
COMMENT	Contact: Beom-Seok Park

Email: p.poonwila.go.ki
 BAC end sequence of *Brassica rapa* ssp. *pekinensis* HindIII BAC clone
 KBRH001K19
 Seq primer: M13 Reverse
 Class: BAC ends.

```

/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBRH001K19"
/tissue_type="young leaves"
/lab_host="E. coli DH10B"
/clone_lib="KBrH, Brassica rapa HindIII BAC library"
/notes="Vector: pCUGIBac1; Site1: HindIII; Brassica rapa
spp. pekinensis inbred line Chiifu BAC library (KBrH BAC)
is provided by Yong-Pvo Lim."

```

```
Query Match          0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT	1378
DU834188/c	
LOCUS	DU834188
DEFINITION	KBrS013J15F KBrS, Brassica rapa Sau3AI BAC library
	subsp. pekinensis genomic clone KBrS013J15, genomic survey
	sequence.
	linear GSS 22-DEC-2005
	20 bp DNA

Query Match	0.7%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.1e+03;		
Matches 20;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

```

RESULT 1379
DU835125
LOCUS      DU835125      20 bp      DNA      linear      GSS 22-DEC-2005
DEFINITION KBR5016A17f KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBR5016A17, genomic survey
            sequence.
ACCESSION  DU835125
VERSION     DU835125.1  GI:839871721
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM    Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE       End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL     Unpublished (2005)
COMMENT     Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1670
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa Sau3AI (KBrS) BAC clone

FEATURES             source
            source
            1..20
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBr5016A17"
            /lab_host="E. coli DH10B"
            /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
            /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
            subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
            available at NTAB."
            Query Match      0.7%; Score 20; DB 1; Length 20;
            Best Local Similarity 100.0%; Pred. No. 1.1e+03;
            Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2728
Db       1  AAAAAAAAAAAAAAAAAAAAAA 20

FEATURES             source
            source
            1..20
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBr5016A17"
            /lab_host="E. coli DH10B"
            /clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
            /note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
            subsp. pekinensis var. Chiifu BAC library (KBrS BAC) is
            available at NTAB."
            Query Match      0.7%; Score 20; DB 1; Length 20;
            Best Local Similarity 100.0%; Pred. No. 1.1e+03;
            Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709  AAAAAAAAAAAAAAAAAAAAAA 2728
Db       1  AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1380
DX045751
LOCUS      DX045751      20 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION KBR5047C15F KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBR5047C15, genomic survey
            sequence.
ACCESSION  DX045751
VERSION     DX045751.1  GI:84740048
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM    Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
TITLE       End sequence of Brassica rapa BamHI (KBrB) BAC clone
JOURNAL     Unpublished (2005)
COMMENT     Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1670
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

FEATURES             source
            source
            1..20
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBr5047C15"
            /lab_host="E. coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBR5060D05, genomic survey
            sequence."
            Accession        DX055580
            Version          DX055580.1  GI:84749877
            Keywords         GSS.
            Source           Brassica rapa subsp. pekinensis
            Organism          Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
            Reference        1 (bases 1 to 20)
            Authors          Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
            Title            End sequence of Brassica rapa BamHI (KBrB) BAC clone
            Journal          Unpublished (2005)
            Comment          Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1670
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

FEATURES             source
            source
            1..20
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBr5047C15"
            /lab_host="E. coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library"
            /note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
            pekinensis var. Chiifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
            Query Match      0.7%; Score 20; DB 1; Length 20;
            Best Local Similarity 100.0%; Pred. No. 1.1e+03;
            Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708  TAAAAAAAAAAAAAAAAAAAAA 2727
Db       1  TAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1381
DX055580
LOCUS      DX055580      20 bp      DNA      linear      GSS 10-JAN-2006
DEFINITION KBR5060D05R KBrB, Brassica rapa BamHI BAC library Brassica rapa
            subsp. pekinensis genomic clone KBR5060D05, genomic survey
            sequence.
ACCESSION  DX055580
VERSION     DX055580.1  GI:84749877
KEYWORDS    GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM    Brassica rapa subsp. pekinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
            Reference        1 (bases 1 to 20)
            Authors          Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
            Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
            Hahn,J.H. and Park,B.S.
            Title            End sequence of Brassica rapa BamHI (KBrB) BAC clone
            Journal          Unpublished (2005)
            Comment          Contact: Beom-Seok Park
            Brassica Genomics Team
            National Institute of Agricultural Biotechnology
            225 Seodun-Dong, Suwon, 441-707, Korea
            Tel: +82-31-299-1670
            Fax: +82-31-299-1670
            Email: pbeom@da.go.kr
            BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

FEATURES             source
            source
            1..20
            /organism="Brassica rapa subsp. pekinensis"
            /mol_type="genomic DNA"
            /cultivar="Chiifu"
            /sub_species="pekinensis"
            /db_xref="taxon:51351"
            /clone="KBr5060D05"
            /lab_host="E. coli DH10B"
            /clone_lib="KBrB, Brassica rapa BamHI BAC library Brassica rapa ssp
            pekinensis var. Chiifu BAC library (KBrB BAC) is provided
            by Yong-Pyo Lim (CNU)."
            Query Match      0.7%; Score 20; DB 1; Length 20;
            Best Local Similarity 100.0%; Pred. No. 1.1e+03;
            Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708  TAAAAAAAAAAAAAAAAAAAAA 2727
Db       1  TAAAAAAAAAAAAAAAAAAAAA 20

```

/clone="KBrB060D05"
 /lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1382
 DX070282/c

LOCUS DX070282 20 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBrB079J23F KBrB, Brassica rapa BamHI BAC library Brassica rapa
 subsp. pekinensis genomic clone KBrB079J23, genomic survey
 sequence.

ACCESSION DX070282
 VERSION DX070282.1 GI:84764578
 KEYWORDS GSS.

SOURCE

ORGANISM Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

AUTHORS Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M.,
 Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
 Hahn, J.H. and Park, B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL Unpublished (2005)

COMMENT Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-293-1670

Fax: +82-31-293-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone

KBrB079J23

Seq primer: T7

Class: BAC ends.

FEATURES

source

Location/Qualifiers
 1..20
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"

/clone="KBrB079J23"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/notes="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1383
 BX556006/c

LOCUS BX556006 21 bp mRNA linear EST 10-OCT-2003

DEFINITION

Accession BX556006

VERSION

KEYWORDS BX556006.1 GI:33379965

SOURCE

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscidae; Glossinidae; Glossina.

REFERENCE

AUTHORS 1 (bases 1 to 21)

TITLE

Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

PUBMED 14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix glc are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

Location/Qualifiers
 1..21
 /organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse24c09_p1c"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/notes="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match

Best Local Similarity 0.7%; Score 20; DB 1; Length 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1384

CF276638/c

LOCUS

DEFINITION

CF276638 21 bp mRNA linear EST 14-AUG-2003
 14ETL--01-N19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
 Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--01-N19,
 mRNA sequence.

ACCESSION CF276638

VERSION

KEYWORDS CF276638.1 GI:33654024

SOURCE

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; BEP

clade; Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE

AUTHORS 1 (bases 1 to 21)

TITLE

JOURNAL

COMMENT Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

[illegible]

```

i. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--07-G07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cdna library (ABF)"
/note="vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 21)

REFERENCE

AUTHORS

Baliya, V.S., Nascimben, L.U. and McCombie, W.R.

TITLE

ESTs from Canis familiaris left cardiac ventricle (dog)

JOURNAL

Unpublished (2004)

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org.

Location/Qualifiers

1. .21

/organism="Canis familiaris"

/mol_type="mRNA"

/db_xref="taxon:9615"

/sex="Unknown"

/tissue_type="Cardiac muscle"

/dev_stage="3 month old normal canine"

/lab_host="X110 Gold"

/clone_lib="Left Cardiac Ventricle (DOGEST7)"

/note="Organ: Heart; Vector: pBluescript II SK; Site: 1:

EcoRI; Site 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected

between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD,

Pathology and Medical Genetics, School of Veterinary

Medicine, University of Pennsylvania, 3800 Spruce Street,

Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727

Db 20 TAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1388

DT496709

LOCUS

DEFINITION

WS01124.BR D19 PT-P-FL-A-2 Populus trichocarpa cDNA clone

EST. 29-AUG-2005

Accession 21 bp mRNA linear

Version 100.0%; Pred. No. 1.1e+03;

Keywords 0; Mismatches 0; Indels 0; Gaps 0;

Source 0; Mismatches 0; Indels 0; Gaps 0;

Organism 0; Mismatches 0; Indels 0; Gaps 0;

Reference 0; Mismatches 0; Indels 0; Gaps 0;

Authors 0; Mismatches 0; Indels 0; Gaps 0;

Title 0; Mismatches 0; Indels 0; Gaps 0;

Journal 0; Mismatches 0; Indels 0; Gaps 0;

Comment 0; Mismatches 0; Indels 0; Gaps 0;

Genome BC forest genomics program

University of British Columbia

Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,

Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-2114

Email: bohlmann@msl.ubc.ca

Plate: WS01124 row: D column: 19

High quality sequence stop: 116
POLYA=Yes.

FEATURES

source

1. .21

/organism="Populus trichocarpa"

/mol_type="mRNA"

/cultivar="383-2499 (Nisqually-1)"

/db_xref="taxon:3694"

/clone="WS01124_D19"

/sex="Female"

/lab_host="E. coli DH10B T1 phage resistant cells"

/clone_lib="PT-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site: 1: SstI (5'

end of cDNA); Site 2: XhoI (3' end of cDNA); Phloem and

cambium from 8 year old trees harvested within the Boise

Cascade region of Washington state on May 15th, 2001. cDNA

was prepared from 20 micrograms of mRNA according to the

full-length cDNA library construction method described by

Carninci P. et al. (2000), Genome Research

10(10):1617-1630 and directionally ligated into the

pBluescript II SK (+) XR vector digested with SstI (5'

end) and XhoI (3'). Plasmid DNA was then transformed by

electroporation into DH10B cells (Invitrogen) for

propagation."

Query Match 0.7%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 2 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1389

AZ461824

LOCUS

DEFINITION

1M0267B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0267B23 R, genomic survey sequence.

Accession 21 bp DNA linear

Version 100.0%; Pred. No. 1.1e+03;

Keywords 0; Mismatches 0; Indels 0; Gaps 0;

Source 0; Mismatches 0; Indels 0; Gaps 0;

Organism 0; Mismatches 0; Indels 0; Gaps 0;

Reference 0; Mismatches 0; Indels 0; Gaps 0;

Authors 0; Mismatches 0; Indels 0; Gaps 0;

Title 0; Mismatches 0; Indels 0; Gaps 0;

Journal 0; Mismatches 0; Indels 0; Gaps 0;

Comment 0; Mismatches 0; Indels 0; Gaps 0;

Genome BC forest genomics program

University of Utah

University of Utah Genome Center

Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0267 row: B column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0267B23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1390

AZ493766
 LOCUS 1M0328C11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0328C11 R, genomic survey sequence.

ACCESSION AZ493766
 VERSION AZ493766.1 GI:10667750
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0328 row: C column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

FEATURES

source

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"
 /clone="UUGC1M0328C11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.le+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 DB 2 TAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1391

DX056270/c

LOCUS

DX056270 21 bp DNA linear GSS 10-JAN-2006
 DEFINITION KBrB061B22F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB061B22, genomic survey sequence.

ACCESSION DX056270 GI:84750567

VERSION DX056270.1

KEYWORDS GSS.

SOURCE Brassica rapa subsp. pekinensis

ORGANISM

Brassica rapa subsp. pekinensis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.

End sequence of Brassica rapa BamHI (KBrB) BAC clone

Unpublished (2005)

JOURNAL

Unpublished (2005)

COMMENT

Contact: Beom-Seok Park

Brassica Genomics Team

National Institute of Agricultural Biotechnology

225 Seodun-Dong, Suwon, 441-707, Korea

Tel: +82-31-299-1670

Fax: +82-31-299-1672

Email: pheom@da.go.kr

BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..21

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB061B22"

/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/notes="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1392

DX081159

LOCUS DX081159 21 bp DNA linear GSS 10-JAN-2006
DEFINITION KBrB093P23R KBrB, Brassica rapa BamHI BAC library Brassica rapa
subsp. pekinensis genomic clone KBrB093P23, genomic survey
sequence.

ACCESSION DX081159

VERSION DX081159.1 GI:84775455

KEYWORDS GSS.

SOURCE

ORGANISM

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eutrosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 21)

AUTHORS Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S.

TITLE End sequence of Brassica rapa BamHI (KBrB) BAC clone

JOURNAL

COMMENT

Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672

Email: pbeom@da.go.kr

BAC end sequence of Brassica rapa spp. pekinensis BamHI BAC clone
KBrB093P23

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1..21

/organism="Brassica rapa subsp. pekinensis"

/mol_type="genomic DNA"

/cultivar="Chiifu"

/sub_species="pekinensis"

/db_xref="taxon:51351"

/clone="KBrB093P23"

/lab_host="E.coli DH10B"

/clone_lib="KBrB, Brassica rapa BamHI BAC library"

/notes="vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa spp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727

Db 2 TAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1393

CF310486

LOCUS CF310486 22 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--05-C16.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--05-C16, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..22

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF-05-C16"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="vector: pCR4-TOPO. Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match

Best Local Similarity 0.7%; Score 20; DB 1; Length 22;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2727

Db 3 TAAAAAAAAAAAAAAAAAAAAA 22

RESULT 1394

DR073660

LOCUS

DEFINITION

ik82h05.g1

22 bp

mRNA

linear

EST 08-JUN-2005

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ginkgo biloba

(maidenhair tree)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

REFERENCE 1 (bases 1 to 22)

AUTHORS

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org
Original 3 prime EST has been reverse completed to be in 5 prime direction

Seq primer: -21M13UnivRev.

FEATURES

Location/Qualifiers
1. .22
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The library was size-fractionated to enrich for large inserts."

Query Match 0.7%; Score 20; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAA 2727

DB 3 TAAAAAATAAAAA 22

RESULT 1395

AL587621/c

LOCUS 23 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587621 BP Chicken Brain Library Gallus gallus cDNA clone
ROS059H07, mRNA sequence.

ACCESSION AL587621.1 GI:13192655

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 23)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbrc.ac.uk
GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech

(*6854-

Seq primer: M13F.

FEATURES

Location/Qualifiers
1. .23
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059H07"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORI1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match 0.7%; Score 20; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAA 2729

Db 23 AAAAAAATAAAAA 3

RESULT 1396

AZ315640

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0033004"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAA 2728

Db 4 AAAAAAAAAAAAAAAAAAAAAA 23

RESULT 1397
 AZ621676 23 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0455J07F Mouse 10kb plasmid UGClM library Mus musculus genomic
 DEFINITION clone UGClM0455J07 F, genomic survey sequence.
 ACCESSION AZ621676
 VERSION AZ621676.1 GI:11743962
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0455 row: J column: 07
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
 source
 1..23
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGClM0455J07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGClM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1398
 AZ817623 23 bp DNA linear GSS 20-FEB-2001
 LOCUS 2M0087N09F Mouse 10kb plasmid UGClM library Mus musculus genomic
 DEFINITION clone UUGC2M0087N09 F, genomic survey sequence.
 ACCESSION AZ817623
 VERSION AZ817623.1 GI:12987531
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 23)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0087 row: N column: 09
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 23.

FEATURES
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0087N09"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGClM library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728

TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1. .24
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000045_P10"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAGAAAAAAGAAAAA 2727
|||||
Db 20 TAAAGAAAAAAGAAAAA 1

RESULT 1401
AJ663467
LOCUS 25 bp mRNA linear EST 28-JUN-2004
DEFINITION CSEQRAN09 Sus scrofa cDNA clone C0000027_007, mRNA sequence.
ACCESSION AJ663467
VERSION AJ663467.1 GI:49347590
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 25)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.I.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1: EcoRI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1. .25
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000027_007"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

```

NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1402
DX071965/c
LOCUS
DEFINITION
KBrB081N24F KBrB, Brassica rapa BamHI BAC library GSS 10-JAN-2006
subsp. pekinensis genomic clone KBrB081N24, genomic survey
sequence.
ACCESSION
DX071965
VERSION
DX071965.1 GI:84766261
SOURCE
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 25)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J.H. and Park,B.S
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-298-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis BamHI BAC clone
KBrB081N24
Seq primer: T7
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..25
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB081N24"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site 1: BamHI; Brassica rapa ssp
pekinensis var. Chiifu BAC library (KBrB BAC) is provided
by Yong-Pyo Lim (CNU)."
```

Query Match 0.7%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
Db 25 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1403
BX568055/c
LOCUS
DEFINITION
BX568055 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse91f03_plc, mRNA sequence.
ACCESSION
BX568055.1 GI:33434952

```

KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
Location/Qualifiers
source
1..23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse91f03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2708 TAAAAA AAAAAAAAAAAAAAAAAA 2730
Db 23 TATATA AAAAAAAAAAAAAAAAAA 1

RESULT 1404
CF297907/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B05, mRNA
sequence.
ACCESSION
CF297907
VERSION
CF297907.1 GI:33669668
KEYWORDS
EST.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 23)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
```


JOURNAL
COMMENT

Unpublished (2000)
Contact: Staben C
School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY
40506-0225, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.
Location/Qualifiers

FEATURES
source

1. .23
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
P. carinii organisms (3x10e9) from a single rat [99-1-6,
sacrificed on 3/17/99] at Cincinnati VA facilities.
Trizol extracted RNA. Oligo dT priming, standard
conditions described by vendor, Stratagene. Further
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 23 AAAAAAAAAAAAAAAAAACCAG 1

RESULT 1408

AZ447220
LOCUS
DEFINITION
A2447220 23 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0244E15 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: E column: 15
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244E15"

FEATURES
source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244E15"

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 1.2e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2731
|||||
Db 1 AAAAAAAAAATAAAAAAAAAAAAA 23

RESULT 1409

AZ662734
LOCUS
DEFINITION
AZ662734 23 bp DNA linear GSS 14-DEC-2000
clone UUGC1M0542D04 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0542 row: D column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends

High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542D04"

FEATURES
source

1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0542D04"


```

/clone_lib="566 (synonym: hfkid2)"
/notes="vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2728
Db 1 TCAAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1413
BX548564/c
LOCUS
DEFINITION
BX548564 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse101g03_plc, mRNA sequence.
ACCESSION
BX548564
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 21)
Lehane, M.J., Aksoy, S., Gibson, M., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..21
/mol_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse101g03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAAAAAAAAAGAAAAA 1

RESULT 1414
CF276747/c
LOCUS
DEFINITION
CF276747 21 bp mRNA linear EST 14-AUG-2003
14ETL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--02-A06,
mRNA sequence.

/clone_lib="566 (synonym: hfkid2)"
/notes="vector: pAMPl; Site_1: NotI; Site_2: SalI"

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db 21 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1415
CF296213/c
LOCUS
DEFINITION
CF296213 21 bp mRNA linear EST 14-AUG-2003
30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION
CF296213
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db 21 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1415
CF296213/c
LOCUS
DEFINITION
CF296213 21 bp mRNA linear EST 14-AUG-2003
30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION
CF296213
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="14ETL--02-A06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match
Best Local Similarity 0.7%; Score 19.4; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db 21 ACCAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1415
CF296213/c
LOCUS
DEFINITION
CF296213 21 bp mRNA linear EST 14-AUG-2003
30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-H19, mRNA
sequence.
ACCESSION
CF296213
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..21

```

```

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-H19"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
      |||||
Db 21 AAAAAAAAAACAAAAAAAAAAAA 1

RESULT 1416
CF302218/c
LOCUS
DEFINITION
7LEAF--07-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--07-117, mRNA
sequence.
ACCESSION
CF302218
VERSION
CF302218.1 GI:33673979
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-L11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-L11"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
      |||||
Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1418
DR073305/c
LOCUS
DEFINITION
ik77a11 g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION
DR073305
VERSION
DR073305.1 GI:67051167
KEYWORDS
EST.
SOURCE
Ginkgo biloba (maidenhair tree)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 21)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory

```

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mconbie@cshl.org

Original 3 prime EST has been reverse completed to be in 5 prime

direction

Seq primer: -21M13UnivRev.

Location/Qualifiers

1. .21

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"

/clone_lib="Ginkgo female leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;

Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.

The library was size-fractionated to enrich for large

inserts."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAA 2728

Db 1 TCAAAAAA 21

RESULT 1419

AZ317208/c

LOCUS AZ317208 21 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0035J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0035J02 R, genomic survey sequence.

ACCESSION AZ317208

VERSION A2317208.1 GI:10365804

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0035 row: J column: 02

Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0035J02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;

Best Local Similarity 95.2%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAGAAAAA 2729

Db 21 AAAAAAAGAAAAA 1

RESULT 1420

AZ486776/c

LOCUS

DEFINITION

AZ486776 21 bp DNA linear GSS 05-OCT-2000
clone UUGC1M0315M10 F, genomic survey sequence.

ACCESSION AZ486776

VERSION A2486776.1 GI:10653882

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: M column: 10

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315M10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1421

AZ792613/c
 LOCUS AZ792613 21 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0045M12 F, genomic survey sequence.

ACCESSION AZ792613
 VERSION AZ792613.1 GI:12936725
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0045 row: M column: 12

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0045M12"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.4; DB 1; Length 21;
 Best Local Similarity 95.2%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1422

AZ822825
 LOCUS AZ822825 21 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0096I20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0096I20 F, genomic survey sequence.

ACCESSION AZ822825
 VERSION AZ822825.1 GI:12992733
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0096 row: I column: 20

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

source

1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0096I20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.

Best Local Similarity 95.2%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0; Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAATAAAAAAAAAAAAAAAAAA 2728
Db 22 TATATAAAAAAAAAAAAAAAAAA 2

RESULT 1429
CL693160
LOCUS
DEFINITION
Prionionchus pacificus
stage fosmid library of P. pacificus var. California Prionionchus
pacificus genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Prionionchus pacificus
Prionionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Prionionchus.
1 (bases 1 to 22)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Prionionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1..22
/organism="Prionionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/notes="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19.4; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2729
Db 1 AAAAAAAAAAAAAAAAAA 21

RESULT 1429
AJ666332/c
LOCUS
DEFINITION
AJ666332 CSEQRAN09 Sus scrofa cDNA clone C0000033_H19, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 23)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and

embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES
source
1..23
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_H19"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAAAAAAAAAAAAA 2727
Db 21 CCAAAAAAAAAAAAAAAAA 1

RESULT 1430
AL048745
LOCUS
DEFINITION
AL048745 DKF2p566K213_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL048745.1 GI:4727816
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 23)
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..23
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p566K213"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 19.4; DB 1; Length 23;
Best Local Similarity 95.2%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2728
Db 3 TCAAAAAAAAAAAAAAAAA 23

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 693 ATGAAGAGCAGGAGGAGACAG 716
Db 24 AAGAGAGTAGAGGAGAGAGAG 1

RESULT 1434
AZ309553
LOCUS
DEFINITION
1M0016B10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION
AZ309553
VERSION
AZ309553.1 GI:10350837
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: B column: 10
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends

High quality sequence stop: 24.
Location/Qualifiers
1. .24

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0016B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAA 2726
Db 1 TTTTAAAAA 24

RESULT 1435
AZ448207
LOCUS
DEFINITION
1M0245E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION
AZ448207
VERSION
AZ448207.1 GI:10600777
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)

AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0245 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 24.
Location/Qualifiers
1. .24

FEATURES
source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0245E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male); was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2702 TTGTACTAAAAA 2725
Db 1 TTTTAAAAA 24

RESULT 1436
AZ814559/c

LOCUS AZ814559 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0082P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0082P18 F, genomic survey sequence.

ACCESSION AZ814559
VERSION AZ814559.1 GI:12984467
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0082 row: P column: 18

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

FEATURES
source

1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAA 2732
Db 24 AAAAAAGAAAGAAAAAGAAA 1

RESULT 1437
CL676551/c

LOCUS CL676551 24 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0118d_H07_2 - PRI0118d_BR (24) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL676551
VERSION CL676551.1 GI:50182187
KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 24)

AUTHORS

TITLE Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
ApADB: an AcedB database for the nematode satellite organism Pristionchus pacificus

JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)

PUBMED 14681447

COMMENT Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..24
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2709 AAAAAA 2732
Db 24 AAAAAAGAAAGAAAAAGAAA 1

RESULT 1438
AJ668179/c

```

LOCUS      AJ668179      19 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ668179 CSEQRAN09 Sus scrofa cDNA clone C0000045_L19, mRNA
sequence.
ACCESSION  AJ668179
VERSION     AJ668179.1  GI:49352630
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE      Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
JOURNAL     Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross match with the -minscore 20
            and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institute,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES   Location/Qualifiers
            1..19
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0000045_L19"
            /tissue_type="placenta"
            /clone_lib="CSEQRAN09"
            /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
            NotI; Single pass sequencing. Normalised library
            constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||||
Db   19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1439
LOCUS      AJ669138      19 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ669138 CSEQRAN09 Sus scrofa cDNA clone C0000048_O12, mRNA
sequence.
ACCESSION  AJ669138
VERSION     AJ669138.1  GI:49353592
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE      Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
JOURNAL     Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:

```

```

EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES   Location/Qualifiers
            1..19
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0000048_O12"
            /tissue_type="placenta"
            /clone_lib="CSEQRAN09"
            /note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site_2:
            NotI; Single pass sequencing. Normalised library
            constructed from pooled tissue from day 30 placentas."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||||
Db   19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1440
LOCUS      BQ588729      19 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION S013713-024-014-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
            cDNA Clone 024-014-B24 3-PRIME, mRNA sequence.
ACCESSION  BQ588729
VERSION     BQ588729.1  GI:26118312
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
            12472698
            Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weissshaab@mpiz-koeln.mpg.de
            Insert Length: 19 Std Error: 0.00
            Plate: 14 row: B column: 24
            Seq primer: 77; GTAATACGACTCACTATAGGCG.

FEATURES   Location/Qualifiers
            1..19
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:187281"
            /db_xref="taxon:161934"
            /clone="024-014-B24"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzaucht AG Binbeck, Germany, contact:
            b.schul@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

```

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1441
CF279008/c
LOCUS
DEFINITION OR 2032F05 010529_Y1 Adult mouse olfactory epithelium library Mus EST 09-OCT-2003
muSculus cDNA clone 2032F05 5', mRNA sequence.
ACCESSION CBI174047
VERSION CBI174047
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 19)
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Trask, B.J.

TITLE Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
JOURNAL Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcr.org
Seq primer: M13 Reverse

FEATURES
source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2032F05"
/tissue_type="olfactory and respiratory epithelium"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector: LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library was provided by Leslie Vossahl. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's lambdaZAPII-XR vector."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1442
CF279008/c
LOCUS
DEFINITION OR 2032F05 010529_Y1 Adult mouse olfactory epithelium library Mus EST 14-AUG-2003
muSculus cDNA clone 2032F05 5', mRNA sequence.
ACCESSION CBI174047
VERSION CBI174047
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@ggi.bio.com, bhnam@bio.myongji.ac.kr

FEATURES
source
1..19
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--05-C13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

Oy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1443
CF291089/c
LOCUS

DEFINITION 14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA sequence.
ACCESSION CF291089
VERSION CF291089
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnam@ggi.bio.com, bhnam@bio.myongji.ac.kr

FEATURES
Location/Qualifiers

```

source      1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-G03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
        |||||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1444
CF291090
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
sequence.
ACCESSION
CF291090.1 GI:33660123
VERSION
CF291090
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1. (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-G03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
        |||||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1444
CF291090
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 14ROOT--01-G03, mRNA
sequence.
ACCESSION
CF291090.1 GI:33660123
VERSION
CF291090
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1. (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--01-G03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
        |||||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 1445
CF299598/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K23, mRNA
sequence.
ACCESSION
CF299598
VERSION
CF299598.1 GI:33671139
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1. (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--03-K23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2727
        |||||||
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1446
CF302327/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L24, mRNA
sequence.
ACCESSION
CF302327
VERSION
CF302327.1 GI:33674088
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1. (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea

```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
    source
        1..19
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="7LEAF--07-L24"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1447
CF304589/c
LOCUS
DEFINITION
    CF304589 19 bp mRNA linear EST 15-AUG-2003
    ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage
    cDNA library (ABF1) Oryza sativa (japonica cultivar-group) CDNA
    clone ABF1--05-G10, mRNA sequence.
ACCESSION
    CF304589
VERSION
    CF304589.1 GI:33676350
KEYWORDS
    EST.
SOURCE
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
    clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
    1 (bases 1 to 19)
    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
    Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.
    Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
    of Bioscience and Bioinformatics, Myongji University
    Yongin, Kyeonggi, Korea
    Tel: 82 31 330 6193
    Fax: 82 31 321 6355
    Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
    source
        1..19
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="ABF1--05-G10"
            /tissue_type="leaf"
            /dev_stage="14 days after germination"
            /lab_host="E.coli SOLR"
            /clone_lib="ABF3-overexpressing transgenic rice lambda
            phage cDNA library (ABF1)"
            /note="Vector: pBluescript SK(+); Site1: EcoRI; Site 2:
            XhoI; Leaf was dried for 2hrs. cDNA was inserted into
            lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
            with XhoI site. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

```

```

Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1448
CF309801/c
LOCUS
DEFINITION
  CF309801.1 19 bp mRNA linear EST 15-AUG-2003
  ABF--04-C04.g1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
  ABF--04-C04, mRNA sequence.
ACCESSION
  CF309801
VERSION
  CF309801.1 GI:33681562
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
REFERENCE
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, Greengene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
    1..19
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultiivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF--04-C04"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH108"
    /clone_lib="ABF3-overexpressing transgenic rice plasmid
    cDNA library (ABF)"
    /notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
    for 2hrs. Oligo-capped mRNA was reverse transcribed and
    then used for PCR. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1449
CF309943
LOCUS
DEFINITION
  CF309943.1 19 bp mRNA linear EST 15-AUG-2003
  ABF--04-F15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
  ABF--04-F15, mRNA sequence.
ACCESSION
  CF309943
VERSION
  CF309943.1 GI:33681704
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-F15"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1450
CF3111496/c

LOCUS ABF--06-L18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L18, mRNA sequence.
CF3111496
CF3111496.1 GI:33683257

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"

/clone="ABF--06-L18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1451
CF3111513/c

LOCUS ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-M03, mRNA sequence.
CF3111513
CF3111513.1 GI:33683274

EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source

1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-M03"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

```

RESULT 1452
CF312403          19 bp  mRNA  linear  EST 15-AUG-2003
LOCUS
DEFINITION
ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--08-C07, mRNA sequence.
ACCESSION
CF312403
VERSION
CF312403.1 GI:33684164
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-C07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1453
CF315299          19 bp  mRNA  linear  EST 15-AUG-2003
LOCUS
DEFINITION
HD--04-C17.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-C17, mRNA sequence.
ACCESSION
CF315299
VERSION
CF315299.1 GI:33687060
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

```

```

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--04-C17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1454
CF316480          19 bp  mRNA  linear  EST 15-AUG-2003
LOCUS
DEFINITION
HD--05-M14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-M14, mRNA sequence.
ACCESSION
CF316480
VERSION
CF316480.1 GI:33688241
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-M14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

```



```

/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-08-G19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1458
CF333507
LOCUS
DEFINITION
JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-G23, mRNA sequence.
CF333507
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1460
CF334014/c
LOCUS
DEFINITION
JMT--03-C09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-C09, mRNA sequence.
CF334014
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-G23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

```

```

RESULT 1459
CF333753
LOCUS
DEFINITION
JMT--02-M08.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--02-M08, mRNA sequence.
CF333753
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--02-M08"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1460
CF334014/c
LOCUS
DEFINITION
JMT--03-C09.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
JMT--03-C09, mRNA sequence.
CF334014
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JWT--03-C09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1461

CN545602/c
LOCUS
DEFINITION
EST 17546 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL003H10 3', mRNA sequence.

ACCESSION
CN545602

VERSION
CN545602.1 GI:46910227

KEYWORDS
EST.

SOURCE
Vitis vinifera

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
1 (bases 1 to 19)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

JOURNAL

COMMENT

Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

source
1. .19
Location/Qualifiers
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL003H10"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/notes="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

|||||

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1462

CN545922/c
LOCUS
DEFINITION
EST 17866 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006D07 3', mRNA sequence.

ACCESSION
CN545922

VERSION
CN545922.1 GI:46910547

KEYWORDS
EST.

SOURCE
Vitis vinifera

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE
1 (bases 1 to 19)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F.,
Couture, C., Dedaldecamp, F., Delrot, S., Glissant, D., Grimplet, J.,
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (skin, pulp
or seeds) at Various Developmental Stages
Unpublished (2002)

JOURNAL

COMMENT

Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche
Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex,
France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7.

FEATURES

Location/Qualifiers
1. .19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D07"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1:
SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

|||||

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1463

CN545964/c
LOCUS
DEFINITION
EST 17912 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
clone B3CS00RL006H10 3', mRNA sequence.

ACCESSION
CN545964

VERSION
CN545964.1 GI:46910589

KEYWORDS
EST.

SOURCE
Vitis vinifera

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Abbal, P., Agase, A., Agorces, A., Atanasova, R., Barrieu, F., Couture, C., Dedadechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
 TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
 source
 1..19
 Location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="B3CS00RL006H10"
 /dev_stage="ripening stage"
 /clone_lib="Ripe Grape Skin Triplex2 Library"
 /note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1464
 CN546303/c
 LOCUS EST 18255 Green Grape Berry Lambda Triplex2 Library Vitis vinifera
 DEFINITION cDNA clone B3CS1XGB015E10 3', mRNA sequence.
 ACCESSION CN546303
 VERSION CN546303.1 GI:46910928
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Abbal, P., Agase, A., Agorces, A., Atanasova, R., Barrieu, F., Couture, C., Dedadechamp, F., Delrot, S., Glissant, D., Grimplet, J., Hamdi, S., Romieu, C. and Terrier, N.
 TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
 JOURNAL Unpublished (2002)
 COMMENT Contact: Hamdi S.
 UMR 619 - Equipe Biologie de la Vigne
 Universite de Bordeaux I, Institut National de la Recherche Agronomique
 71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
 Tel: 00-33-(0)5-57-12-25-50
 Fax: 00-33-(0)5-57-12-25-48
 Email: s.hamdi@bordeaux.inra.fr
 Seq primer: T7.

FEATURES
 source
 1..19
 Location/Qualifiers
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"
 /clone="B3CS1XGB015E10"
 /dev_stage="green stage"
 /clone_lib="Green Grape Berry Lambda Triplex2 Library"
 /note="Organ: Fruit without seeds; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1465
 CX003880
 LOCUS iv25a12.bl Brain - Cerebellum Library (DOGE8T8) Canis familiaris
 DEFINITION cDNA, mRNA sequence.
 ACCESSION CX003880
 VERSION CX003880.1 GI:56275296
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Balijs, V., Nascimento, L.U. and McCombie, W.R.
 TITLE ESTs from Canis familiaris cerebellum (dog)
 JOURNAL Unpublished (2004)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org.

FEATURES
 source
 1..19
 Location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /sex="Unknown"
 /tissue_type="Cerebellum"
 /dev_stage="3 month old normal canine"
 /lab_host="XL10 Gold"
 /clone_lib="Brain - Cerebellum Library (DOGE8T8)"
 /note="Organ: Brain; Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1466
 CX007355/c
 LOCUS io27h10.g1 Whole Heart Library (DOGE8T5) Canis familiaris cDNA,
 DEFINITION mRNA sequence.
 ACCESSION CX007355

```

CX007355.1 GI:56389584
EST.
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 19)
Baliya, V.S., Nascimento, L.U. and McCombie, W.R.
ESTs from Canis familiaris whole heart (dog)
Unpublished (2004)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Location/Qualifiers
1..19
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Whole Heart Library (DOGSST5)"
EcoRI; Site 2: XhoI; Vector: pBluescript II SK; Site 1:
XR kit from Stratagene. Cloned cDNA was size selected
between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
Medical Genetics, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA 19104-6051

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1467
DN954273/c
LOCUS
DEFINITION
it71a04.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
DN954273
VERSION
DN954273.1 GI:63026411
KEYWORDS
EST.
SOURCE
Gnetum gnemon
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R.W.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;
1 (bases 1 to 19)
Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,
O'Shaughnessy, A.L., Baliya, V., Martienssen, R.A., McCombie, R
```

```

sequence.
ACCESSION DN955630
VERSION DN955630.1 GI:63027768
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetales; Gnetaceae; Gnetum.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"
/clone_lib="Gnetum female cone (NYBG)"
/vector="pBK-CMV; Site 1: XhoI; Site 2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The
library was size-fractionated to enrich for large inserts.
Sample: NYBG accession number #436/84"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR062165 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq09e02.g1 Cytas sporophyll (w/o ovule) (NYBG) Cytas rumphii cDNA
ACCESSION DR062165
VERSION DR062165.1 GI:66985731
KEYWORDS EST.
SOURCE Cytas rumphii
ORGANISM Cytas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cytas ovules (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cytas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cytas ovule (NYBG)"
/vector="pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1470
LOCUS DR063459 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq24h10.g1 Cytas ovule (NYBG) Cytas rumphii cDNA 3', mRNA sequence.
ACCESSION DR063459
VERSION DR063459.1 GI:66986609
KEYWORDS EST.
SOURCE Cytas rumphii
ORGANISM Cytas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cytas ovules (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cytas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cytas ovule (NYBG)"
/vector="pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1472
LOCUS DR063459/c 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq09e02.g1 Cytas sporophyll (w/o ovule) (NYBG) Cytas rumphii cDNA
ACCESSION DR063459/c
VERSION DR063459/c.1 GI:66985731
KEYWORDS EST.
SOURCE Cytas rumphii
ORGANISM Cytas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cytas sporophyll (w/o ovule) (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19

```

```

/organism="Cytas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cytas sporophyll (w/o ovule) (NYBG)"
/notes="Organ: Sporophyll with ovules detached.; Vector:
pBK-CMV; Site 1: Xho I; Site 2: Eco RI; Date: Completed
08/09/2002. Submitted to CSHL 08/21/2002. Sample: Young
emergent sporophyll with ovules detached (ovules used to
make a separate library). From New York Botanical Garden
Conservatory accession number 808/59 A. (collected
06/04/2002). Library: Made using Stratagene's ZAP Express
Vector Kit. Library was size fractionated for large
inserts."

```

```

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

```

```

RESULT 1471
LOCUS DR063041 19 bp mRNA linear EST 06-JUN-2005
DEFINITION iq24h10.g1 Cytas ovule (NYBG) Cytas rumphii cDNA 3', mRNA sequence.
ACCESSION DR063041
VERSION DR063041.1 GI:66986609
KEYWORDS EST.
SOURCE Cytas rumphii
ORGANISM Cytas rumphii
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Cytas ovules (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..19
/organism="Cytas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cytas ovule (NYBG)"
/vector="pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

```

```

FEATURES
source
1..19
/organism="Cytas rumphii"
/mol_type="mRNA"
/db_xref="taxon:58031"
/sex="female"
/clone_lib="Cytas ovule (NYBG)"
/notes="Organ: Ovules; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

```

```

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

```

```

RESULT 1472
LOCUS DR063459/c 19 bp mRNA linear EST 06-JUN-2005

```

```

DEFINITION ip65g04_g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR063459
VERSION DR063459.1 GI:66987027
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo megasporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
     source
     1..19
     /organism="Ginkgo biloba"
     /mol_type="mRNA"
     /db_xref="taxon:3311"
     /sex="Female"
     /clone_lib="Ginkgo megasporophyll (NYBG)"
     /note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1473
DR065256/c
LOCUS
DEFINITION ip92c10_g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
mRNA sequence.
ACCESSION DR065256
VERSION DR065256.1 GI:66988824
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
     source
     1..19
     /organism="Ginkgo biloba"
     /mol_type="mRNA"
     /db_xref="taxon:3311"
     /sex="Female"
     /clone_lib="Ginkgo microsporophyll (NYBG)"
     /note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1473
DR065256/c
LOCUS
DEFINITION ip65g04_g1 Ginkgo megasporophyll (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR063459
VERSION DR063459.1 GI:66987027
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo megasporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
     source
     1..19
     /organism="Ginkgo biloba"
     /mol_type="mRNA"
     /db_xref="taxon:3311"
     /sex="Female"
     /clone_lib="Ginkgo megasporophyll (NYBG)"
     /note="Organ: megasporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1473
DR065256/c
LOCUS
DEFINITION ip92c10_g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
mRNA sequence.
ACCESSION DR065256
VERSION DR065256.1 GI:66988824
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo microsporophyll (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
     source
     1..19
     /organism="Ginkgo biloba"
     /mol_type="mRNA"
     /db_xref="taxon:3311"
     /sex="Female"
     /clone_lib="Ginkgo microsporophyll (NYBG)"
     /note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1475
DR074208
LOCUS
DEFINITION il53h03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074208
VERSION DR074208.1 GI:67052176
KEYWORDS EST.

```

```

/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="male"
/clone_lib="Ginkgo microsporophyll (NYBG)"
/note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1474
DR073123/c
LOCUS
DEFINITION ik86f08.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR073123
VERSION DR073123.1 GI:67050974
KEYWORDS EST.
SOURCE Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 19)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES             source
     source
     1..19
     /organism="Ginkgo biloba"
     /mol_type="mRNA"
     /db_xref="taxon:3311"
     /sex="female"
     /clone_lib="Ginkgo female leaf (NYBG)"
     /note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI;
Site_2: Eco RI; Stratagene ZAP Express cDNA
Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."
Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1475
DR074208
LOCUS
DEFINITION il53h03.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
ACCESSION DR074208
VERSION DR074208.1 GI:67052176
KEYWORDS EST.

```

```

SOURCE      Ginkgo biloba (maidenhair tree)
ORGANISM    Ginkgo biloba
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
              1 (bases 1 to 19)
O'Shaughnessy A.L., Twigg R.W., Runko S.J., Katari, M.S., Dedhia, N.N.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Martiniussen, R.A., McCombie, R.W.,
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES    Location/Qualifiers
source      1..19
              /organism="Ginkgo biloba"
              /mol_type="mRNA"
              /db_xref="taxon:3311"
              /sex="male"
              /clone_lib="Ginkgo male leaf (NYBG)"
              /note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:
              Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
              library was size-fractionated to enrich for large
              inserts."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||
      1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1476
AZ307313
LOCUS      AZ307313
DEFINITION 1M0008H20R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0008H20 R, genomic survey sequence.
ACCESSION  AZ307313
VERSION     AZ307313.1 GI:10346192
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
              Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
              Niederhausern, A. and Wright, D., Weiss, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0008 row: H column: 20
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.

SOURCE      Ginkgo biloba (maidenhair tree)
ORGANISM    Ginkgo biloba
REFERENCE    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
              1 (bases 1 to 19)
O'Shaughnessy A.L., Twigg R.W., Runko S.J., Katari, M.S., Dedhia, N.N.,
Benfey, P., Coruzzi, G. and Stevenson, D.
Martiniussen, R.A., McCombie, R.W.,
Expressed tag sequences from Ginkgo male leaf (NYBG)
Unpublished (2005)
CONTACT: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES    Location/Qualifiers
source      1..19
              /organism="Ginkgo biloba"
              /mol_type="mRNA"
              /db_xref="taxon:3311"
              /sex="male"
              /clone_lib="Ginkgo male leaf (NYBG)"
              /note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:
              Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The
              library was size-fractionated to enrich for large
              inserts."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
      |||
      1 AAAAAAAAAAAAAAAAAAAAAA 19

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1477
AZ310079/c
LOCUS      AZ310079/c
DEFINITION 1M0018K17R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0018K17 R, genomic survey sequence.
ACCESSION  AZ310079
VERSION     AZ310079.1 GI:10351709
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
              Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
              Niederhausern, A. and Wright, D., Weiss, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0018 row: K column: 17
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.

```


FEATURES
source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1478
AZ310105/c

LOCUS AZ310105 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0018E21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0018E21 R, genomic survey sequence.

ACCESSION AZ310105
VERSION AZ310105.1 GI:10351761
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: E column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0018E21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1479
AZ317743

LOCUS AZ317743 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0036B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0036B18 R, genomic survey sequence.

ACCESSION AZ317743
VERSION AZ317743.1 GI:10366848
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: B column: 18
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0036B18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1480
AZ340311/c

LOCUS AZ340311 19 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UUGC1M0072H15 F, genomic survey sequence.

ACCESSION AZ340311
VERSION AZ340311.1 GI:10415441
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0072 row: H column: 15

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0072H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1481
AZ350519/c

LOCUS AZ350519 19 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UUGC1M0089A10 F, genomic survey sequence.

ACCESSION AZ350519
VERSION AZ350519.1 GI:10429756
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: A column: 10

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0110B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1482

AZ364226
LOCUS
DEFINITION
1M0110B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0110B24 F, genomic survey sequence.
ACCESSION
AZ364226
VERSION
AZ364226.1 GI:10477926
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0110 row: B column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0110B24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1483

AZ365696
LOCUS
DEFINITION
1M0112A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0112A07 R, genomic survey sequence.
ACCESSION
AZ365696
VERSION
AZ365696.1 GI:10479396
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: A column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
Source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0112A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1484

AZ374409
LOCUS AZ374409 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0127D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127D10 F, genomic survey sequence.

ACCESSION AZ374409
VERSION AZ374409.1 GI:10488109
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: D column: 10
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0127D10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1485

AZ374619
LOCUS AZ374619 19 bp DNA linear GSS 02-OCT-2000
DEFINITION IM0127F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0127F04 R, genomic survey sequence.

ACCESSION AZ374619
VERSION AZ374619.1 GI:10488319
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: F column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

FEATURES                                     Location/Qualifiers
  source                                     1..19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0127F04"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1486
AZ385952
LOCUS      19 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION  IM0144L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0144L10 R, genomic survey sequence.
ACCESSION  AZ385952
VERSION    AZ385952.1 GI:10499652
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D..Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0144 row: L column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
  source                                     1..19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0144L10"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1487
AZ391509
LOCUS      19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION  1M0153K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0153K08 R, genomic survey sequence.
ACCESSION  AZ391509
VERSION    AZ391509.1 GI:10506552
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D..Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0153 row: K column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

```

FEATURES
source
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0153K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1489
AZ414050
LOCUS
DEFINITION
1M0182P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0182P04 F, genomic survey sequence.
ACCESSION
AZ414050
VERSION
AZ410050.1 GI:10534063
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seq primer: CGTTGTAAACACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0182P04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1489
AZ414413
LOCUS
DEFINITION
1M0189013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0189013 R, genomic survey sequence.
ACCESSION
AZ414413
VERSION
AZ414413.1 GI:10538426
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0188 row: O column: 13
Seq primer: CACACAGGAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

```

FEATURES                                     Location/Qualifiers
  source                                     1. .19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0188013"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1490
AZ422604
LOCUS          19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION    IM0201B21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone, UUGC1M0201B21 F, Genomic survey sequence.
ACCESSION     AZ422604
VERSION       AZ422604.1 GI:10546617
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0201 row: B column: 21
              Seq primer: CGTTGTAAACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
  source                                     1. .19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0201B21"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match          0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1491
AZ424716/c
LOCUS          19 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION    IM0204020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0204020 F, genomic survey sequence.
ACCESSION     AZ424716
VERSION       AZ424716.1 GI:10548729
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0204 row: O column: 20
              Seq primer: CGTTGTAAACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 19.

```

```

FEATURES
source
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0204020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1492
AZ441329/c
LOCUS
DEFINITION 1M0233D01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0233D01 F, genomic survey sequence.
ACCESSION AZ441329
VERSION AZ441329.1 GI:10565342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: D column: 01
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0233D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1493
AZ442365/c
LOCUS
DEFINITION 1M0236C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0236C13 F, genomic survey sequence.
ACCESSION AZ442365
VERSION AZ442365.1 GI:10566378
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0236 row: C column: 13
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

```


FEATURES
source

Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0236C13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1494

AZ450180
LOCUS
1M0248K13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0248K13 R, genomic survey sequence.

ACCESSION
AZ450180
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0248 row: K column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0248K13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2707 CTAATAAAAAAAAAAAAAAAAAA 2725
|||||
Db 1 CTAATAAAAAAAAAAAAAAAAAA 19

RESULT 1495

AZ453930/c
LOCUS
1M0255G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0255G11 R, genomic survey sequence.

ACCESSION
AZ453930
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: G column: 11
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0255G11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1496

AZ460906
LOCUS AZ460906 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0266E03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0266E03 R, genomic survey sequence.

ACCESSION AZ460906
VERSION AZ460906.1 GI:10619031
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: E column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0266E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1497

AZ471494/c
LOCUS AZ471494 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0286E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286E11 F, genomic survey sequence.

ACCESSION AZ471494
VERSION AZ471494.1 GI:10629619
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0286 row: E column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0286E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1498
AZ476576/c

LOCUS 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0295F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0295F04 R, genomic survey sequence.

ACCESSION AZ476576
VERSION AZ476576.1 GI:10634701

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0295 row: F column: 04

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0295F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1499
AZ486786/c

LOCUS 19 bp DNA linear GSS 05-OCT-2000
DEFINITION 1M0315D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315D21 F, genomic survey sequence.

ACCESSION AZ486786
VERSION AZ486786.1 GI:10653902

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 21

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

```

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0315D21"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1500
LOCUS
DEFINITION
  AZ490652 19 bp DNA linear GSS 05-OCT-2000
  1M0323E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0323E17 R, genomic survey sequence.
ACCESSION
  AZ490652
VERSION
  AZ490652.1 GI:10661595
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0323 row: E column: 17
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0315D21"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1500
LOCUS
DEFINITION
  AZ490652/c 19 bp DNA linear GSS 05-OCT-2000
  1M0323E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0323E17 R, genomic survey sequence.
ACCESSION
  AZ490652/c
VERSION
  AZ490652.1 GI:10661595
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0323 row: E column: 17
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

```

```

FEATURES                                     Location/Qualifiers
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0350B04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
DB 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1502
AZ579119
LOCUS
DEFINITION
1M0363M16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0363M16 F, genomic survey sequence.
ACCESSION
AZ579119
VERSION
GI:11693580
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0363 row: M column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363M16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
DB 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1503
AZ583970
LOCUS
DEFINITION
1M0388M11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0388M11 F, genomic survey sequence.
ACCESSION
AZ583970
VERSION
GI:11704386
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0388 row: M column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

```

FEATURES		Location/Qualifiers					
source	1. .19	/organism="Mus musculus"					
		/mol_type="genomic DNA"					
		/strain="C57BL/6J"					
		/db_xref="taxon:10090"					
		/clone="UUGC1M038M11"					
		/sex="Male"					
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"					
		/clone_lib="Mouse 10kb plasmid UUGC1M library"					
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource					
		(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor mouse DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."					
		Query Match		0.7%;	Score 19; DB 1; Length 19;		
		Best Local Similarity		100.0%;	Pred. No. 1.2e+03;		
		Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	2709	AAAAAAAAAAAAAAAAAAAAA 2727					
Db	1	AAAAAAAAAAAAAAAAAAAAA 19					
				RESULT 1504			
				AZ585865			
				LOCUS			
				DEFINITION			
				1M0391D21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391D21 F, genomic survey sequence.			
				ACCESSION			
				VERSION			
				KEYWORDS			
				SOURCE			
				ORGANISM			
				REFERENCE			
				AUTHORS			
				TITLE			
				JOURNAL			
				COMMENT			
				<p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0391 row: D column: 21</p> <p>Seq primer: CGTTGTAAACGACGCCAGT</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>			

FEATURES		Location/Qualifiers					
source	1. .19	/organism="Mus musculus"					
		/mol_type="genomic DNA"					
		/strain="C57BL/6J"					
		/db_xref="taxon:10090"					
		/clone="UUGC1M0391D21"					
		/sex="Male"					
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"					
		/clone_lib="Mouse 10kb plasmid UUGC1M library"					
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource					
		(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor mouse DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."					
		Query Match		0.7%;	Score 19; DB 1; Length 19;		
		Best Local Similarity		100.0%;	Pred. No. 1.2e+03;		
		Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	2709	AAAAAAAAAAAAAAAAAAAAA 2727					
Db	1	AAAAAAAAAAAAAAAAAAAAA 19					
				RESULT 1505			
				AZ593210			
				LOCUS			
				DEFINITION			
				1M0404C09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0404C09 R, genomic survey sequence.			
				ACCESSION			
				VERSION			
				KEYWORDS			
				SOURCE			
				ORGANISM			
				REFERENCE			
				AUTHORS			
				TITLE			
				JOURNAL			
				COMMENT			
				<p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0404 row: C column: 09</p> <p>Seq primer: CACACAGGAACGCTATGACC</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>			

FEATURES
source

Location/Qualifiers
1. .19

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0404C09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1506

AZ616154/c
LOCUS
DEFINITION
1M045P16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0445P16 R, genomic survey sequence.

ACCESSION
AZ616154
VERSION
GSS.
KEYWORDS
SOURCE
MUS musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

1 (bases 1 to 19)

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0445 row: P column: 16

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0445P16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 1

RESULT 1507

AZ627844/c
LOCUS
DEFINITION
1M0474005F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474J05 F, genomic survey sequence.

ACCESSION
AZ627844
VERSION
GSS.
KEYWORDS
SOURCE
MUS musculus (house mouse)

ORGANISM

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

1 (bases 1 to 19)

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: J column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0489H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0507D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1510

AZ643659
LOCUS
DEFINITION
1M0507D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0507D18 F, genomic survey sequence.

ACCESSION
AZ643659
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0507 row: D column: 18
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

JOURNAL
COMMENT

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1511

AZ644698/C
LOCUS
DEFINITION
1M0508E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0508E17 R, genomic survey sequence.

ACCESSION
AZ644698
VERSION
GSS.
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0508 row: E column: 17
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

JOURNAL
COMMENT

FEATURES		Location/Qualifiers	
Source		1..19	
		/organism="Mus musculus"	
		/mol_type="genomic DNA"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/clone="UUGC1M0517L16"	
		/sex="Male"	
		/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"	
		/clone_lib="Mouse 10kb plasmid UUGC1M library"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
Query Match		0.7%; Score 19; DB 1; Length 19;	
Best Local Similarity		100.0%; Pred. No. 1.2e+03;	
Matches		19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	2709	AAAAAAAAAAAAAAAAAAAAA	2727
Db	19	AAAAAAAAAAAAAAAAAAAAA	1
RESULT 1512			
AZ648335			
LOCUS			
DEFINITION			
AZ648335			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

FEATURES
source

Location/Qualifiers

```

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0519E15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1514
AZ764497

LOCUS AZ764497 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION IM0560H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0560H03 R, genomic survey sequence.

ACCESSION AZ764497
 VERSION AZ764497.1 GI:12879521

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: H column: 03
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

```

1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560H03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match 0.7%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1515

LOCUS AZ764522 19 bp DNA linear GSS 16-FEB-2001
 DEFINITION IM0560E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0560E16 R, genomic survey sequence.

ACCESSION AZ764522
 VERSION AZ764522.1 GI:12879571

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: E column: 16
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

```

FEATURES             Location/Qualifiers
  source              1..19
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC1M0560P14"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /vector="PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1516
A2764534
LOCUS             19 bp DNA linear GSS 16-FEB-2001
DEFINITION       1M0560P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560P14 R, genomic survey sequence.
ACCESSION        A2764534
VERSION          A2764534.1 GI:12879595
KEYWORDS         GSS.
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE        1 (bases 1 to 19)
AUTHORS          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE            Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 14
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES             Location/Qualifiers
  source              1..19
                        /organism="Mus musculus"
                        /mol_type="genomic DNA"
                        /strain="C57BL/6J"
                        /db_xref="taxon:10090"
                        /clone="UUGC1M0560E16"
                        /sex="Male"
                        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                        /vector="PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1516
A2764534
LOCUS             19 bp DNA linear GSS 16-FEB-2001
DEFINITION       1M0560P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560P14 R, genomic survey sequence.
ACCESSION        A2764534
VERSION          A2764534.1 GI:12879595
KEYWORDS         GSS.
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE        1 (bases 1 to 19)
AUTHORS          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE            Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 14
Seq primer: CACACGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

```

FEATURES
source

Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0571L23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1518
AZ778858

LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0014O20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0014O20 F, genomic survey sequence.

ACCESSION AZ778858
VERSION AZ778858.1 GI:12908925
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source

Location/Qualifiers

1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014O20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1519
AZ779901

LOCUS 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0016L16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0016L16 R, genomic survey sequence.

ACCESSION AZ779901
VERSION AZ779901.1 GI:12911024
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES		Location/Qualifiers			
source	1.	19			
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC2M0016E16"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUGC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
Query Match		0.7%;	Score 19; DB 1; Length 19;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+03;		
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2727			
	1	AAAAAAAAAAAAAAAAAAAAA 19			
Db	1	AAAAAAAAAAAAAAAAAAAAA 19			
	1	AAAAAAAAAAAAAAAAAAAAA 19			
RESULT 1520					
AZ781876					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
<p>19 bp DNA linear GSS 16-FEB-2001</p> <p>2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021003 R, genomic survey sequence.</p> <p>2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034M12 F, genomic survey sequence.</p> <p>GI:12915007</p> <p>Mus musculus (house mouse)</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0021 row: 0 column: 03</p> <p>Seq primer: CACACAGGAACAGCTATGACC</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>					

FEATURES		Location/Qualifiers			
source	1.	19			
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC2M0016E16"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUGC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
Query Match		0.7%;	Score 19; DB 1; Length 19;		
Best Local Similarity		100.0%;	Pred. No. 1.2e+03;		
Matches		19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Qy	2709	AAAAAAAAAAAAAAAAAAAAA 2727			
	1	AAAAAAAAAAAAAAAAAAAAA 19			
Db	1	AAAAAAAAAAAAAAAAAAAAA 19			
	1	AAAAAAAAAAAAAAAAAAAAA 19			
RESULT 1521					
AZ787634					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
<p>19 bp DNA linear GSS 16-FEB-2001</p> <p>2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034M12 F, genomic survey sequence.</p> <p>2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034M12 F, genomic survey sequence.</p> <p>GI:12926621</p> <p>Mus musculus (house mouse)</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.</p> <p>1 (bases 1 to 19)</p> <p>Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.</p> <p>Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts</p> <p>Unpublished (2000)</p> <p>Contact: Robert B. Weiss</p> <p>University of Utah Genome Center</p> <p>University of Utah</p> <p>Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA</p> <p>Tel: 801 585 5606</p> <p>Fax: 801 585 7177</p> <p>Email: ddunn@genetics.utah.edu</p> <p>Insert Length: 10000 Std Error: 0.00</p> <p>Plate: 0034 row: M column: 12</p> <p>Seq primer: CTTGTAAAACGACGGCAGT</p> <p>Class: plasmid ends</p> <p>High quality sequence stop: 19.</p>					

FEATURES
sourceLocation/Qualifiers
1. .19

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1522
AZ788058/c

LOCUS AZ788058 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0034I24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0034I24 R, genomic survey sequence.

ACCESSION AZ788058
VERSION AZ788058.1 GI:12927475
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0034 row: I column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES
sourceLocation/Qualifiers
1. .19

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0034I24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note: Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1523
AZ789590/c

LOCUS AZ789590 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0037G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037G06 R, genomic survey sequence.

ACCESSION AZ789590
VERSION AZ789590.1 GI:12930573
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0037 row: G column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

```

FEATURES             Location/Qualifiers
  source              1..19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0037G06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1524
A2792713/c
LOCUS           19 bp DNA linear GSS 16-FEB-2001
DEFINITION     2M0045C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045C22 F, genomic survey sequence.
ACCESSION     A2792713
VERSION       A2792713.1 GI:12936930
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunne@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0045 row: C column: 22
               Seq primer: CGTTGTAACGACGCCGAGT
               Class: plasmid ends
               High quality sequence stop: 19.

FEATURES             Location/Qualifiers
  source              1..19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0045C22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1524
A2792713/c
LOCUS           19 bp DNA linear GSS 16-FEB-2001
DEFINITION     2M0045C22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0045C22 F, genomic survey sequence.
ACCESSION     A2792713
VERSION       A2792713.1 GI:12936930
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunne@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0045 row: C column: 22
               Seq primer: CGTTGTAACGACGCCGAGT
               Class: plasmid ends
               High quality sequence stop: 19.

```



```

FEATURES                                     Location/Qualifiers
  source
  1..19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0049C12"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1526
AZ801970/c
LOCUS
DEFINITION
  2M0060112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0060112 R, genomic survey sequence.
ACCESSION
  AZ801970
VERSION
  AZ801970.1 GI:12954293
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0060 row: 1 column: 12
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
  source
  1..19
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0049C12"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /notes="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1527
AZ822225/c
LOCUS
DEFINITION
  2M0095E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0095E17 F, genomic survey sequence.
ACCESSION
  AZ822225
VERSION
  AZ822225.1 GI:12992133
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0095 row: 5 column: 17
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 19.

```

```

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0139G08"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adapted vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1529
AZ841581
LOCUS
DEFINITION
  AZ841581 19 bp DNA linear GSS 20-FEB-2001
  2M0139G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0139G08 R, genomic survey sequence.
ACCESSION
  AZ841581
VERSION
  AZ841581.1 GI:13011489
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunne@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0139 row: G column: 08
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0095E17"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adapted DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adapted mouse DNA was annealed to
        adapted vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1529
AZ841581
LOCUS
DEFINITION
  AZ841581 19 bp DNA linear GSS 20-FEB-2001
  2M0139G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0139G08 R, genomic survey sequence.
ACCESSION
  AZ841581
VERSION
  AZ841581.1 GI:13011489
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 19)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunne@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0139 row: G column: 08
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.

```

```

FEATURES                                     Location/Qualifiers
  source
1..19
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0139A16"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1530
LOCUS      AZ861896                19 bp    DNA        linear    GSS 21-FEB-2001
DEFINITION 2M0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ861896
VERSION    AZ861896.1  GI:13058674
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0168 row: P column: 10
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.

FEATURES                                     Location/Qualifiers
  source
1..19
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC2M0139A16"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1M library"
  /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db   1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1531
LOCUS      AZ936798                19 bp    DNA        linear    GSS 26-APR-2001
DEFINITION 2M0193L10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION  AZ936798
VERSION    AZ936798.1  GI:13795379
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 19)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D. Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0193 row: L column: 10
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.

```

FEATURES		Location/Qualifiers	
source		1. 19	
		/organism="Mus musculus"	
		/mol_type="genomic DNA"	
		/strain="C57BL/6J"	
		/db_xref="taxon:10090"	
		/clone="UUGC2M0193L10"	
		/sex="Female"	
		/lab_hosts="E. coli strain XL10-Gold, Tl-resistant, F-"	
		/clone_lib="Mouse 10kb plasmid UUGC2M library"	
		/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	
Query Match		0.7%; Score 19; DB 1; Length 19;	
Best Local Similarity		100.0%; Pred. No. 1.2e+03;	
Matches		19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy		2709 AAAAAAAAAAAAAAAAAAAAAA 2727	
Db		1 AAAAAAAAAAAAAAAAAAAAAA 19	
RESULT 1533			
AZ985501		19 bp DNA linear GSS 27-APR-2001	
LOCUS		2M0267821F Mouse 10kb plasmid UUGC2M library Mus musculus genomic	
DEFINITION		clone UUGC2M0267E21 F, genomic survey sequence.	
ACCESSION		AZ985501	
VERSION		AZ985501.1 GI:13856728	
KEYWORDS		GSS.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
AUTHORS		1 (bases 1 to 19)	
		Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.	
TITLE		Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0267 row: E column: 21 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 19.	

FEATURES
source

Location/Qualifiers
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288121"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1534

LOCUS
DEFINITION
CL680736 19 bp DNA linear GSS 09-JUL-2004
PRI012a_H07_2 - PRI012a.BR (19) Note: Recurring String Mixed stage
pacificus genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CL680736.1 GI:50187696
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 19)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source

Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"

/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1535

LOCUS
DEFINITION
CL685439 19 bp DNA linear GSS 09-JUL-2004
PRI0141b_A04_2 - PRI0141b.BR (19) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CL685439.1 GI:50193696
GSS.
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 19)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppADB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source

Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1536

LOCUS
DEFINITION
CL693186 19 bp DNA linear GSS 10-JUL-2004
PRI0160c_B05_2 - PRI0160c.BR (19) Note: Recurring String Mixed
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
CL693186
CL693186.1 GI:50215094
GSS.

```

SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..19
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1537
LOCUS
DEFINITION CL693191 19 bp DNA linear GSS 10-JUL-2004
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION CL693191.1 GI:50215099
KEYWORDS GSS.
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1537
LOCUS
DEFINITION CL693191 19 bp DNA linear GSS 10-JUL-2004
stage fosmid library of P. pacificus var. California Pristionchus
pacificus genomic, genomic survey sequence.
ACCESSION CL693191
VERSION CL693191.1 GI:50215099
KEYWORDS GSS.
SOURCE
ORGANISM
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism
JOURNAL Pristionchus pacificus
PUBMED Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT 14681447
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: r7
Class: fosmid ends.
FEATURES
Location/Qualifiers
1..19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

```

```

/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
Query Match 0.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19
RESULT 1538
LOCUS
DEFINITION AL038507 20 bp mRNA linear EST 06-JUL-2004
DKFP566D1846_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFP566D1846_mRNA sequence.
ACCESSION AL038507
VERSION AL038507.1 GI:49682146
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 20)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
EST (Ottewaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP566D1846"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xi-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"
Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2708 TAAAAAAAAAAAAAAAAAAAAA 2726
Db 2 TAAAAAAAAAAAAAAAAAAAAA 20
RESULT 1539
LOCUS
DEFINITION AL038576 20 bp mRNA linear EST 06-JUL-2004
DKFP566F0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFP566F0346_mRNA sequence.
ACCESSION AL038576
VERSION AL038576.1 GI:49682161
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 20)
Ottewaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and

```

```

Wiemann,S.
EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p566P1746"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAA 2726
|||||
Db 2 TAAAAAATAAAAA 20

RESULT 1540
AL038754
LOCUS 20 bp mRNA linear EST 06-JUL-2004
DEFINITION DKF2p566M1346_r1.566 (synonym: hfk2) Homo sapiens cDNA clone
ACCESSION DKF2p566M1346, mRNA sequence.
VERSION AL038754
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
TITLE EST (Ottenwaelder, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKF2p566M1346"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAA 2726
|||||
Db 2 TAAAAAATAAAAA 20

RESULT 1541
AL038754
LOCUS 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587759 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION ROS061G06, mRNA sequence.
VERSION AL587759
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Murray, P.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCCCGCTTTT TTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech
(*6854-

Seq primer: M13P.
Location/Qualifiers
1..20
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS061G06"
/tissue_type="Brain"
/dev_stage="Unknown"

```

/lab_host="DH10B"
 /clone_lib="BP Chicken Brain Library"
 /note="Vector: pSPT11; Site_1: NotI; Site_2: SalI; Cloned
 unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
 5' TCGACTCTGAG 3' ; 3' adaptor sequence: 5'
 GCGCGCGTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
 Clontech (*6854-1)"

Query Match 0.7%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAATAAAAAAAAAA 2726

Db 20 TAAAAAATAAAAAAAAAA 2

RESULT 1543

CF318278/c

LOCUS HD--08-F13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
 HD--08-F13, mRNA sequence.

ACCESSION CF318278

VERSION CF318278

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 20)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

TITLE Contact: Nahm B.H.

JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

COMMENT of Bioscience and Bioinformatics, Myongui University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .20

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD--08-F13"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAATAAAAAAAAAA 2727

Db 20 AAAAAAATAAAAAAAAAA 2

RESULT 1544

CN754148

LOCUS CN754148 20 bp mRNA linear EST 19-MAY-2004

DEFINITION ID0AAA12AG12RM1 ApMS Acyrthosiphon pisum cDNA clone ID0AAA12AG12

5', mRNA sequence.

ACCESSION CN754148

VERSION CN754148.1 GI:47519145

KEYWORDS EST.

SOURCE Acyrthosiphon pisum (pea aphid)

ORGANISM Acyrthosiphon pisum

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;

Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.

1 (bases 1 to 20)

Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,

Stern, D., Tagu, D. and Wincker, P.

An expressed sequence tags database for the pea aphid Acyrthosiphon

pisum

Unpublished (2004)

CONTACT: D. Tagu

INRA Rennes

UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France

Tel: +33 2.23.48.51.65

Fax: +33 2.23.48.51.50

Risk of contamination by bacterial sequences from obligatory

(Buchner) or facultative endosymbionts. These sequences were

obtained in the frame of the International Consortium of Aphid

Genomics in collaboration with Genoscope

PCR Primers

FORWARD: CAGGAACAGCTATGACC

Plate: 12 row: G column: 12.

Location/Qualifiers

1. .20

/organism="Acyrthosiphon pisum"

/mol_type="mRNA"

/cultivar="developmentstage"

/db_xref="taxon:7029"

/clones="ID0AAA12AG12"

/tissue_type="whole insect"

/dev_stage="nymphs and adults (parthenogenetic females)"

/lab_hosts="XLI-Blue"

/clone_lib="ApMS"

/note="Vector: pBS-SK minus; Site_1: EcoRI; Site_2: XhoI;

Sample name: ID0AAA; Plant growth place: Department of

Ecology & Evolutionary Biology, Princeton University ;

Soil conditions: Soil ; Sowing date: 01/06/1999 ;

Harvesting date: 01/06/1999 ; Stress date: no stress ;

Description: Aphids inoculated on one-week old Vicia faba

under non-sterile conditions. All parthenogenetic stages

and both winged and wingless adults were collected for

library construction. ; experimental condition: long

photoperiod (16-hr light/8-hr dark at 18 c)"

Query Match 0.7%; Score 19; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2728

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 1545

DN955202

LOCUS DN955202 20 bp mRNA linear EST 04-MAY-2005

DEFINITION i83bf09.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA

sequence.

ACCESSION DN955202

VERSION DN955202

KEYWORDS EST.

SOURCE Gnetum gnemon

ORGANISM Gnetum gnemon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales;

1 (bases 1 to 20)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.,

AUTHORS


```

O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES
    source
        1..20
            /organism="Gnetum gnemon"
            /mol_type="mRNA"
            /db_xref="taxon:3382"
            /sex="female"
            /clone_lib="Gnetum female cone (NYBG)"
            /note="Organ: mature, unfertilized reproductive strobili;
            Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
            Completed 02/11/02, submitted for sequencing 02/12/02.
            Library: Stratagene ZAP Express cDNA Synthesis Kit. The
            library was size-fractionated to enrich for large inserts.
            Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
    |||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1546
AZ341237
LOCUS
DEFINITION
    AZ341237 20 bp DNA linear GSS 29-SEP-2000
    clone UUGC1M0073G03 R, genomic survey sequence.
ACCESSION
    AZ341237
VERSION
    AZ341237.1 GI:10417288
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 20)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0073 row: G column: 03
    Seq primer: CACACAGGAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 10.
    Location/Qualifiers
        1..20
            /organism="Mus musculus"
            /mol_type="genomic DNA"

O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Seq primer: -21M13UnivRev.
FEATURES
    source
        1..20
            /organism="Gnetum gnemon"
            /mol_type="mRNA"
            /db_xref="taxon:3382"
            /sex="female"
            /clone_lib="Gnetum female cone (NYBG)"
            /note="Organ: mature, unfertilized reproductive strobili;
            Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
            Completed 02/11/02, submitted for sequencing 02/12/02.
            Library: Stratagene ZAP Express cDNA Synthesis Kit. The
            library was size-fractionated to enrich for large inserts.
            Sample: NYBG accession number #436/84"
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
    |||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1547
AZ579178
LOCUS
DEFINITION
    AZ579178 20 bp DNA linear GSS 13-DEC-2000
    clone UUGC1M0363F11 F, genomic survey sequence.
ACCESSION
    AZ579178
VERSION
    AZ579178.1 GI:11693523
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 20)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0363 row: F column: 11
    Seq primer: CGTTGTAAACGACGCCAGT
    Class: plasmid ends
    High quality sequence stop: 20.
    Location/Qualifiers
        1..20
            /organism="Mus musculus"
            /mol_type="genomic DNA"

```

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0073G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
    |||||
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1547
AZ579178
LOCUS
DEFINITION
    AZ579178 20 bp DNA linear GSS 13-DEC-2000
    clone UUGC1M0363F11 F, genomic survey sequence.
ACCESSION
    AZ579178
VERSION
    AZ579178.1 GI:11693523
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
    Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
    1 (bases 1 to 20)
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
TITLE
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
JOURNAL
    Unpublished (2000)
COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0363 row: F column: 11
    Seq primer: CGTTGTAAACGACGCCAGT
    Class: plasmid ends
    High quality sequence stop: 20.
    Location/Qualifiers
        1..20
            /organism="Mus musculus"
            /mol_type="genomic DNA"

```

```
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0363F11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 2 AAAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 1548
LOCUS AZ638704 20 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0498E13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0498E13 R, genomic survey sequence.
ACCESSION AZ638704
VERSION AZ638704.1 GI:11760894
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: E column: 13
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
```

```
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0498E13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```
Query Match      0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
Db 2 AAAAAAAAAAAAAAAAAAAAAA 20
```

```
RESULT 1549
LOCUS AZ849506 20 bp DNA linear GSS 21-FEB-2001
DEFINITION ZM0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION AZ849506
VERSION AZ849506.1 GI:13033596
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
```


TITLE
JOURNAL
COMMENT

Niederhauern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 Plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduhn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0017 row: N column: 14
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1. .22

FEATURES
 source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0017N14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1553
CX002873/c
LOCUS
DEFINITION
 iV34c07.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 23)
 Balija, V.S., Nascimento, L.U. and McCombie, M.R.
 ESTs from Canis familiaris left cardiac ventricle (dog)
 Unpublished (2004)

COMMENT

Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org.

FEATURES
 source

Location/Qualifiers
 1. .23
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1: EcoRI; Site 2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
Db 23 AAAAAAAAAAAAAAAAAA 5

RESULT 1554

LOCUS
DEFINITION
 DX032218 KBrB029E14R KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB029E14, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

1 (bases 1 to 23)
 Yang, T.J., Kwon, S.J., Kim, J.A., Kim, J.S., Lim, K.B., Jin, M., Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S., Hann, J.H. and Park, B.S.
 End sequence of Brassica rapa BamHI (KBrB) BAC clone Unpublished (2005)
 Contact: Beom-Seok Park
 Brassica Genomics Team
 National Institute of Agricultural Biotechnology
 225 Seodun-Dong, Suwon, 441-707, Korea
 Tel: +82-31-299-1670
 Fax: +82-31-299-1672
 Email: pbeom@da.go.kr

TITLE
JOURNAL
COMMENT

FEATURES
 source

Location/Qualifiers
 1. .23
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrB029E14"

/lab_host="E.coli DH10B"
 /clone_lib="KBrB, Brassica rapa BamHI BAC library"
 /notes="vector: PCUGIBAC1; Site 1: BamHI; Brassica rapa spp
 pekinensis var. Chiifu BAC library (KBrB BAC) is provided
 by Yong-Pyo Lim (CNU)."

Query Match 0.7%; Score 19; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1555
 AZ442146/c
 LOCUS 22 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0234B16r Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0234B16 R, genomic survey sequence.

ACCESSION AZ442146
 VERSION AZ442146.1 GI:10566159
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0234 row: B column: 16
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 22.
 FEATURES
 source
 1. .22
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0234B16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.7%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAACAAAAAAAAA 1

RESULT 1556
 CT017313/c
 LOCUS 22 bp DNA linear GSS 09-AUG-2005
 DEFINITION KBrH128J11 genomic clone, KBrH (HindIII) BAC library Brassica rapa
 subsp. pekinensis, genomic survey sequence.

ACCESSION CT017313
 VERSION CT017313.1 GI:71471431
 KEYWORDS GSS.
 SOURCE Brassica rapa subsp. pekinensis
 ORGANISM Brassica rapa subsp. pekinensis

REFERENCE 1
 AUTHORS Viehoever, P., Holtgraewe, D. and Weisshaar, B.
 TITLE BAC end sequences of Brassica rapa
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 22)
 AUTHORS Li, Y. and Weisshaar, B.

TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
 Institute for Genome Research, Universitaetstrasse 25, D-33594
 Bielefeld, Germany
 COMMENT Contact: Bernd Weisshaar
 Bielefeld University, Institute for Genome Research
 Universitaetstrasse 25, D-33594 Bielefeld, Germany Email:
 bernd.weisshaar@uni-bielefeld.de

BAC end sequences of Brassica rapa BAC clone KBrH128J11; generated
 as contribution to the 'Multinational Brassica rapa Sequencing
 Project' Seq primer: sp6B ATTAGGTGACTATAG
 Class: BAC ends.

FEATURES
 source
 1. .22
 Location/Qualifiers
 /organism="Brassica rapa subsp. pekinensis"
 /mol_type="genomic DNA"
 /strain="Chiifu type 401-42"
 /cultivar="Chiifu"
 /sub_species="pekinensis"
 /db_xref="taxon:51351"
 /clone_lib="KBrH128J11"
 /clone="KBrH128J11"
 /clone_lib="KBrH, Brassica rapa HindIII BAC library
 GF-SCF-1002, Vector: pCUGIBAC1"
 /lab_host="E.coli DH10B"

Query Match 0.7%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2730
 |||||
 Db 22 AAAAAAAAAACAAAAAAAAA 1

RESULT 1557
 CF291486/c
 LOCUS 23 bp mRNA linear EST 14-AUG-2003
 DEFINITION 14ROOT--01-021.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa (japonica cultivar-group) cDNA clone 14ROOT--01-021, mRNA


```
VERSION AL587572.1 GI:13192606
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE MURRAY,F.
AUTHORS BP Chicken Brain Library
TITLE Unpublished (2001)
JOURNAL Contact: Frazer Murray
COMMENT Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech
(*6854-

FEATURES
source
    1. .20
        Location/Qualifiers
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /db_xref="taxon:9031"
            /clone="ROS05B11"
            /tissue_type="Brain"
            /dev_stage="Unknown"
            /lab_host="DH108"
            /clone_lib="BP Chicken Brain Library"
            /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
            unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
            5' TCACCTCGAG 3' ; 3' adaptor sequence: 5'
            GCGGCGCTTTTCTTTTCTTTT 3' Poly A RNA purchased from
            Clontech (*6854-1)"

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2707 CTAAAAAATAAAAAAAAAA 2726
Db 20 CCAAAAAAAAAAAAAAAAAA 1

RESULT 1561
CF299570/c
LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--03-K09, mRNA
sequence.
ACCESSION CF299570.1 GI:33671331
VERSION CF299570
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
    1. .20
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="ABF--03-A01"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH108"
        /clone_lib="ABF3-overexpressing transgenic rice plasmid
        cDNA library (ABF)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
        for 2hrs. Oligo-capped mRNA was reverse transcribed and
        then used for PCR. mRNA was prepared from ABA-responsive
        element binding transcription factor 3 overexpression
        line."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAAAAAAA 2728
Db 20 CAAAAAATAAAAAAAAAA 1
```

```
source
    1. .20
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="7LEAF--03-K09"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH108"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2705 TACTAAAAAATAAAAAAAAAA 2724
Db 20 TAGTAAAAAATAAAAAAAAAA 1

RESULT 1562
CF308984/c
LOCUS 20 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-A01, mRNA sequence.
ACCESSION CF308984
VERSION CF308984.1 GI:33680745
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
    1. .20
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="ABF--03-A01"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH108"
        /clone_lib="ABF3-overexpressing transgenic rice plasmid
        cDNA library (ABF)"
        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
        for 2hrs. Oligo-capped mRNA was reverse transcribed and
        then used for PCR. mRNA was prepared from ABA-responsive
        element binding transcription factor 3 overexpression
        line."

Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAAAAAAA 2728
Db 20 CAAAAAATAAAAAAAAAA 1
```

```

Db      20 AAAAAAAAAAAAAAAAACAAAAAA 1

RESULT 1563
CF316662/c
LOCUS   HD--06-A20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION
HD--06-A20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
Library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--06-A20, mRNA sequence.
CF316662
CF316662.1 GI:33688423
EST.
SOURCE  Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Eharctoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--06-A20"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2707 CTAATAAAAAAAAAAAAAAAAAA 2726
| | | | | | | | | | | | | | | | | |
Db      20 CCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1564
DR073483
LOCUS   ik85b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
ik85b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR073483
DR073483.1 GI:67051364
EST.
SOURCE  Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2707 CTATAAAAAAAAAAAAAAAAAA 2726
| | | | | | | | | | | | | | | | | |
Db      20 CCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1565
DR073483
LOCUS   ik85b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
DEFINITION
ik85b11.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
sequence.
DR073483
DR073483.1 GI:67051364
EST.
SOURCE  Ginkgo biloba (maidenhair tree)
ORGANISM Ginkgo biloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoales; Ginkgoales; Ginkgoaceae; Ginkgo.
1 (bases 1 to 20)
Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Ginkgo female leaf (NYBG)

JOURNAL COMMENT
Unpublished (2005)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@csuhl.org
Original 3 prime EST has been reverse completed to be in 5 prime
direction
Seq primer: -21M13UnivRev.
Location/Qualifiers
1..20
/organism="Ginkgo biloba"
/mol_type="mRNA"
/db_xref="taxon:3311"
/sex="female"
/clone_lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
The library was size-fractionated to enrich for large
inserts."

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2728
| | | | | | | | | | | | | | | | | |
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1565
AZ375620
LOCUS   AK0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION
clone UUGC1M0129A08 F, genomic survey sequence.
ACCESSION AK375620
VERSION AK375620.1 GI:10489320
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: A column: 08
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0129A08"

```


/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.78; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 1566

AZ486787/c

LOCUS 20 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0315D23 F, genomic survey sequence.

ACCESSION AZ486787
 VERSION AZ486787.1 GI:10653904
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 23

Seq primer: CGTTGTAAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315D23"

FEATURES

source

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315D23"

/sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.78; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
 |||||
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1567

AZ579122

LOCUS 20 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0363G19 F, genomic survey sequence.

ACCESSION AZ579122

VERSION AZ579122.1 GI:11693583

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0363 row: G column: 19

Seq primer: CGTTGTAAACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0363G19"

```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1/4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
    ||| ||||| ||||| |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

```

RESULT 1568

```

AZ645312/C
LOCUS
DEFINITION
  1M0510K11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0510K11 R, genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
  AZ645312.1 GI:11774684
  GSS.

```

```

ORGANISM
  Mus musculus
  Mus musculus (house mouse)

```

```

REFERENCE
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

JOURNAL
COMMENT
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0510 row: K column: 11
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.

```

FEATURES

```

source
  1..20
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0510K11"

```

```

/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1/4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
    ||| ||||| ||||| |||||
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

```

RESULT 1569

```

AZ821905
LOCUS
DEFINITION
  2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0094D20 R, genomic survey sequence.

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
  AZ821905.1 GI:12991813
  GSS.

```

```

ORGANISM
  Mus musculus
  Mus musculus (house mouse)

```

```

REFERENCE
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts

```

```

JOURNAL
COMMENT
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0094 row: D column: 20
  Seq primer: CACACAGGAAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 20.

```

FEATURES

```

source
  1..20
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0094D20"

```


Best Local Similarity 95.0%; Pred. No. 1.3e+03; Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1572
DX071064/c
LOCUS
DEFINITION
KBRB080L01F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB080L01, genomic survey sequence.
DX071064
DX071064.1 GI:84765360
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosids; eucotyledons II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 20)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L01

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/lab_host="E.coli DH10B"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1572
DX071064/c
LOCUS
DEFINITION
KBRB080L01F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB080L01, genomic survey sequence.
DX071064
DX071064.1 GI:84765360
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosids; eucotyledons II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 20)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L01

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 20 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1573
DX071075
LOCUS
DEFINITION
KBRB080L07F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB080L07, genomic survey sequence.
DX071075
DX071075.1 GI:84765371
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucotyledons II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 20)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L07

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucotyledons II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 20)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L07

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L07

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAGAAAAAAAAA 20

RESULT 1574
BX558161/c
LOCUS
DEFINITION
BX558161 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse37a05_plc, mRNA sequence.
BX558161
BX558161.1 GI:33429302
EST.
KEYWORDS
SOURCE
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 21)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
14519198
PUBMED
CONTACT: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L01

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAGAAAAAAAAA 20

RESULT 1574
BX558161/c
LOCUS
DEFINITION
BX558161 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse37a05_plc, mRNA sequence.
BX558161
BX558161.1 GI:33429302
EST.
KEYWORDS
SOURCE
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 21)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
14519198
PUBMED
CONTACT: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L01

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
|||||
Db 1 AAAAAAAAAAGAAAAAAAAA 20

RESULT 1573
DX071075
LOCUS
DEFINITION
KBRB080L07F KBrB, Brassica rapa BamHI BAC library Brassica rapa subsp. pekinensis genomic clone KBrB080L07, genomic survey sequence.
DX071075
DX071075.1 GI:84765371
GSS.
ORGANISM
Brassica rapa subsp. pekinensis
Brassica rapa subsp. pekinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eucotyledons II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 20)
Yang,T.J., Kwon,S.J., Kim,J.A, Kim,J.S., Lim,K.B., Jin,M., Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S., Hahn,J.H. and Park,B.S.
End sequence of Brassica rapa BamHI (KBrB) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa subsp. pekinensis BamHI BAC clone KBrB080L07

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .20
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone_lib="KBrB, Brassica rapa BamHI BAC library"
/note="Vector: pCUGIBAC1; Site_1: BamHI; Brassica rapa subsp pekinensis var. Chiifu BAC library (KBrB BAC) is provided by Yong-Pyo Lim (CNU)."
Query Match 0.7%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Park, J.Y., Lim, M.H., Kim, H.I., Choi, B.S., Seol, Y.J., Park, D.S.,
Hahn, J. H. and Park, B.S.
End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa esp. pekinensis Sau3AI BAC clone
KBrS004D04
Seq primer: T7
Class: BAC ends.

FEATURES

source
1..21
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS004D04"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/note="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC library (KBrS BAC) is
available at NIAB."

Query Match 0.7%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2727
|||||
Db 20 TAAAAAATAAAAAAAAAA 1

RESULT 1578

AL048750
LOCUS
DEFINITION
DKFZp566L123.r1.566 (synonym: hfk2) Homo sapiens cDNA clone

ACCESSION
AL048750
VERSION
AL048750.1 GI:4727821
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 22)
AUTHORS
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE
EST (Koehler, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
1..22
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566L123"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfk2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2727
|||||
Db 3 TCAAAAAATAAAAAAAAA 22

RESULT 1579

CT019890/c
LOCUS
DEFINITION
KBrH130A15 genomic clone, KBrH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.

ACCESSION
CT019890
VERSION
CT019890.1 GI:71468840
KEYWORDS
GSS.
SOURCE
Brassica rapa subsp. pekinensis

ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 Viehoever, P., Holtgraewe, D. and Weisshaar, B.
AUTHORS
BAC end sequences of Brassica rapa
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 23)
AUTHORS
Li, Y. and Weisshaar, B.
TITLE
Direct Submission
JOURNAL
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitaetsstrasse 25, D-33594
Bielefeld, Germany

COMMENT
Contact: Bernd Weisshaar
Bielefeld University, Institute for Genome Research
Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBrH130A15; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project' Seq primer: ml3f TGTAAGAAGGACGCCAGT
Class: BAC ends.

FEATURES
source
1..23
Location/Qualifiers
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/strain="Chiifu type 401-42"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrH130A15"
/clone_lib="KBrH, Brassica rapa HindIII BAC library
GF-SCF-1002, Vector: pCUGIBAC1"
/lab_host="E.coli DH10B"

Query Match 0.7%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAAAAAAA 2728
|||||
Db 23 AAAAAAATAAAAAAAAAA 4

DEFINITION
DKFZp566J0846.r1.566 (synonym: hfk2) Homo sapiens cDNA clone
ACCESSION
AL038692
VERSION
AL038692.1 GI:49682190
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 18)

RESULT 1580

AL038692
LOCUS
DEFINITION
DKFZp566J0846.r1.566 (synonym: hfk2) Homo sapiens cDNA clone

ACCESSION
AL038692
VERSION
AL038692.1 GI:49682190
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 18)

AUTHORS Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Ottenwaelder, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany.

FEATURES

source

Location/Qualifiers

1..18

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566J0846"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1581

BQ582676/c

LOCUS

DEFINITION BQ582676 18 bp mRNA linear EST 06-DEC-2002

CDNA clone 024-007-P18-SP6 MP12-ADIS-024-inflorescence Beta vulgaris

CDNA clone 024-007-P18 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 7 row: P column: 18

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES Location/Qualifiers

source

1..18

/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:184018"
/db_xref="taxon:161934"
/clone="024-007-P18"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1582

BQ590027/c

LOCUS

DEFINITION BQ590027 18 bp mRNA linear EST 06-DEC-2002

CDNA clone 024-019-E24-T7 MP12-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-E24 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 18 Std Error: 0.00

Plate: 19 row: E column: 24

Seq primer: T7; GTAATACGACTACTATAGGC.

FEATURES Location/Qualifiers

source

1..18

/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:190095"
/db_xref="taxon:161934"
/clone="024-019-E24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT-PCR."

Query Match 0.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1586

CF299674/c

LOCUS CF299674 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--03-M14, mRNA sequence.

ACCESSION CF299674.1 GI:33671435

VERSION CF299674

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source Location/Qualifiers

1..18 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-M14"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/notes="Vector: pCR4-TOPO; Site1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.7%; Score 18; DB 1; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1587

CF301151/c

LOCUS CF301151 18 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--05-005.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-005, mRNA sequence.

ACCESSION CF301151

VERSION CF301151.1 GI:33672912

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..18 /organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--06-Cl2"

/tissue_type="leaf"

/dev_stage="7 days after germination"

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1

Query Match 0.7%; Score 18; DB 1; Length 18;

/lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1589

CF301760/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--06-L22, mRNA
 sequence.

ACCESSION CF301760

VERSION CF301760.1 GI:33673521

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--06-L22"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 18; DB 1; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1590

CF302409/c

LOCUS 18 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--07-N19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--07-N19, mRNA
 sequence.

ACCESSION CF302409

VERSION CF302409.1 GI:33674170

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--07-N19"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.7%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2707 CTAATAAAAAAAAAAAAA 2724

|||||

Db 18 CTAATAAAAAAAAAAAAA 1

RESULT 1591

DE073142/c

LOCUS 18 bp mRNA linear EST 08-JUN-2005

DEFINITION qs66c01.g1 Ginkgo female leaf (NYBG) Ginkgo biloba cDNA 3', mRNA

sequence.

ACCESSION DE073142

VERSION DE073142.1 GI:67050994

KEYWORDS

EST.

SOURCE

Ginkgo biloba (maidenhair tree)

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 18)

Brenner, E.D., Twigg, R.W., Runko, S.J., Katari, M.S., Dedhia, N.N.,

O'Shaughnessy, A.L., Balija, V., Martienssen, R.A., McCombie, R.W.,

Benfey, P., Coruzzi, G. and Stevenson, D.

Expressed tag sequences from Ginkgo female leaf (NYBG)

Unpublished (2005)

JOURNAL

COMMENT

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

FEATURES

source

1..18

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="female"
 /clone_lib="Ginkgo female leaf (NYBG)"
 /note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI;
 Site_2: Eco RI; Stratagene ZAP Express cDNA Synthesis Kit.
 The library was size-fractionated to enrich for large
 inserts."

Query Match 0.7%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1592

DR074121/c 18 bp mRNA linear EST 08-JUN-2005
 LOCUS 1K98C05.g1 Ginkgo male leaf (NYBG) Ginkgo biloba cDNA 3', mRNA
 DEFINITION

ACCESSION

DR074121

VERSION

DR074121.1 GI:67052070

KEYWORDS

EST.

SOURCE

Ginkgo biloba (maidenhair tree)

ORGANISM

Ginkgo biloba

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.

1 (bases 1 to 18)

REFERENCE

AUTHORS

Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,

O'Shaughnessy,A.L., Baliya,V., Martienssen,R.A., McCombie,R.W.,

Benfey,P., Coruzzi,G. and Stevenson,D.

Expressed tag sequences from Ginkgo male leaf (NYBG)

Unpublished (2005)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Seq primer: -21M13UnivRev.

FEATURES

source

1..18

/organism="Ginkgo biloba"

/mol_type="mRNA"

/db_xref="taxon:3311"

/sex="male"

/clone_lib="Ginkgo male leaf (NYBG)"

/note="Organ: leaf; Vector: pBK-CMV; Site_1: XhoI; Site_2:

Eco RI; Stratagene ZAP Express cDNA Synthesis Kit. The

library was size-fractionated to enrich for large

inserts."

Query Match

Best Local Similarity 0.7%; Score 18; DB 1; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1593

CF293167/c

LOCUS

DEFINITION

30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

sativa (japonica cultivar-group) cDNA clone 30DGS--02-E02, mRNA

sequence.

ACCESSION

CF293167

VERSION

CF293167.1 GI:33662200

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-M05"

```

/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1596
CF309821/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P22, mRNA
sequence.
ACCESSION
CF302456
VERSION
CF302456.1 GI:33674217
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--07-P22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1596
CF309821
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA library II (7LEAF) "
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1596
CF309821/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA library II (7LEAF) "
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

ACCESSION
CF309821
VERSION
CF309821.1 GI:33681582
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--04-C17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
18 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1597
CF311778/c
LOCUS
DEFINITION
ABF--07-D01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--07-D01, mRNA sequence.
ACCESSION
CF311778
VERSION
CF311778.1 GI:33683539
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

```

```

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="ABF--07-D01"
        /tissue_type="leaf"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH108"
        /clone_lib="ABF3-overexpressing transgenic rice plasmid
        cDNA library (ABF)"
        /notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
        for 2hrs. Oligo-capped mRNA was reverse transcribed and
        then used for PCR. mRNA was prepared from ABA-responsive
        element binding transcription factor 3 overexpression
        line."
      Query Match
      Best Local Similarity 0.7%; Score 18; DB 1; Length 19;
      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
      Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1598
CF331361/c
LOCUS
DEFINITION
  NACL--07-H08.b1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa (japonica cultivar-group) cDNA clone NACL--07-H08, mRNA
  sequence.
ACCESSION
  CF331361
VERSION
  CF331361.1 GI:33810941
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Gyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..19
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="NACL--07-H08"
      /tissue_type="callus"
      /dev_stage="proliferated callus on 2N6 media for 30 days"
      /lab_host="E.coli DH108"
      /clone_lib="Rice callus plasmid cDNA library (NACL)"
      /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."
    Query Match
    Best Local Similarity 0.0%; Score 18; DB 1; Length 19;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726

```

```

      Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1599
CF335293/c
LOCUS
DEFINITION
  JMT--04-O17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
  library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
  JMT--04-O17, mRNA sequence.
ACCESSION
  CF335293
VERSION
  CF335293.1 GI:33818938
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Gyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
  Location/Qualifiers
    1..19
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:39947"
      /clone="JMT--04-O17"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH108"
      /clone_lib="AtJMT-overexpressing transgenic rice plasmid
      cDNA library (JMT)"
      /notes="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
      was reverse transcribed and then used for PCR. mRNA was
      prepared from Arabidopsis Jasmonate Carboxyl
      methyltransferase overexpression line."
    Query Match
    Best Local Similarity 0.7%; Score 18; DB 1; Length 19;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
      Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1600
CN545923/c
LOCUS
DEFINITION
  CN545923
  EST 17867 Ripe Grape Skin Triplex2 Library Vitis vinifera cDNA
  clone B3CS00RL006D08 3', mRNA sequence.
ACCESSION
  CN545923
VERSION
  CN545923.1 GI:46910548
KEYWORDS
  EST.
SOURCE
  Vitis vinifera
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  rosids; Vitaceae; Vitis.
  1 (bases 1 to 19)
  Abbal,P., Agasse,A., Ageorges,A., Atanaseova,R., Barrieu,F.,
  Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimpet,J.,
  Hamdi,S., Romieu,C. and Terrier,N.

```

TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages
JOURNAL Unpublished (2002)
COMMENT Contact: Hamdi S.
UMR 619 - Equipe Biologie de la Vigne
Universite de Bordeaux I, Institut National de la Recherche Agronomique
71, Avenue Edouard Bourleaux, BP 81, 33883 Villenave D'Ornon Cedex, France
Tel: 00-33-(0)5-57-12-25-50
Fax: 00-33-(0)5-57-12-25-48
Email: s.hamdi@bordeaux.inra.fr
Seq primer: T7

FEATURES source
1..19
/organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="B3CS00RL006D08"
/dev_stage="ripening stage"
/clone_lib="Ripe Grape Skin Triplex2 Library"
/note="Organ: Fruit skin; Vector: Lambda Triplex2; Site_1: SfiIA; Site_2: SfiIB; Oriented library"

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
|||||

Db 19 AAAAAAAAAAAAAAAAAA 2

RESULT 1601
CX002732/c
LOCUS
DEFINITION 19 bp mRNA linear EST 03-DEC-2004
iv33e03.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA, mRNA sequence.

ACCESSION CX002732
VERSION CX002732.1 GI:56274148
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 19)
AUTHORS Baliya,V.S., Nascimento,L.U. and McCombie,W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Cold Spring Harbor Laboratory
Columbia University
PO Box 100 Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org.

FEATURES source
1..19
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site_1: EcoRI; Site_2: XhoI; Library constructed using pBluescript XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary

Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2726
|||||

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1602

LOCUS
DEFINITION 19 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0080H09 R, genomic survey sequence.

ACCESSION AZ345795

VERSION AZ345795.1 GI:10425032

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: H column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0080H09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725
|||||
Db 2 TAAAAAAAAAAAAAAAAA 19

RESULT 1603

LOCUS AJ650575 19 bp DNA linear GSS 14-DEC-2000
DEFINITION M0520P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0520P13 R, genomic survey sequence.

ACCESSION AJ650575
VERSION AJ650575.1 GI:11785200

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

Mus whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: P column: 13

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0520P13"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.7%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725
|||||
Db 2 TAAAAAAAAAAAAAAAAA 19

RESULT 1604

LOCUS AJ666275/c 20 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ666275 CSEQRAN09 Sus scrofa cDNA clone C0000033_B07, mRNA sequence.

ACCESSION AJ666275
VERSION AJ666275.1 GI:49350726

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

1 (bases 1 to 20)

Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by crossmatch with the -minscore 20
and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:

ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK

Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

Location/Qualifiers

1..20

FEATURES

source

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_B07"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site 1: EcorI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

Query Match 0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
|||||
Db 20 AAAAAAAAAAAAAAAAAA 3

RESULT 1605

LOCUS AL587727/c 20 bp mRNA linear EST 02-MAR-2001
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ROS061D01, mRNA sequence.

ACCESSION AL587727

VERSION AL587727.1 GI:13192761

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 20)

REFERENCE

AUTHORS

TITLE BP Chicken Brain Library

JOURNAL Unpublished (2001)

COMMENT

Contact: Frazer Murray

Dept Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk

CGCGCCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech

(*6854-

Seq primer: M13F.

Location/Qualifiers

1. .20

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="ROS061D01"

/tissue_type="Brain"

/dev_stage="Unknown"

/lab_host="DH10B"

/clone_lib="BP Chicken Brain Library"

/note="Vector: pSPOT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGCGCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"

Query Match

Best Local Similarity 0.7%; Score 18; DB 1; Length 20;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2709 AAAAAAAAAAAAAAAAAA 2726

Db

19 AAAAAAAAAAAAAAAAAA 2

RESULT 1606

CA853586/c

LOCUS

DEFINITION B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone

B09H12 5', mRNA sequence.

CA853586

CA853586.1 GI:33390391

EST.

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 20)

/organism="Glycine max"

/mol_type="mRNA"

/db_xref="taxon:5082"

/clone="B09H12"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

RT-PCR."

/cultivar="Peking"

/db_xref="taxon:3847"

/clone="B09H12"

/tissue_type="Roots"

/dev_stage="Seedlings"

/clone_lib="cDNA Peking library 12hr SCN3"

/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."

SK- phagemid."


```

LOCUS       CF320843                20 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  HD-11-001.gi OsHDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD-11-001, mRNA sequence.
ACCESSION   CF320843
VERSION     CF320843.1    GI:33692604
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 20)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD-11-001"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDACL1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
Query Match      0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2726
      |||||
Db   19 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1609
AZ345856/c
LOCUS       AZ345856                20 bp    DNA    linear    GSS 29-SEP-2000
DEFINITION  1M0080G17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080G17 R, genomic survey sequence.
ACCESSION   AZ345856
VERSION     AZ345856.1    GI:10425093
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss

LOCUS       CF320843                20 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION  HD-11-001.gi OsHDACL1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD-11-001, mRNA sequence.
ACCESSION   CF320843
VERSION     CF320843.1    GI:33692604
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 20)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD-11-001"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDACL1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /notes="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
Query Match      0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2726
      |||||
Db   19 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1609
AZ345856/c
LOCUS       AZ345856                20 bp    DNA    linear    GSS 29-SEP-2000
DEFINITION  1M0080G17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080G17 R, genomic survey sequence.
ACCESSION   AZ345856
VERSION     AZ345856.1    GI:10425093
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss

```

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1..20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080G17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptor DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptor mouse DNA was annealed to
                     adaptor vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
Query Match      0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2709 AAAAAAAAAAAAAAAAAAAAAA 2726
      |||||
Db   20 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1610
AZ370699/c
LOCUS       AZ370699                20 bp    DNA    linear    GSS 02-OCT-2000
DEFINITION  1M0121N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0121N17 R, genomic survey sequence.
ACCESSION   AZ370699
VERSION     AZ370699.1    GI:10484399
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss

```

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 row: N column: 17
Seq primer: CACACAGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.
2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.	2. Scalability: The model is designed to handle large-scale data and complex tasks, making it suitable for enterprise-level applications.
3. Interpretability: The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.	3. Interpretability: The model provides clear and understandable explanations for its predictions, enhancing transparency and trust.
4. Robustness: The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.	4. Robustness: The model is highly robust to noise and outliers, ensuring reliable performance in real-world scenarios.
5. Efficiency: The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.	5. Efficiency: The model is optimized for fast processing and low resource consumption, making it ideal for resource-constrained environments.

```

1. .20
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0121N17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of Plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```
Query Match      0.7%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT	1611
AL048772	
LOCUS	21 bp mRNA linear EST 04-SEP-2003
DEFINITION	DKFZ566N143_r1_566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION	DKFZ566N143_mRNA sequence.
VERSION	AL048772
KEYWORDS	AL048772.1 GI:4727843
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 21)
AUTHORS	Koehler K., Beyer A., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE	EST (Koehler, et al.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS MIPS
FEATURES	IngoIsstaedter Landstr.1, D-85764 Neuherberg, Germany.
	Location/Qualifiers
	1..21

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N143"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match          0.7%  Score 18;  DB 1;  Length 21;
Best Local Similarity 100.0%;  Pred No. 1.4e+03;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAA 2725
      |||||
Db 4 TAAAAAAAAAAAAAAAAA 21

```

```

Query Match      0.7%;      Score 18;  DB 1;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 1.4e-03;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      2709  AAAAAAAAAAAAAAAAAAAAAA 2725
Db      21    AAAAAAAAAAAAAAAAAAAAAA 4

```

RESULT	1613			
AZ610868/c				
LOCUS	AZ610868	21 bp	DNA	linear
DEFINITION	1M0436G12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0436G12 F, genomic survey sequence.			GSS 13-DEC-2000

```

ACCESSION      AZ610868
VERSION        AZ610868.1  GI:11733058
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0436 row: G column: 12
               Seq primer: CGTTGTAACACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 21.
               Location/Qualifiers
               1..21
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0436G12"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

Query Match      0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 18 TAAAAA

RESULT 1614
AZ6764492
LOCUS          21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION    IM0560D04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC1M0560D04 R, genomic survey sequence.

```

```

ACCESSION      AZ764492
VERSION        AZ764492.1  GI:12879511
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0560 row: D column: 04
               Seq primer: CACACAGGAACAGCTATGACC
               Class: plasmid ends
               High quality sequence stop: 21.
               Location/Qualifiers
               1..21
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC1M0560D04"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /notes="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

Query Match      0.7%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAA
Db 4 TAAAAA

RESULT 1615
CF328832/c
LOCUS          22 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION    NACL--03-020.b1 Rice callus plasmid cDNA library (NACL) Oryza
               sativa (japonica cultivar-group) cDNA clone NACL--03-020, mRNA

```

```

sequence.
ACCESSION CF328832
VERSION CF328832.1 GI:33805905
KEYWORDS EST.
SOURCE Oriza sativa (japonica cultivar-group)
ORGANISM Oriza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          Clade; Ehrhartoideae; Oryzeae; Oriza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongui University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     1..22
     /organism="Oriza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultiVar="Nackdong"
     /db_xref="taxon:39947"
     /clone="NACL--03-020"
     /tissue type="callus"
     /dev stages="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."
Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1616
AZ843648
LOCUS 2M0142807R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0142807 R, genomic survey sequence.
ACCESSION AZ843648
VERSION AZ843648.1 GI:13013556
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177

sequence.
ACCESSION CF328832
VERSION CF328832.1 GI:33805905
KEYWORDS EST.
SOURCE Oriza sativa (japonica cultivar-group)
ORGANISM Oriza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
          Clade; Ehrhartoideae; Oryzeae; Oriza.
REFERENCE 1 (bases 1 to 22)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongui University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     1..22
     /organism="Oriza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultiVar="Nackdong"
     /db_xref="taxon:39947"
     /clone="NACL--03-020"
     /tissue type="callus"
     /dev stages="proliferated callus on 2N6 media for 30 days"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice callus plasmid cDNA library (NACL)"
     /note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
           with oligoribonucleotides and then used as templates for
           RT-PCR."
Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 18 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1616
AZ843648
LOCUS 2M0142807R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0142807 R, genomic survey sequence.
ACCESSION AZ843648
VERSION AZ843648.1 GI:13013556
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
          Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
          University of Utah Genome Center
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0142 row: B column: 07
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
     1..22
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC2M0142B07"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (male) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adapted DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adapted mouse DNA was annealed to
           adapted vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
Query Match      0.7%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
Db 1 AAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1617
TA231E08Q
LOCUS T. brucei sheared genomic DNA clone 231e08, reverse sequence,
DEFINITION genomic survey sequence.
ACCESSION AL480935
VERSION AL480935.1 GI:11846704
KEYWORDS GSS.
SOURCE Trypanosoma brucei
          Trypanosoma brucei
          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
          Trypanosoma
          1 (bases 1 to 22)
REFERENCE Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
          Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
          Melville,S.E., Rajandream,M.A. and Barrell,B.G.
          Direct Submission
          Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
          project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
          Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
          nh@sanger.ac.uk
          Constructed at the Institute for Genomic Research (TIGR),
          Rockville, MD. Genomic DNA isolated from a cloned population of
          Trypanosoma brucei (TSEU927/4 GUTat 10.1) was mechanically sheared
          to give a tight size distribution (
          4 kb). The v + i method used for the library construction is
          described in detail in Smith, H. and Venter, J.C. (Making small
          insert libraries for whole genome shotgun sequencing projects. In

```

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="231e08"

Query Match 0.7%; Score 18; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1618

TA386H07Q/c

LOCUS 22 bp DNA linear GSS 13-DEC-2000

DEFINITION T. brucei sheared genomic DNA clone 386h07, reverse sequence,

Genomic survey sequence.

ACCESSION AL498291

VERSION AL498291.1 GI:11874013

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

REFERENCE 1 (bases 1 to 22)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nhl@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared

to give a tight size distribution (

4 kb). The v + i method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

1..22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="386h07"

Query Match 0.7%; Score 18; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1619

BX564412/c

LOCUS

DEFINITION

21 bp mRNA linear EST 10-OCT-2003

morsitans morsitans adult infected gut Glossina

BX564412

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all pic reads are from

the 3' end.

FEATURES

source

1..21

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse71e10_pic"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match 0.6%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAA 2726

Db 21 ATTCAAAAAAAAAAAAAAAAAA 1

RESULT 1620

CF330439/c

LOCUS

DEFINITION

21 bp mRNA linear EST 18-AUG-2003

NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa (japonica cultivar-group) cDNA clone NACL--06-C12, mRNA

sequence.

ACCESSION CF330439

VERSION CF330439.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Unpublished (2003)

1 (bases 1 to 21)
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes
 Genome Biol. 4 (10), R63 (2003)
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J.Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all pic reads are from
 the 3' end.
 Location/Qualifiers
 1..21
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse71e10_pic"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"
 Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2706 ACTAAAAAAAAAAAAAAAAA 2726
 Db 21 ATTCAAAAAAAAAAAAAAAAAA 1
 RESULT 1620
 CF330439/c
 LOCUS
 DEFINITION
 21 bp mRNA linear EST 18-AUG-2003
 NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--06-C12, mRNA
 sequence.
 ACCESSION CF330439
 VERSION CF330439.1
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Unpublished (2003)

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1. .21
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL-06-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2703 TGTACTAAAAAAAAAAAAA 2723

Db 21 TGTATTAAAAAAAAAAAAA 1
|||||

RESULT 1621

AW248782/c

LOCUS

DEFINITION AW248782 21 bp mRNA linear EST 07-JAN-2000
mRNA sequence.

ACCESSION AW248782

VERSION AW248782.1 GI:6591775

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

1 (bases 1 to 21)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2821017.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF DNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.

Plate: LLCM5 row: L column: 10

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821017"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 7"
/note="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
Query Match 0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2729
|||||

Db 21 AAAAAAAAAATTAAAAAAAAA 1
|||||

RESULT 1622

DV751812 21 bp mRNA linear EST 21-NOV-2005
LOCUS ID0AAH9BD052M1 ID0AAH Acyrthosiphon pisum cDNA clone ID0AAH9BD05
DEFINITION 5', mRNA sequence.
ACCESSION DV751812 GI:82580156
VERSION DV751812.1
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE 1 (bases 1 to 21)
AUTHORS Stern,D.L., Wincker,P. and Tagu,D.
TITLE Large-scale gene discovery in the pea aphid Acyrthosiphon pisum
(Hemiptera)
JOURNAL Unpublished (2005)
COMMENT Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: TCCGAGATCTGGACGAC
Plate: 9B row: D column: 5.
Location/Qualifiers
1. .21
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/db_xref="taxon:7029"
/clone="ID0AAH9BD05"
/tissue_type="salivary gland"
/dev_stage="adult parthenogenetic females"
/lab_host="E. coli BM25.8"
/clone_lib="ID0AAH"
/note="Vector: pTriplex2; Site.1: SfiIA; Site.2: SfiIB;
Sample name: ID0AAH Plant growth place: 9 Gerad REECK
Soil conditions: none Sowing date: 01/07/2004 Harvesting
date: 01/08/2004 Description: Small description of
dissection protocole and RNA extraction: Aphid heads were
obtained by a cut between head and thorax. A second cut
was made along the top of the heads. Brain and salivary
glands were gently pushed out of the heads and salivary
principal gland and, usually, an accompanying accessory
gland). Total RNA was isolated using the Micro RNA
isolation kit from Stratagene (La Jolla, CA). experimental
condition: see description"

```

Query Match      0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2700 GTTTGTACTAAAAA 2720
Db 1 GTTTGTCTAAAAA 21

RESULT 1623
AZ597932/c
LOCUS
DEFINITION
  IM0412D33F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0412D23 F, genomic survey sequence.
ACCESSION
  AZ597932
VERSION
  AZ597932.1 GI:11720122
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 21)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D..Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0412 row: D column: 23
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 21.
FEATURES
  Location/Qualifiers
    1..21
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0412D23"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male); was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptedore DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptedore mouse DNA was annealed to
      adaptedore vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

```

```

Query Match      0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2729
Db 21 AAAAAAAAAAGAAAAA 1

RESULT 1624
AZ627840/c
LOCUS
DEFINITION
  1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0474B05 F, genomic survey sequence.
ACCESSION
  AZ627840
VERSION
  AZ627840.1 GI:11750126
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 21)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D..Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0474 row: B column: 05
  Seq primer: CGTTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 21.
FEATURES
  Location/Qualifiers
    1..21
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0474B05"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male); was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptedore DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptedore mouse DNA was annealed to
      adaptedore vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

```

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1625

A2647578/c

LOCUS

DEFINITION A2647578 21 bp DNA linear GSS 14-DEC-2000
 1M0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0514117 F, genomic survey sequence.

ACCESSION

A2647578

VERSION

A2647578.1

KEYWORDS

GSS.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0514 row: I column: 17

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0514117"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1626

CL693188

LOCUS

DEFINITION CL693188 21 bp DNA linear GSS 10-JUL-2004
 PR10160c.F06.2 - PR10160c.BR (21) Note: Recurring String Mixed
 stage fosmid library of P. pacificus var. California Pristionchus
 pacificus genomic, genomic survey sequence.

ACCESSION

CL693188

VERSION

CL693188.1

KEYWORDS

GSS.

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

JOURNAL

Nucleic Acids Res. 32 (1), D421-D422 (2004)

PUBMED

14681447

COMMENT

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..21

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.6%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

||||| ||||| ||||| ||||| |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1627

DUB834197

LOCUS

DEFINITION

DUB834197 21 bp DNA linear GSS 22-DEC-2005

KB-S013K03F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa

subsp. pekinensis genomic clone KBRs013K03, genomic survey

sequence.

ACCESSION

DUB834197

VERSION

DUB834197.1

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1625

A2647578/c

LOCUS

DEFINITION A2647578 21 bp DNA linear GSS 14-DEC-2000
 1M0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0514117 F, genomic survey sequence.

ACCESSION

A2647578

VERSION

A2647578.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0514 row: I column: 17

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1..21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0514117"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1626

CL693188

LOCUS

DEFINITION CL693188 21 bp DNA linear GSS 10-JUL-2004
 PR10160c.F06.2 - PR10160c.BR (21) Note: Recurring String Mixed
 stage fosmid library of P. pacificus var. California Pristionchus
 pacificus genomic, genomic survey sequence.

ACCESSION

CL693188

VERSION

CL693188.1

KEYWORDS

GSS.

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

REFERENCE

1 (bases 1 to 21)

AUTHORS

Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.

AppADB: an AcedB database for the nematode satellite organism

Pristionchus pacificus

JOURNAL

Nucleic Acids Res. 32 (1), D421-D422 (2004)

PUBMED

14681447

COMMENT

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end

sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

Location/Qualifiers

1..21

/organism="Pristionchus pacificus"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Mixed stage fosmid library of P. pacificus

var. California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.6%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729

||||| ||||| ||||| ||||| |||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1627

DUB834197

LOCUS

DEFINITION

DUB834197 21 bp DNA linear GSS 22-DEC-2005

KB-S013K03F KBRs, Brassica rapa Sau3AI BAC library Brassica rapa

subsp. pekinensis genomic clone KBRs013K03, genomic survey

sequence.

ACCESSION

DUB834197

VERSION

DUB834197.1

Query Match 0.6%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAAAAAA 2729
 ||||| ||||| ||||| ||||| |||||
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1625

A2647578/c

LOCUS

DEFINITION A2647578 21 bp DNA linear GSS 14-DEC-2000
 1M0514117F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0514117 F, genomic survey sequence.

ACCESSION

A2647578

VERSION

A2647578.1

KEYWORDS

GSS.

SOURCE


```

REFERENCE
AUTHORS      1 (bases 1 to 21)
Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
TITLE
JOURNAL      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
COMMENT      Unpublished (2005)
Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS013K03
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..21
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013K03"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is
available at NIAB."
Query Match      0.6%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      ||||| ||||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAAAAA 21

RESULT 1628
DU831616/c      22 bp DNA linear GSS 22-DEC-2005
LOCUS      KBrS008L22F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS008L22, genomic survey
sequence.
ACCESSION      DU831616
VERSION      DU831616.1 GI:83868212
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS013D12
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013D12"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is
available at NIAB."
Query Match      0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      ||||| ||||| ||||| ||||| |||||
1 AAAAAAAAAAAAAAAAAAAAAA 22

```

```

/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS008L22"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is
available at NIAB."
Query Match      0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2706 ACTAAAAAAAAAAAAAAAAAAAAA 2726
Db      ||||| ||||| ||||| ||||| |||||
21 ACACAAAAAAAAAAAAAAAAAAAA 1

RESULT 1629
DU833993/c      22 bp DNA linear GSS 22-DEC-2005
LOCUS      KBrS013D12F KBrS, Brassica rapa Sau3AI BAC library Brassica rapa
DEFINITION      subsp. pekinensis genomic clone KBrS013D12, genomic survey
sequence.
ACCESSION      DU833993
VERSION      DU833993.1 GI:83870589
KEYWORDS      GSS.
SOURCE      Brassica rapa subsp. pekinensis
ORGANISM      Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE      1 (bases 1 to 22)
AUTHORS      Yang,T.J., Kwon,S.J., Kim,J.A., Kim,J.S., Lim,K.B., Jin,M.,
Park,J.Y., Lim,M.H., Kim,H.I., Choi,B.S., Seol,Y.J., Park,D.S.,
Hahn,J. H. and Park,B.S.
TITLE      End sequence of Brassica rapa Sau3AI (KBrS) BAC clone
JOURNAL      Unpublished (2005)
COMMENT      Contact: Beom-Seok Park
Brassica Genomics Team
National Institute of Agricultural Biotechnology
225 Seodun-Dong, Suwon, 441-707, Korea
Tel: +82-31-299-1670
Fax: +82-31-299-1672
Email: pbeom@da.go.kr
BAC end sequence of Brassica rapa ssp. pekinensis Sau3AI BAC clone
KBrS013D12
Seq primer: T7
Class: BAC ends.
FEATURES
source
1..22
/organism="Brassica rapa subsp. pekinensis"
/mol_type="genomic DNA"
/cultivar="Chiifu"
/sub_species="pekinensis"
/db_xref="taxon:51351"
/clone="KBrS013D12"
/lab_host="E. coli DH10B"
/clone_lib="KBrS, Brassica rapa Sau3AI BAC library"
/notes="Vector: pCUGIBAC1; Site 1: Sau3AI; Brassica rapa
ssp pekinensis var. Chiifu BAC_library (KBrS BAC) is
available at NIAB."
Query Match      0.6%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAAAAAA 2729
Db      ||||| ||||| ||||| ||||| |||||
22 AAAAAAAAAAAAAAAAAAAAAA 22

```

RESULT 1630
CF291665/c

LOCUS CF291665 19 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665.1 GI:33660698
VERSION EST.

KEYWORDS

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-D01"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAA 2726

|||||

19 TCAAAAAAAAAA 1

Db

RESULT 1631

CF291899/c

LOCUS CF291899 19 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-I08, mRNA sequence.

ACCESSION CF291899.1 GI:33660932

VERSION

EST.

KEYWORDS

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-I08"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;

Best Local Similarity 94.7%; Pred. No. 1.4e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAA 2727

|||||

19 AAAAAAAAAA 1

Db

RESULT 1632

CF292072/c

LOCUS CF292072 19 bp mRNA linear EST 14-AUG-2003
DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-M03, mRNA sequence.

ACCESSION CF292072.1 GI:33661105

VERSION

EST.

KEYWORDS

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 320 6193

Fax: 82 31 321 6355

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ROOT--02-M03"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1633

CF292144/c

LOCUS 14ROOT--02-N17.b1 19 bp mRNA linear EST 14-AUG-2003
 DEFINITION sativa (japonica cultivar-group) cDNA clone 14ROOT--02-N17, mRNA sequence.

ACCESSION CF292144
 VERSION CF292144.1 GI:33661177
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19 Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="14ROOT--02-N17"

/tissue_type="root"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1634

CF310688

LOCUS

DEFINITION ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

ABF--05-H18, mRNA sequence.

ACCESSION CF310688

VERSION CF310688.1 GI:33682449

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="ABF--05-H18"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match

Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727

Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1635

CF329136/c

LOCUS

DEFINITION

CF329136 19 bp mRNA linear EST 18-AUG-2003
 NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-F15, mRNA sequence.

ACCESSION CF329136

VERSION CF329136.1 GI:33806509

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="NACL--04-F15"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site.1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAGAAAAAAAAAAAAAAAAAAAA 1

RESULT 1636
CF334610/c
LOCUS
DEFINITION
JMT--03-P13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT--03-P13, mRNA sequence.
CF334610
CF334610.1 GI:33817556
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ekhartolidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ekhartolidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1..19
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="JMT--03-P13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site.1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAA 2723
|||||
Db 19 TAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1637
AW248747/c
LOCUS
DEFINITION
AW248747
2821119.3prime NTH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ekhartolidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821119.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 7 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 19 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LiCM5 row: P column: 16
High quality sequence stop: 7.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821119"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
|||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1638
AZ363907/c
LOCUS
DEFINITION
AZ363907
1M0109113R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0109113 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Query Match 0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2705 TACTAAAAAAAAAAAAAAAAAAAA 2723
|||||
Db 19 TAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 1637
AW248747/c
LOCUS
DEFINITION
AW248747
2821119.3prime NTH_MGC_7 Homo sapiens cDNA clone IMAGE:2821119 3', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ekhartolidae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: I column: 13
 Seq primer: CACACAGCAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0109113"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1639
 AZ513919/c
 LOCUS
 DEFINITION
 1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0360E13 F, genomic survey sequence.
 ACCESSION
 AZ513919
 VERSION
 AZ513919.1 GI:10695235
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: E column: 13
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0360E13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

FEATURES
 source

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1640
 AZ645841/c
 LOCUS
 DEFINITION
 1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0511G04 R, genomic survey sequence.
 ACCESSION
 AZ645841
 VERSION
 AZ645841.1 GI:11775726
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0511 row: G column: 04
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0511G04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1641

AZ650252
 LOCUS AZ650252 19 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0520N17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0520N17 F, genomic survey sequence.
 ACCESSION AZ650252
 VERSION AZ650252.1 GI:11784550
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 AUTHORS

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0520 row: N column: 17
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0520N17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAGAAAAAAAAA 19

RESULT 1642

AZ654747/c
 LOCUS AZ654747 19 bp DNA linear GSS 14-DEC-2000
 DEFINITION IM0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0529F08 F, genomic survey sequence.
 ACCESSION AZ654747
 VERSION AZ654747.1 GI:11791893
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0529 row: F column: 08
 Seq primer: CGTTGTAACACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source
 1. .19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0529F08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 1643

CL693177 19 bp DNA linear GSS 10-JUL-2004
 PRI0160b.G03.2 - PRI0160b.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL693177.1 GI:50215085
 VERSION GSS.
 KEYWORDS

SOURCE
 ORGANISM
 Pristionchus pacificus
 Pristionchus pacificus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

REFERENCE
 1 (bases 1 to 19)
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.

TITLE

AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)
 14681447
 Contact: Sommer RJ
 Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 00497071601371
 Fax: 00497071601498
 Email: ralf.sommer@tuebingen.mpg.de
 This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
 Seq primer: T7
 Class: fosmid ends.

FEATURES

source
 1. .19
 Location/Qualifiers
 /organism="Pristionchus pacificus"
 /mol_type="genomic DNA"
 /strain="California"
 /db_xref="taxon:54126"
 /clone_lib="Mixed stage fosmid library of P. pacificus var. California"
 /note="Vector: pEpifos-5 Fosmid vector"

Query Match 0.6%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 1644

CF319428/c 20 bp mRNA linear EST 15-AUG-2003
 LOCUS
 DEFINITION
 HD--09-020.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--09-020, mRNA sequence.

ACCESSION CF319428
 VERSION CF319428.1 GI:33691189
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 (bases 1 to 20)

AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

CONTACT: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .20
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="HD--09-020"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0012 row: H column: 15

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES

source

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0012H15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 19 row: E column: 19

Seq primer: T7; GTAATACGACTACTATAGGC.

Location/Qualifiers

1. .17

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:189986"

/db_xref="taxon:161934"

/clone="024-019-E19"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MPIZ-ADIS-024-storage root"

/notes="Vector: pCMVSPORT6; Site1: Sali; Site 2: NotI; DNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:"

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

RESULT 1649

BQ590687

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Query Match 0.6%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2727

|||||

Db 21 AAAAAAAAAACAAAAA 3

RESULT 1648

BQ590128/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

BQ590128 17 bp mRNA linear EST 06-DEC-2002

E012843-024-019-E19-T7 MPIZ-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-E19 3-PRIME, mRNA sequence.

BQ590128

BQ590128.1 GI:26119711

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 17)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

/db_xref="GABI:189432"
 /db_xref="taxon:161934"
 /clone="024-018-B24"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-storage root"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1650

BQ591177/c

LOCUS

DEFINITION BQ591177 17 bp mRNA linear EST 06-DEC-2002
 cDNA clone 024-017-B22-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ591177

VERSION BQ591177.1

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

PUBMED

COMMENT

Contact: Weisshaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 17 Std Error: 0.00
 Plate: 17 row: B column: 22
 Seq primer: T7; GTAATACGACTCTACTATAGGCG.

FEATURES

source

1. .17
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:188948"
 /db_xref="taxon:161934"
 /clone="024-017-B22"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeener Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:

SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1651

CF290854/c

LOCUS

DEFINITION CF290854 17 bp mRNA linear EST 14-AUG-2003
 14ROOT--01-A21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa (japonica cultivar-group) cDNA clone 14ROOT--01-A21, mRNA
 sequence.

ACCESSION CF290854

VERSION CF290854.1

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 320 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .17
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="14ROOT--01-A21"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1652

CF294668/c

LOCUS

DEFINITION CF294668 17 bp mRNA linear EST 14-AUG-2003
 30DGS--04-El7.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 sativa (japonica cultivar-group) cDNA clone 30DGS--04-El7, mRNA
 sequence.

ACCESSION CF294668

VERSION CF294668.1

GI:33663701

```

KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--04-E17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1653
CF295988/c
LOCUS 30DGS--06-C17.b1 17 bp mRNA linear EST 14-AUG-2003
DEFINITION sative (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1653
CF295988/c
LOCUS 30DGS--06-C17.b1 17 bp mRNA linear EST 14-AUG-2003
DEFINITION sative (japonica cultivar-group) cDNA clone 30DGS--06-C17, mRNA
sequence.
ACCESSION CF295988
VERSION CF295988.1 GI:33665021
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"

```

```

/db_xref="taxon:39947"
/clone="30DGS--06-C17"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAATAAAAAAAAAA 2724
Db 17 TAAAAAATAAAAAAAAAA 1

RESULT 1654
CF298589/c
LOCUS 7LEAF--02-A18.b1 17 bp mRNA linear EST 15-AUG-2003
DEFINITION sative (japonica cultivar-group) cDNA clone 7LEAF--02-A18, mRNA
sequence.
ACCESSION CF298589
VERSION CF298589.1 GI:33670350
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1. .17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A18"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAATAAAAAAAAAA 2725
Db 17 AAAAAAATAAAAAAAAAA 1

RESULT 1655
CF310219/c
LOCUS ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION ABF--04-M02.g1 17 bp mRNA linear EST 15-AUG-2003

```

library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
 ABF--04-M02, mRNA sequence.
 CF310219 GI:33681980
 EST.
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 17)
 REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
 1..17
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="ABF--04-M02"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."
 Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1656
 CF334566/c
 LOCUS
 DEFINITION
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--03-O13, mRNA sequence.
 CF334566
 CF334566.1 GI:33817460
 EST.
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 17)
 REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193

FEATURES

source
 1..17
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--03-O13"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."
 Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 1657
 CF336950/c
 LOCUS
 DEFINITION
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone
 JMT--07-D04, mRNA sequence.
 CF336950
 CF336950.1 GI:33822280
 EST.
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 17)
 REFERENCE
 AUTHORS
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 TITLE
 JOURNAL
 COMMENT
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source
 1..17
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="JMT--07-D04"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."
 Query Match 0.6%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;

```

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAAAAAA 2724
Db 17 TAAAAAAAAAAAAAAAAA 1

RESULT 1658
CX309551/c
LOCUS
DEFINITION
  17 bp mRNA linear EST 03-JAN-2005
  Drosophila melanogaster Embryo Larva Pupa Adult
  Drosophila melanogaster cDNA clone AM02384 3, mRNA sequence.
ACCESSION
CX309551
VERSION
CX309551.1 GI:57011768
KEYWORDS
SOURCE
  Drosophila melanogaster (fruit fly)
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 17)
  Yandell,M., Bailey,A.M., Misra,S., Shu,S., Wiel,C., Evans-Holm,M.,
  Celnikier,S.E. and Rubin,G.M.
  A computational and experimental approach to validating annotations
  and gene predictions in the Drosophila melanogaster genome
  Proc. Natl. Acad. Sci. U.S.A. 102 (5), 1566-1571 (2005)
JOURNAL
PUBMED
15668397
COMMENT
  Other ESTs: AM02384.5prime
  Contact: Stapleton, M.
  BDGP,
  Lawrence Berkeley National Lab
  One Cyclotron Rd, Berkeley, CA 94720, USA
  Fax: 510 486 6798
  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
  Plate: AM-23 row: G column: 12
  High quality sequence stop: 17.

FEATURES
  source
    1..17
      Location/Qualifiers
        /organism="Drosophila melanogaster"
        /mol_type="mRNA"
        /db_xref="taxon:7227"
        /clone="AM02384"
        /sex="male and female"
        /dev_stage="0 to 24 hours mixed stage embryonic, late
        third instar larvae, mixed stage pupae, mixed age adults"
        /clone_lib="AM Drosophila melanogaster Embryo Larva Pupa
        Adult"
        /note="RT-PCR products were amplified with pairs of
        gene-specific primers from template RNA representing
        pooled Drosophila stages. Products were directly
        sequenced from both ends with the same oligos used to
        prime PCR."

Query Match 0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2725
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1659
CF301057/c
LOCUS
DEFINITION
  18 bp mRNA linear EST 15-AUG-2003
  7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M05, mRNA
  sequence.
ACCESSION
CF301057
VERSION
CF301057.1 GI:33672818
KEYWORDS
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
  source
    1..18
      Location/Qualifiers
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="7LEAF--05-M05"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2725
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 1660
CF320046/c
LOCUS
DEFINITION
  18 bp mRNA linear EST 15-AUG-2003
  HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
  HD--10-M11, mRNA sequence.
ACCESSION
CF320046
VERSION
CF320046.1 GI:33691807
KEYWORDS
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
  source
    1..18
      Location/Qualifiers
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="HD--10-M11"
        /tissue_type="callus"

```

/dev stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.6%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAATAAAAAAAAAAAAAA 2724

|||||
 Db 17 TAAATAAAAAAAAAAAAAA 1

RESULT 1661

CF320418/c

LOCUS

DEFINITION HD-11-E22.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD-11-E22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1..18

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="HD-11-E22"

/tissue_type="callus"

/dev stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli DH10B"

/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725

|||||

Db 18 AAAAAAAAAAAAAAAAAA 2

RESULT 1662

AZ853220

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0156

row: J

column: 15

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0156J15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [G14732114]gb[AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725

|||||

Db 3 AAAAAAAAAAAAAAAAAA 19

RESULT 1663

AZ853220

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

University of Utah

Rm. 308, Biomedical

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000

Std Error: 0.00

Plate: 0156

row: J

column: 15

Seq primer: CGTTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0156J15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 [G14732114]gb[AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725

|||||

Db 3 AAAAAAAAAAAAAAAAAA 19

RESULT 1663

```

CF298207      20 bp  mRNA  linear  EST 15-AUG-2003
LOCUS         7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
sequence.
ACCESSION     CF298207.1 GI:33669968
VERSION       CF298207
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     1 (bases 1 to 20)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
FEATURES             source
    1..20
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="7LEAF--01-H23"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."
    Query Match      0.6%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
        |||||
Db       1 AAAAAAAAAAAAAAAAAA 17

RESULT 1664
AZ818055
LOCUS         2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    clone UUGC2M0087B23 R, genomic survey sequence.
ACCESSION     AZ818055
VERSION       AZ818055.1 GI:12987963
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center

CF298207      20 bp  mRNA  linear  EST 15-AUG-2003
LOCUS         7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa (japonica cultivar-group) cDNA clone 7LEAF--01-H23, mRNA
sequence.
ACCESSION     CF298207.1 GI:33669968
VERSION       CF298207
KEYWORDS      EST.
SOURCE        Oryza sativa (japonica cultivar-group)
ORGANISM      Oryza sativa (japonica cultivar-group)
REFERENCE     1 (bases 1 to 20)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
FEATURES             source
    1..20
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:39947"
        /clone="7LEAF--01-H23"
        /tissue_type="leaf"
        /dev_stage="7 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."
    Query Match      0.6%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
        |||||
Db       1 AAAAAAAAAAAAAAAAAA 17

RESULT 1664
AZ818055
LOCUS         2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION    clone UUGC2M0087B23 R, genomic survey sequence.
ACCESSION     AZ818055
VERSION       AZ818055.1 GI:12987963
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 20)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center

```

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLÇ, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: B column: 23
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
FEATURES             source
    1..20
        /organism="Mus musculus"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0087B23"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."
    Query Match      0.6%; Score 17; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.5e+03;
    Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2725
        |||||
Db       4 AAAAAAAAAAAAAAAAAA 20

RESULT 1665
DR065210/c
LOCUS         ip91f09.g1 Ginkgo microsporophyll (NYBG) Ginkgo biloba cDNA 3',
DEFINITION    mRNA sequence.
ACCESSION     DR065210
VERSION       DR065210.1 GI:66988778
KEYWORDS      EST.
SOURCE        Ginkgo biloba (maidenhair tree)
ORGANISM      Ginkgo biloba
REFERENCE     1 (bases 1 to 21)
AUTHORS       Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
              O'Shaughnessy,A.L., Ballja,V., Martensen,R.A., McCombie,R.W.,
              Benfey,P., Coruzzi,G. and Stevenson,D.
TITLE         Expressed tag sequences from Ginkgo microsporophyll (NYBG)
JOURNAL       Unpublished (2005)
COMMENT       Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874

```

Email: mcmombie@cshl.org
 Seq primer: -21M3UnivRev.
 Location/Qualifiers
 1..21
 /organism="Ginkgo biloba"
 /mol_type="mRNA"
 /db_xref="taxon:3311"
 /sex="male"
 /clone_lib="Ginkgo microsporophyll (NYBG)"
 /note="Organ: microsporophyll; Vector: pBK-CMV; Site_1:
 XhoI; Site_2: Eco RI; Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts."

Query Match 0.6%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 1666
 AZ943299/c
 LOCUS AZ943299 21 bp DNA linear GSS 26-APR-2001
 DEFINITION 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K21 R, genomic survey sequence.

ACCESSION AZ943299
 VERSION AZ943299.1 GI:13807290

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Bescorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

INSERT LENGTH: 10000 Std Error: 0.00

PLATE: 0203 row: K column: 21

SEQ PRIMER: CACACAGGNAACAGCTATGACC

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 21.

Location/Qualifiers

source

1..21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0203K21"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: pW42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2725
 |||||
 Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 1667

CF298018/c

LOCUS CF298018 20 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CF298018

VERSION CF298018.1 GI:33669779

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

TEL: 82 31 330 6193

FAX: 82 31 321 6355

EMAIL: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

source

1..20
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--01-D19"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 1.6e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAAAAAAAAAAAA 2725

|||||

Db 20 AATCAAAAAAAAAAAAAAAAAA 1


```

RESULT 1668
CF300961/c
LOCUS
DEFINITION
  CF300961
  7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-K03, mRNA
  sequence.
ACCESSION
  CF300961
VERSION
  CF300961.1 GI:33672722
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1. (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
  source
  1. .20
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="7LEAF--05-K03"
    /tissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
    with oligoribonucleotides and then used as templates for
    RT-PCR."
  Query Match          0.6%; Score 16.8; DB 1; Length 20;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2728
  ||| ||||| ||||| ||||| |||||
  Db 20 AAGAGAAAAAAAAAAAAAAAAAAA 1

  RESULT 1670
  CF303777/c
  LOCUS
  DEFINITION
    S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
  ACCESSION
    CF303777
  VERSION
    CF303777.1 GI:6830134
  KEYWORDS
    EST.
  SOURCE
    Pneumocystis carinii
  ORGANISM
    Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
    Pneumocystidaceae; Pneumocystis.
  REFERENCE
    1. (bases 1 to 20)
    Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
    Edman,J.C., Kovacs,J. and Cushion,M.
    Expressed sequence tags from Pneumocystis carinii
    Unpublished (2000)
    Contact: Staben C
    School of Biological Sciences
    University of Kentucky
    101 Morgan Building, University of Kentucky, Lexington, KY
    40506-0225, USA
    Tel: 606 257 2161
    Fax: 606 257 1717
    Email: staben@pop.uky.edu.
  FEATURES
    source
    1. .20
      /organism="Pneumocystis carinii"
      /mol_type="mRNA"
      /db_xref="taxon:4754"
      /lab_host="E. coli"
      /clone_lib="AGS-1"
      /note="Vector: Lambda ZAP II; Site_1: EcoRI; Site_2: XhoI;
      P. carinii organisms (3x10e9) from a single rat (99-1-6,
      sacrificed on 3/17/99) at Cincinnati VA facilities.
      Trizol extracted RNA. Oligo dt priming, standard
      conditions described by vendor, Stratagene. Further
      details see www.uky.edu/Project/Pneumocystis/"
  Query Match          0.6%; Score 16.8; DB 1; Length 20;
  Best Local Similarity 90.0%; Pred. No. 1.6e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 2705 TACTAAAAAAAAAAAAAAAAAAAA 2724
  ||| ||||| ||||| ||||| |||||
  Db 20 TAATATAAAAAAAAAAAAAAAAAAAA 1

```

```

RESULT 1669
CF301101/c
LOCUS
DEFINITION
  CF301101
  7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
  sativa (japonica cultivar-group) cDNA clone 7LEAF--05-N04, mRNA
  sequence.
ACCESSION
  CF301101
VERSION
  CF301101.1 GI:33672862
KEYWORDS
  EST.
SOURCE
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
  clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
  1. (bases 1 to 20)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea

```

```

RESULT 1671
DY223532
LOCUS ID0AA110YJ11M1 ID0AEE Acyrthosiphon pisum cDNA clone ID0AA110YJ11
DEFINITION 20 bp mRNA linear EST 03-FEB-2006
5', mRNA sequence.
ACCESSION DY223532
VERSION DY223532.1 GI:86457660
KEYWORDS EST.
SOURCE Acyrthosiphon pisum (pea aphid)
ORGANISM Acyrthosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
1 (bases 1 to 20)
Stern, D.L., Wincker, P. and Tagu, D.
Large-scale gene discovery in the pea aphid Acyrthosiphon pisum
(Hemiptera)
Unpublished (2005)
Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 10Y row: J column: 11.
Location/Qualifiers
1..20
/organism="Acyrthosiphon pisum"
/mol_type="mRNA"
/cultivar="yr2"
/db_xref="taxon:7029"
/clone="ID0AA110YJ11"
/tissue_type="antennae"
/dev_stage="L3"
/lab_host="Xl1-Blue"
/clone_lib="ID0AEE"
/Note="Vector: pBS-SKminus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID0AEE ; Plant growth place: INRA Rennes, UMR
BIO3P, 35327, 35653 Le Rheu Cedex France ; Soil
conditions: Soil ; Sowing date: 15/04/2004 ; Harvesting
date: 15/04/2004 ; Description: Aphids inoculated on
one-week old Vicia faba under non-sterile conditions. A.
pisum Yr2 is holocyclic, i.e. able to change its
reproductive mode under short photoperiods (sexual) versus
long photoperiods (clonal). experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 degC)"

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2701 TTTGTACTAAAAA 2720
Db 1 TTTTAAATAAAAAA 20

RESULT 1672
AZ343730/c
LOCUS AZ343730
DEFINITION 20 bp DNA linear GSS 29-SEP-2000
Clone UUGC1M0077820 F, genomic survey sequence.
ACCESSION AZ343730
VERSION AZ343730.1 GI:10422288
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

```

```

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0077 row: E column: 20
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0077E20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/Note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAA 2728
Db 20 AGAAAAA 1

RESULT 1673
AZ368518
LOCUS AZ368518
DEFINITION 1M0118G09R Mouse 10Kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0118G09 R, genomic survey sequence.
ACCESSION AZ368518
VERSION AZ368518.1 GI:10482218
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

```


AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .21
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-09-107"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr_ Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.6%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2706 ACTAATAAAAAAAAAAAAAA 2725
|||
Db 20 ACGAATAAAAAAAAAATAAA 1
|||

RESULT 1676
AJ725584
LOCUS AJ725584 riken1 Gallus gallus cDNA clone 2c16r4, mRNA sequence.
DEFINITION AJ725584
ACCESSION AJ725584
VERSION AJ725584.1 GI:53890998
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 18)
Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezzubov, Y., Zaim, J.,
Fiedler, P., Kutter, S., Blagodatcki, A., Kostovska, D., Kotter, M.,
Plachy, J., Carninci, P., Hayashizaki, Y. and Buerstedde, J.M.
Full-length cDNAs from chicken bursal lymphocytes to facilitate
gene function analysis
Genome Biol. 6 (1), R6 (2005)
15642098
Contact: Caldwell RB
GSP - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.

FEATURES
source
1. .18
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="2c16r4"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/clone_lib="riken1"
/note="CB inbred strain"

Query Match 0.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAAATAAAAAAAAAA 2725
|
Db 1 TCAAAAAAAAAAAAAAAAAA 18
|

RESULT 1677
AL048754
LOCUS AL048754 18 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP566L173_r1_566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZP566L173, mRNA sequence.
ACCESSION AL048754
VERSION AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP566L173"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pMPl; Site_1: NotI; Site_2: SalI"

Query Match 0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2708 TAAAAAATAAAAAAAAAA 2725
|
Db 1 TCAAAAAAAAAAAAAAAAAA 18
|

RESULT 1678
BM658677/c
LOCUS BM658677 18 bp mRNA linear EST 27-FEB-2002
DEFINITION LZV602768363.R1_CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
sequence.
ACCESSION BM658677
VERSION BM658677.1 GI:18958948
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 18)
AUTHORS Adelson, D.L. and Gill, C.A.
TITLE Porcine ESTs
JOURNAL Unpublished (2002)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970

```

Email: david.adelson@tamu.edu.
FEATURES
source
  1. .18
    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clone_lib="CSEQFL37 pig adrenal"
    /notes="Organ: adrenal gland; Vector: pBluescript SK+;
    Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert
    (5'-NNN...NNNinsert)
    GCGAATTCGAGCTCCACCGCGTGGCGGCGGCTCGAG. Sequence 3' of
    the inserts (AAGAATTCGATATCAAGCTTATCGATACCTCGACCTCGAG.
    non-normalized library, sequenced 3' with M13R primer."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 18 AAAAAAAAAAGAAAAAAAAA 1

RESULT 1679
LOCUS
CF300456 18 bp mRNA linear EST 15-AUG-2003
DEFINITION
7LEAF--04-N23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-N23, mRNA
sequence.
ACCESSION
CF300456
VERSION
CF300456.1 GI:33672217
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--03-119"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 18 AGAAAAAAAAAAAAAAAAA 1

RESULT 1691
LOCUS
CF329285 18 bp mRNA linear EST 18-AUG-2003
DEFINITION
NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-122, mRNA
sequence.
ACCESSION
CF329285
VERSION
CF329285.1 GI:33806806
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAA 2723
Db 18 AGTAAAAA 1

RESULT 1680
LOCUS
CF309376 18 bp mRNA linear EST 15-AUG-2003
DEFINITION
ABF--03-119.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--03-119, mRNA sequence.
ACCESSION
CF309376
VERSION
CF309376.1 GI:33681137
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--03-119"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAA 2723
Db 18 AGTAAAAA 1

RESULT 1680
LOCUS
CF329285/c 18 bp mRNA linear EST 18-AUG-2003
DEFINITION
NACL--04-122.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa (japonica cultivar-group) cDNA clone NACL--04-122, mRNA
sequence.
ACCESSION
CF329285/c
VERSION
CF329285.1 GI:33806806
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--04-N23"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726
Db 18 AGAAAAAAAAAAAAAAAAA 1

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

```

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-122"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAGAAAAAAAAA 2725
|||
Db 18 TAGAAAAAAAAAAAAAAAAA 1

```

RESULT 1682

CF329484/c

```

LOCUS      CF329484      18 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION  CF329484
VERSION     CF329484.1 GI:33807207
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

```

FEATURES

source

```

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2706 ACTAAAAAAGAAAAAAAA 2723
|||
Db 18 AGTAAAAAAGAAAAAAAAA 1

```

RESULT 1683

```

LOCUS      CF329485      18 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-N06, mRNA sequence.
ACCESSION  CF329485
VERSION     CF329485.1 GI:33807209
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

```

FEATURES

source

```

1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--04-N06"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.6%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2706 ACTAAAAAAGAAAAAAAA 2723
|||
Db 1 AGTAAAAAAGAAAAAAAAA 18

```

RESULT 1684

CR786637

```

LOCUS      CR786637      18 bp      mRNA      linear      EST 01-OCT-2004
DEFINITION DKFZP468J2331.r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DKFZP468J2331-5', mRNA sequence.
ACCESSION  CR786637
VERSION     CR786637.1 GI:53705634
KEYWORDS    EST.
SOURCE      Pongo pygmaeus (orangutan)
ORGANISM    Eukaryota; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Pongo.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

```

TITLE Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
 JOURNAL Unpublished (2004)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKF2);
 Email s.wiemann@dkfz-heidelberg.de; mfoerschung GmbH in Berlin,
 Germany. Please contact RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468J2331
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1. .18
 Location/Qualifiers
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp468J2331"
 /tissue_type="heart"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="468 (synonym: phrt1)"
 /notes="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.6%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 1 AAAAAAAAAAAAAAAAAATA 18
 |||||

RESULT 1685
 AJ666205/c 19 bp mRNA linear EST 28-JUN-2004
 LOCUS AJ666205 CSEQRAN09 Sus scrofa cDNA clone C0000033_E15, mRNA
 DEFINITION sequence.

ACCESSION AJ666205
 VERSION AJ666205.1 GI:49350656

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE 1 (bases 1 to 19)

Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
 Development of cDNA and EST resources for studying reproduction and
 embryo development in pigs and cattle
 Unpublished (2004)

JOURNAL Contact: Anderson SI

COMMENT Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred
 v0.020425.c. Vector identified by cross match with the -m10score 20.
 and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
 EcoRI R. Site 2: NotI Description: Normalised library constructed
 from pooled tissue from day 30 placentas. Clones available from UK
 Centre for Functional Genomics in Farm Animals, Roslin Institute,
 Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source

1. .19
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C000033_E15"
 /tissue_type="placenta"
 /clone_lib="CSEQRAN09"
 /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
 NotI; Single pass sequencing. Normalised library
 constructed from pooled tissue from day 30 placentas."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2726

Db 19 AAAAAAAAAAGAAAAAAAAA 2
 |||||

RESULT 1686

CF298472/c

LOCUS CF298472 19 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-001, mRNA
 sequence.

ACCESSION CF298472

VERSION CF298472.1 GI:33670233

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

JOURNAL Contact: Nahm B.H.

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .19
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF--01-001"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2725

Db 18 TAAAAAAAAAAAAAAAAA 1
 |||||

RESULT 1687

CF326845

LOCUS CF326845 19 bp mRNA linear EST 18-AUG-2003
 DEFINITION NACL--01-B12 g1 Rice callus plasmid cDNA library (NACL) Oryza
 sativa (japonica cultivar-group) cDNA clone NACL--01-B12, mRNA
 sequence.

ACCESSION CF326845

VERSION CF326845.1 GI:33801944

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

QY 2708 TAAAAAAAAAAAAAAAAAAAAA 2725
 Db 1 TCAAAAAAAAAAAAAAAAAAAAAA 18

RESULT 1690
 AZ360314
 LOCUS
 DEFINITION 19 bp DNA linear GSS 02-OCT-2000
 clone UUGC1M0103G03 R, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0103 row: G column: 03
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0103G03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2726
 Db 2 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 1691
 AZ447251/c
 LOCUS
 DEFINITION 19 bp DNA linear GSS 04-OCT-2000
 clone UUGC1M0244J19 F, genomic survey sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0244 row: J column: 19
 Seq primer: CGTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0244J19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      2708 TAAAAAAAAAAAAAAAAA 2725
DB      18 TATAAAAAAAAAAAAAAAAA 1

RESULT 1692
BQ590166/c
LOCUS   16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-K18-T7 MP12-ADIS-024-storage root Beta vulgaris
          CDNA clone 024-019-K18 3-PRIME, mRNA sequence.
ACCESSION BQ590166
VERSION   1
KEYWORDS  Beta vulgaris
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
PUBMED    12472698
COMMENT   Contact: Weishaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weishaar@mpiz-koeln.mpg.de
          Insert Length: 16 Std Error: 0.00
          Plate: 19 row: K column: 18
          Seq primer: T7; GTAATACGACTCACTATAGGCG.
          Location/Qualifiers
            1..16
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:189955"
            /db_xref="taxon:161934"
            /clone="024-019-K18"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MP12-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2708 TAAAAAAAAAAAAAAAAA 2723
DB      16 TAAAAAAAAAAAAAAAAA 1

RESULT 1694
BQ592600
LOCUS   16 bp mRNA linear EST 06-DEC-2002
DEFINITION S013686-024-028-F08-SP6R MP12-ADIS-024-developing root Beta
          vulgaris CDNA clone 024-028-F08 5-PRIME, mRNA sequence.
ACCESSION BQ592600
VERSION   1
KEYWORDS  Beta vulgaris
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 16)
AUTHORS   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
PUBMED    12472698
COMMENT   Contact: Weishaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weishaar@mpiz-koeln.mpg.de
          Insert Length: 16 Std Error: 0.00
          Plate: 19 row: K column: 18
          Seq primer: T7; GTAATACGACTCACTATAGGCG.
          Location/Qualifiers
            1..16
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:189955"
            /db_xref="taxon:161934"
            /clone="024-019-K18"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MP12-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2709 AAAAAAAAAAAAAAAAAA 2724
DB      16 AAAAAAAAAAAAAAAAAA 1

RESULT 1693
BQ590507/c
LOCUS   16 bp mRNA linear EST 06-DEC-2002
DEFINITION E012844-024-019-M04-T7 MP12-ADIS-024-storage root Beta vulgaris
          CDNA clone 024-019-M04 3-PRIME, mRNA sequence.

```

and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

CONTACT: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 28 row: F column: 08
Seq primer: SP6r; ATTTAGTGACACTATAGAGA.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:194262"
/db_xref="taxon:161934"
/clone="024-028-F08"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
|||||
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1695
BQ592965/c
LOCUS
DEFINITION
S01324-024-028-A01-T7 MPZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-028-A01 3-PRIME, mRNA sequence.
ACCESSION
BQ592965
VERSION
BQ592965.1 GI:26122548
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

CONTACT: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00
Plate: 28 row: A column: 01
Seq primer: T7; GTAATACGACTACTATAGGC.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:193895"
/db_xref="taxon:161934"
/clone="024-028-A01"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
|||||
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 1696
BQ595369/c
LOCUS
DEFINITION
S013317-024-022-P02-T7 MPZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION
BQ595369
VERSION
BQ595369.1 GI:26124952
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
Herwig, R., Schulz, B., Weissshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
PUBMED
COMMENT

CONTACT: Weissshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: P column: 02
Seq primer: T7; GTAATACGACTACTATAGGC.
Location/Qualifiers
1. .16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:191489"
/db_xref="taxon:161934"

```

/clone="024-022-P02"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAAAAAAAAAAAAAAAA 2723
Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 1697
LOCUS      BQ595717
DEFINITION BQ595717
ACCESSION BQ595717
VERSION    BQ595717
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
PUBMED    12472698
COMMENT   Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpi2-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 22 row: H column: 07
Seq primer: SP6: CATACGATTGAGTGACACTATAG.

FEATURES             Location/Qualifiers
     1..16
     /organism="Beta vulgaris"
     /mol_type="mRNA"
     /cultivar="KWS2320 (double haploid, monogerm breeding
line)"
     /db_xref="GABI:191134"
     /db_xref="taxon:161934"
     /clone="024-022-H07"
     /tissue_type="developing root"
     /lab_host="EMDH10B"
     /clone_lib="MP1Z-ADIS-024-developing root"
     /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet

```

```

project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1698
LOCUS      CF279325/c
DEFINITION 14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--05-J09,
mRNA sequence.
ACCESSION   CF279325
VERSION     CF279325.1 GI:33656711
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     1..16
     /organism="Oryza sativa (japonica cultivar-group)"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:39947"
     /clone="14ETL--05-J09"
     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
     /notes="vector: PCR4-TOP0; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 1699
LOCUS      CF296130/c
DEFINITION 30DGS--06-F22 b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa (japonica cultivar-group) cDNA clone 30DGS--06-F22, mRNA
sequence.
ACCESSION   CF296130
VERSION     CF296130.1 GI:33665163
KEYWORDS    EST.

```

```

SOURCE          Oryza sativa (japonica cultivar-group)
ORGANISM        Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                clade; Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE           Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT         Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source            1..16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="30DGS--06-F22"
                     /tissue_type="leaf"
                     /dev_stage="30 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
                     /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY   2708 TAAAGAAAAAAGAAAAA 2723
Db    16 TAAAGAAAAAAGAAAAA 1

RESULT 1700
LOCUS CF311057/c
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
          library (ABF), Oryza sativa (japonica cultivar-group) cDNA clone
          ABF--06-C03, mRNA sequence.
ACCESSION CF311057
VERSION    CF311057.1 GI:33682818
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
                clade; Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source            1..16
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"

```

```

RESULT 1702
CF314377/c
LOCUS
DEFINITION
HD--02-001.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--02-001, mRNA sequence.
ACCESSION
CF314377
VERSION
CF314377.1 GI:33686138
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--02-001"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1703
CF315789/c
LOCUS
DEFINITION
HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--04-N10, mRNA sequence.
ACCESSION
CF315789
VERSION
CF315789.1 GI:33687550
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

```

```

COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--04-N10"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1704
CF316056/c
LOCUS
DEFINITION
HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--05-D07, mRNA sequence.
ACCESSION
CF316056
VERSION
CF316056.1 GI:33687817
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6355
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--05-D07"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 1705
CF317718/c
LOCUS
DEFINITION
HD--07-105-g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-105, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--07-105"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 1706
CF320356/c
LOCUS
DEFINITION
HD--11-D14_b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa (japonica cultivar-group) cDNA clone HD--11-D14, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD--11-D14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
|||||
Db 16 AAAAAAAAAAAAAA 1

RESULT 1707
CF327722/c
LOCUS
DEFINITION
NACL--02-F06_b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--02-F06, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE
JOURNAL
COMMENT
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

```

FEATURES
source
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACL--02-F06"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TAAATAAAAAAAAAA 2724
|||||
DB 16 TAAATAAAAAAAAAA 1

RESULT 1708
LOCUS CF329320/c 16 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa (japonica cultivar-group) cDNA clone NACL--04-J17, mRNA sequence.
ACCESSION CF329320
VERSION CF329320
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="JMT--02-E05"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
|||||
DB 1 AAAAAAAAAAAAAAAAAA 16

FEATURES
source
Location/Qualifiers
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clones="JMT--02-E05"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAA 2724
|||||
DB 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1710
LOCUS CR786853 16 bp mRNA linear EST 01-OCT-2004
DEFINITION DRFP468E2231_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone DRFP468E2231_5', mRNA sequence.
ACCESSION CR786853
VERSION CR786853
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Suarchontoglires; Primates; Catarrhini; Homnidae; Pongo.
1 (bases 1 to 16)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehler,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
Contact: MIPS
MIPS

```


Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; mforschung GmbH in Berlin,
Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468E2231>
Further information about the clone and the sequencing project is
available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source
1. .16
Location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp468E2231"
/tissue_type="heart"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="468 (synonym: phrt1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 1 AAAAAAAAAAAAAA 16

RESULT 1711

DT498583
LOCUS
DEFINITION
WS0115_BR M08 PT-P-FL-A-2 Populus trichocarpa cDNA clone WS0115_M08
5', mRNA sequence.
ACCESSION
DT498583
VERSION
DT498583.1 GI:73895845
KEYWORDS
EST.
SOURCE
Populus trichocarpa (Populus balsamifera subsp. trichocarpa)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 16)

Ralph, S., Cooper, D., Kolesova, N., Oddy, C., Butterfield, Y.,
Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G.,
Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,
Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,
Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and
Bohlmann, J.

The poplar transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries

Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282

Fax: 1-604-822-2114
Email: bohlmann@msl.ubc.ca
Plate: WS0115 row: M column: 08
High quality sequence stop: 122
POLYA=Yes.

FEATURES

source
1. .16
Location/Qualifiers
/organism="Populus trichocarpa"
/mol_type="mRNA"
/cultivar="383-2499 (Nisqually-1)"
/db_xref="taxon:3694"
/clone="WS0115_M08"
/sex="Female"
/lab_host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PT-P-FL-A-2"

/note="Vector: pBluescript II SK (+) XR; Site_1: SstI (5'
end of cDNA); Site_2: XhoI (3' end of cDNA); Phloem and
cambium from 8 year old trees harvested within the Boise
Cascade region of Washington state on May 15th, 2001. cDNA
was prepared from 20 micrograms of mRNA according to the
full-length cDNA library construction method described by
Carninci P. et al. (2000), Genome Research
10(10):1617-1630 and directionally ligated into the
pBluescript II SK (+) XR vector digested with SstI (5'
end) and XhoI (3'). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation."

Query Match 0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
Db 1 AAAAAAAAAAAAAA 16

RESULT 1712

BQ591181/c
LOCUS
DEFINITION
BQ591181 17 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris
3-PRIME, mRNA sequence.

ACCESSION
BQ591181
VERSION
BQ591181.1 GI:26120764
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE
1 (bases 1 to 17)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
and Radloff, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

12472698

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 17 row: H column: 16

Seq primer: T7: GTAATACGACTCACTATAGGCG.

Location/Qualifiers

FEATURES

source
1. .17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188932"
/db_xref="taxon:161934"
/clone="024-017-H16"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCWSVSPORT6; Site_1: Sali; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAATAAAAAAAAAA 2723
Db 16 TAAAAAATAAAAAAAAAA 1

RESULT 1713

CF295807/c 17 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--05-012.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa (japonica cultivar-group) cDNA clone 30DGS--05-012, mRNA
sequence.

ACCESSION CF295807

VERSION CF295807.1 GI:33664840

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. .17

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="30DGS--05-012"

/tissue_type="leaf"

/dev_stage="30 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAATAAAAAAAAAA 2724

Db 16 AAAAAAATAAAAAAAAAA 1

RESULT 1714

CF299639/c 17 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--03-L20, mRNA

sequence.

ACCESSION CF299639

VERSION CF299639.1 GI:33671400

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. .17

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--03-L20"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAATAAAAAAAAAA 2724

Db 16 AAAAAAATAAAAAAAAAA 1

RESULT 1715

CF302447/c

LOCUS 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone 7LEAF--07-P11, mRNA

sequence.

ACCESSION CF302447

VERSION CF302447.1 GI:33674208

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. .17

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--07-P11"

/tissue_type="leaf"

/dev_stage="7 days after germination"

```

/lab_host="E.coli DH10B"
/clone_lib="rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1716
CF311499/c
LOCUS
DEFINITION
ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF--06-L20, mRNA sequence.
CF311499
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-L20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1718
CF319075/c
LOCUS
DEFINITION
HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.
CF319075
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--06-L20"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2708 TAAAAAAAAAAAAA 2723
Db 16 TAAAAAAAAAAAAA 1

RESULT 1717
CF313013/c
LOCUS
DEFINITION
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone

```

```

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match          0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAA 2724
Db 16 AAAAAAAAAAAAAA 1

RESULT 1718
CF319075/c
LOCUS
DEFINITION
HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--09-H06, mRNA sequence.
CF319075
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF--08-P19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

```

Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source

Location/Qualifiers
1..17
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HD-09-H06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAAAAAAAAAAAAAA 2723

Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 1719
CF298591/c

LOCUS
DEFINITION
18 bp mRNA linear EST 15-AUG-2003
7LEAF--02-A20 b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-A20, mRNA sequence.

ACCESSION
VERSION
CF298591.1 GI:33670352

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1..18
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="7LEAF--02-A20"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAAAAAAAAAAAAAA 2723

Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 1720

CF278272/c

LOCUS
DEFINITION
19 bp mRNA linear EST 14-AUG-2003
14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-C01, mRNA sequence.

ACCESSION

VERSION

CF278272

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers
1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-C01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2708 TAAAAAAAAAAAAAAAAA 2723

Db 16 TAAAAAAAAAAAAAAAAA 1

RESULT 1721

CF308042/c

LOCUS
DEFINITION
19 bp mRNA linear EST 15-AUG-2003
ABF--01-L07.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone ABF--01-L07, mRNA sequence.

ACCESSION

VERSION

CF308042

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 19)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-01-L07"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2708 TAAATAAAAAAAAAA 2723
|||||
Db 16 TAAATAAAAAAAAAA 1

RESULT 1722
CF311668
LOCUS
DEFINITION 19 bp mRNA linear EST 15-AUG-2003
ABF-07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa (japonica cultivar-group) cDNA clone
ABF-07-A05, mRNA sequence.

ACCESSION CF311668
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF-07-A05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAA 2724
|||||
Db 1 AAAAAAAAAAAAAA 16

RESULT 1723
AZ764517
LOCUS
DEFINITION 19 bp DNA linear GSS 16-FEB-2001
1M0560L07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560L07 R, genomic survey sequence.

ACCESSION AZ764517
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560L07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2724

Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 1724

LOCUS AJ663023 19 bp mRNA linear EST 28-JUN-2004
DEFINITION AJ663023 CSEQPAN09 Sus scrofa cDNA clone C0000024_H21, mRNA sequence.

ACCESSION AJ663023

VERSION AJ663023.1 GI:49347146

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 19)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site 1:

ECORI R. Site 2: NotI Description: Normalised library constructed from pooled tissue from day 30 placentas. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

FEATURES

source

1..19

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0000024_H21"

/tissue_type="placenta"

/clone_lib="CSEQPAN09"

/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled tissue from day 30 placentas."

Query Match 0.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 1 AAACCAAAAAAAAAAAAAAAAA 19

RESULT 1725

LOCUS CF298134 19 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-G09, mRNA sequence.

ACCESSION CF298134

CF298134.1 GI:33669895

VERSION EST.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:39947"

/clone="7LEAF--01-G09"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 1.8e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 1 AAGGAAAAAAAAAAAAAAAAA 19

RESULT 1726

LOCUS CF300236/c

DEFINITION CF300236

7LEAF--04-124.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-124, mRNA sequence.

ACCESSION CF300236

VERSION CF300236.1 GI:33671997

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

1..19

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```

1..19
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="NACI--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 0.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 1 AAAGATAAAAAAAAAA 19

RESULT 1730

AZ345499/c

LOCUS AZ345499 19 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0080F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080F06 F, genomic survey sequence.

ACCESSION AZ345499

VERSION AZ345499.1 GI:10424736

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0080 row: F column: 06

Seq primer: CGTTGTAACGACGCCGCT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

```

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

```

/clone lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2709 AAAAAAAAAAAAAAAAAA 2727

Db 19 AAAAAAAAAAAGAGAAAA 1

RESULT 1731

AZ509929

LOCUS AZ509929 19 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0354A07 F, genomic survey sequence.

ACCESSION AZ509929

VERSION AZ509929.1 GI:10691245

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0354 row: A column: 07

Seq primer: CGTTGTAACGACGCCGCT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

```

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0354A07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

```


/clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAATTAA 19

RESULT 1732

AZ611602/c

LOCUS

DEFINITION

1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0438G03 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0438G03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 1 AAAAAAAAAAAAAAAAAATTAA 19

RESULT 1733

AZ786336/c

LOCUS

DEFINITION

2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0031H17 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0031H17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (G1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2709 AAAAAAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAAACCAAAAA 1

RESULT 1733

AZ786336/c

LOCUS

DEFINITION

2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0031H17 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0031H17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
 Best Local Similarity 89.5%; Pred. No. 1.8e+03;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2709 AAAAAAAAAAAAAAAAAA 2727
 |||||
 Db 19 AAAAAAAAAAGAGAAAAA 1

Search completed: November 7, 2006, 10:40:22
 Job time : 108 secs